



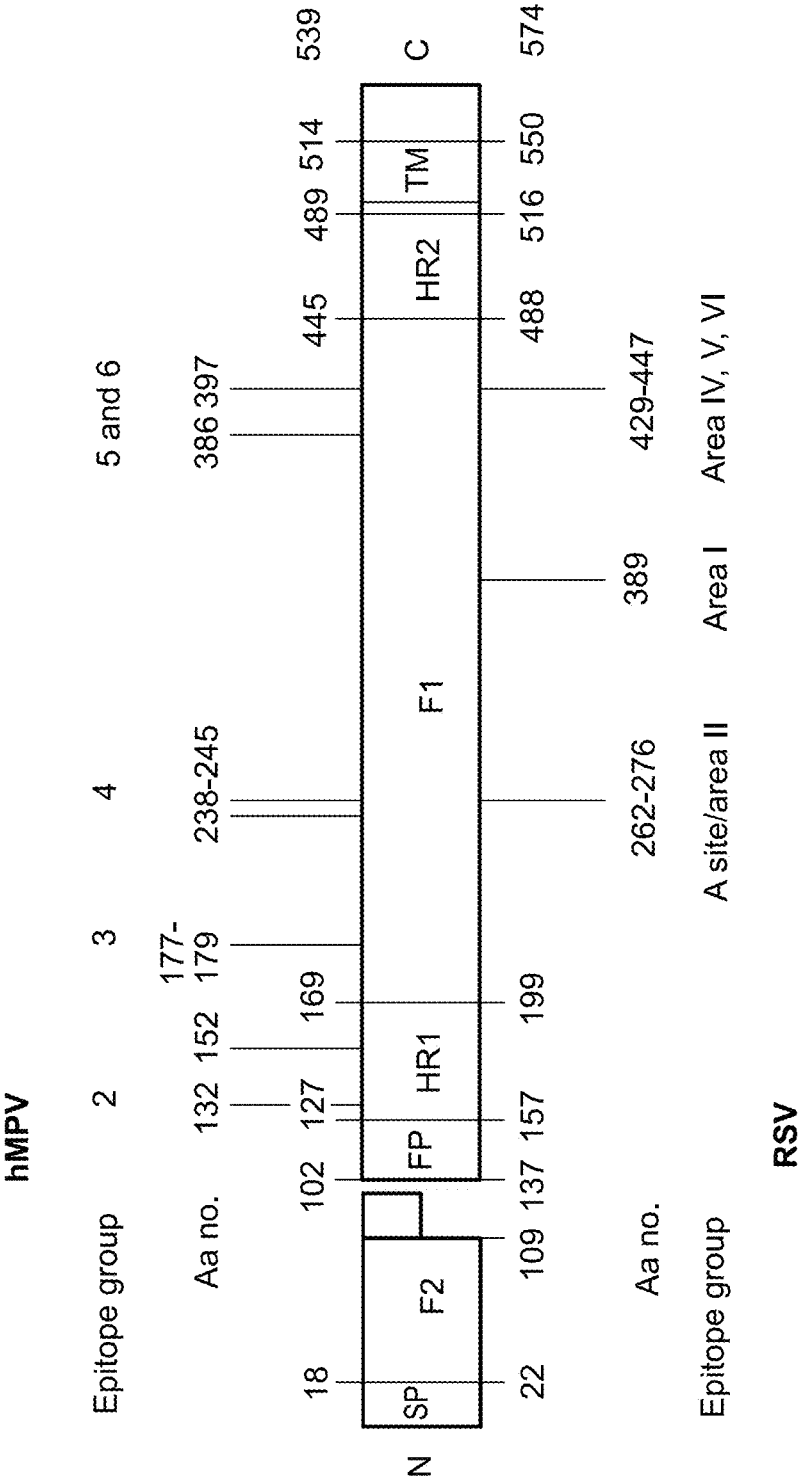
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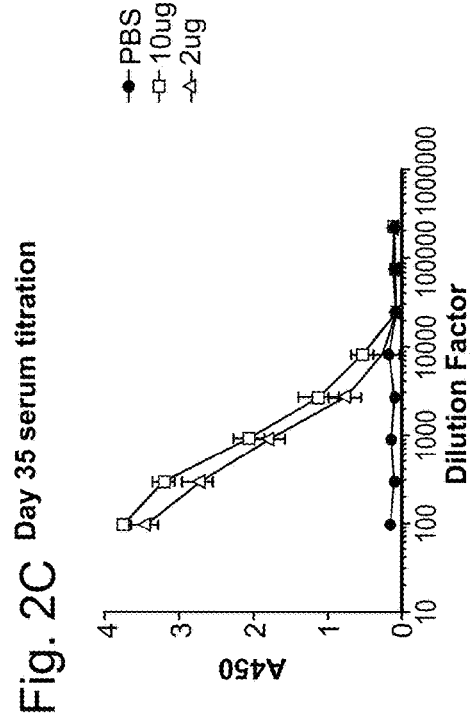
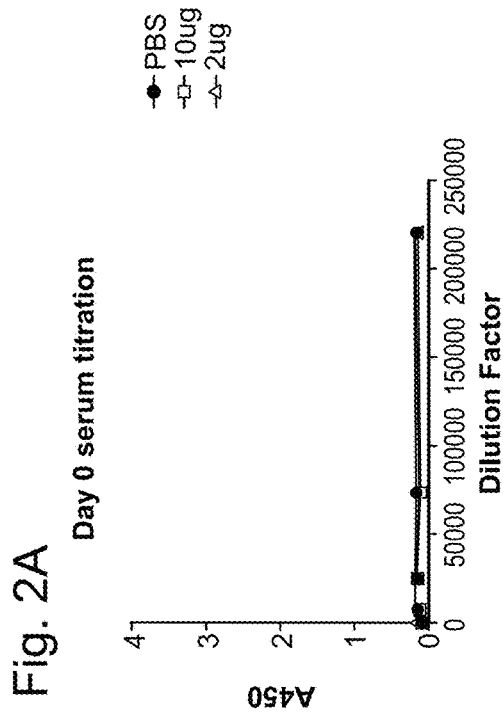
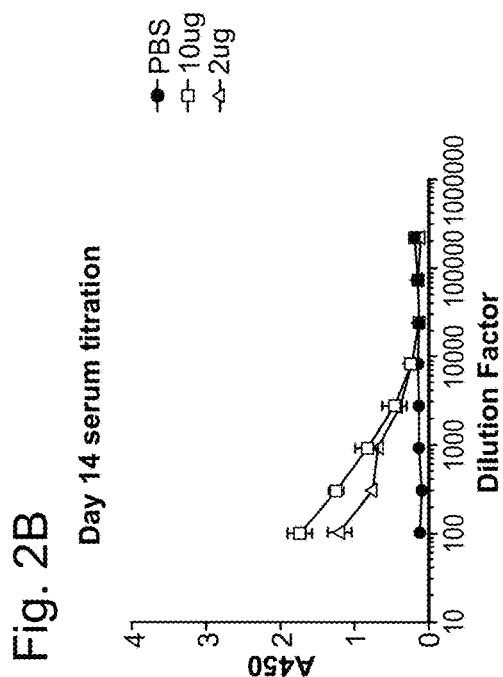
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Ciaramella et al.(10) **Pub. No.: US 2019/0240317 A1**(43) **Pub. Date: Aug. 8, 2019**(54) **HPIV3 RNA VACCINES**(71) Applicant: **ModernaTX, Inc.**, Cambridge, MA
(US)(72) Inventors: **Giuseppe Ciaramella**, Sudbury, MA
(US); **Sunny Himansu**, Winchester,
MA (US)(73) Assignee: **ModernaTX, Inc.**, Cambridge, MA
(US)(21) Appl. No.: **16/368,270**(22) Filed: **Mar. 28, 2019****Related U.S. Application Data**(63) Continuation of application No. 16/040,981, filed on
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continuation of application No. 15/674,599, filed on
Aug. 11, 2017, now Pat. No. 10,064,934, which is a
continuation of application No. PCT/US2016/
058327, filed on Oct. 21, 2016.(60) Provisional application No. 62/247,362, filed on Oct.
28, 2015, provisional application No. 62/247,394,
filed on Oct. 28, 2015, provisional application No.
62/247,483, filed on Oct. 28, 2015, provisional ap-
plication No. 62/247,297, filed on Oct. 28, 2015,provisional application No. 62/244,802, filed on Oct.
22, 2015, provisional application No. 62/244,946,
filed on Oct. 22, 2015, provisional application No.
62/244,813, filed on Oct. 22, 2015, provisional ap-
plication No. 62/244,837, filed on Oct. 22, 2015,
provisional application No. 62/245,031, filed on Oct.
22, 2015.**Publication Classification**(51) **Int. Cl.****A61K 39/155** (2006.01)**C07K 16/10** (2006.01)**A61K 39/12** (2006.01)(52) **U.S. Cl.**CPC **A61K 39/155** (2013.01); **C07K 16/10**
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(2013.01); **C12N 2760/18434** (2013.01)

(57)

ABSTRACTThe disclosure relates to respiratory virus ribonucleic acid
(RNA) vaccines and combination vaccines, as well as meth-
ods of using the vaccines and compositions comprising the
vaccines.**Specification includes a Sequence Listing.**

Fig. 1





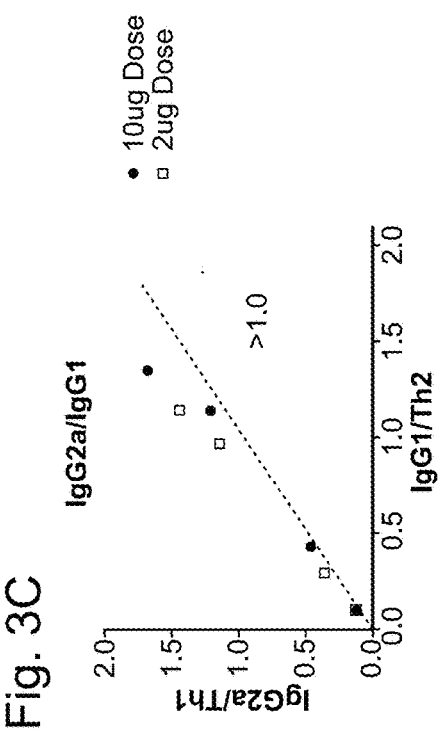
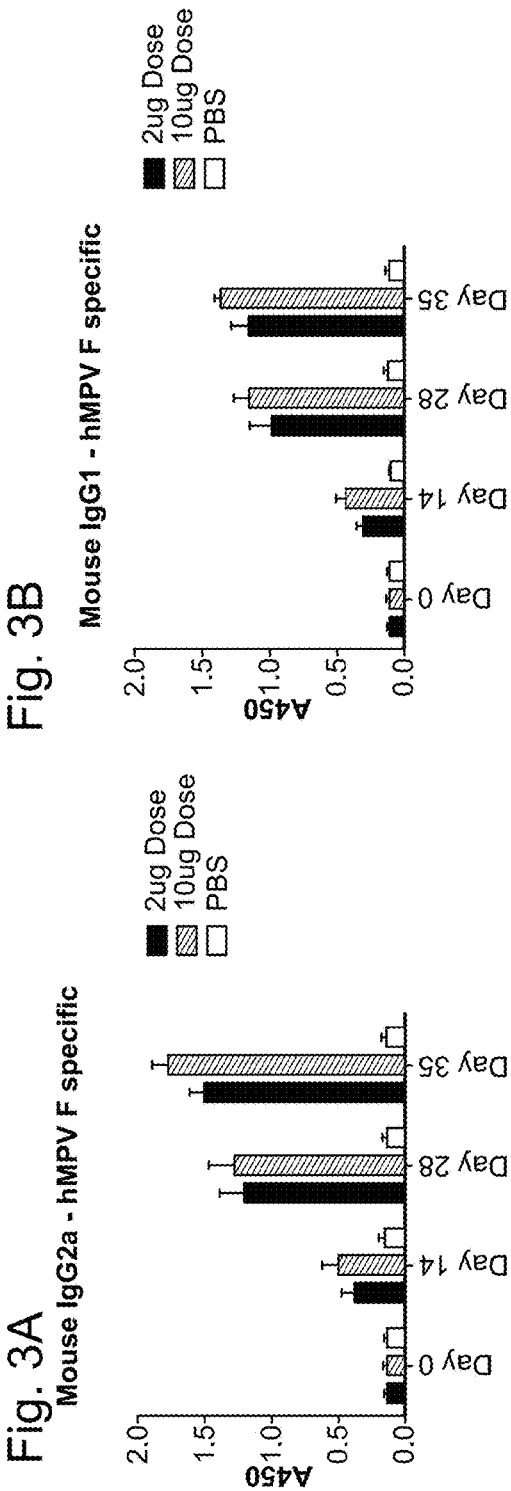
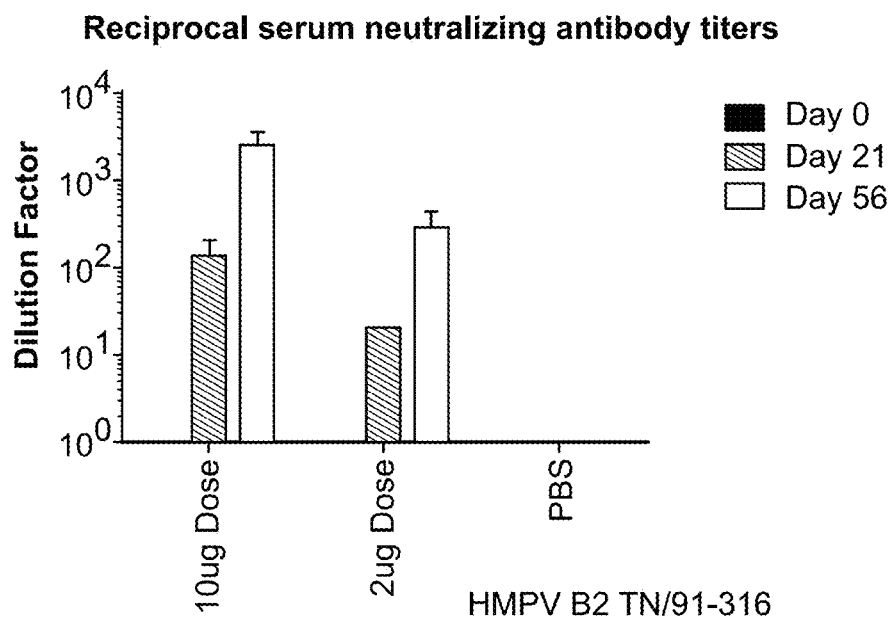
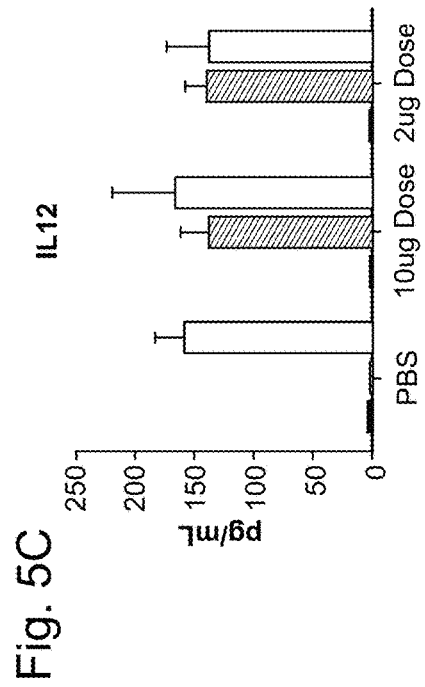
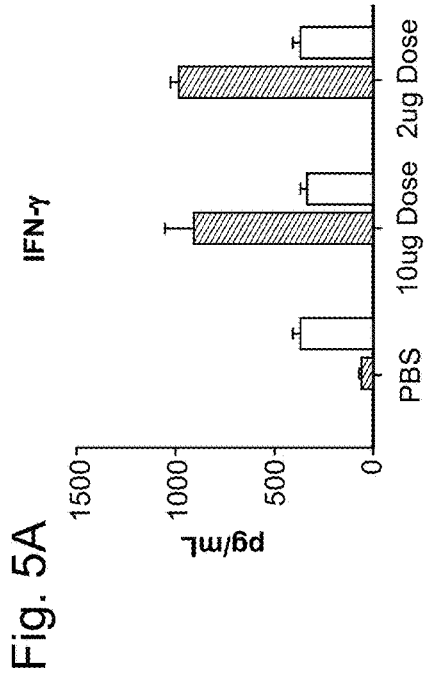
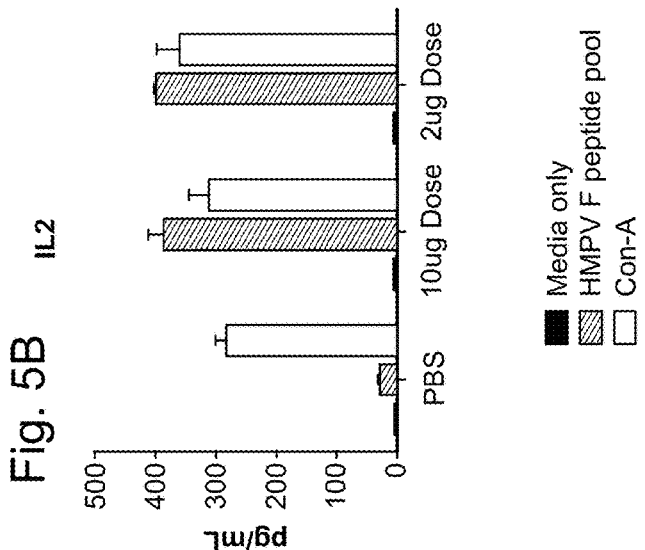
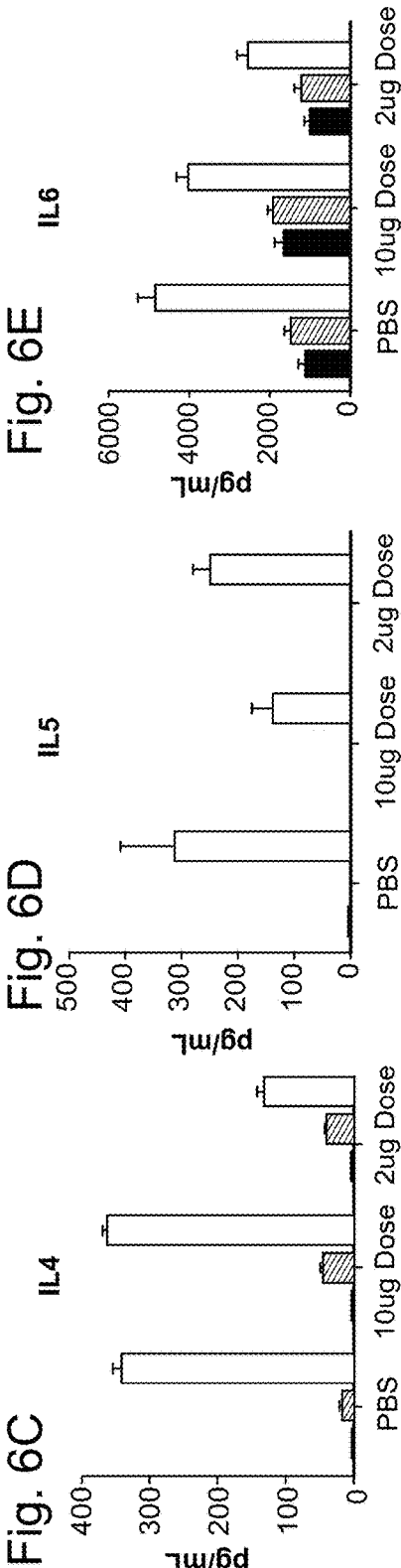
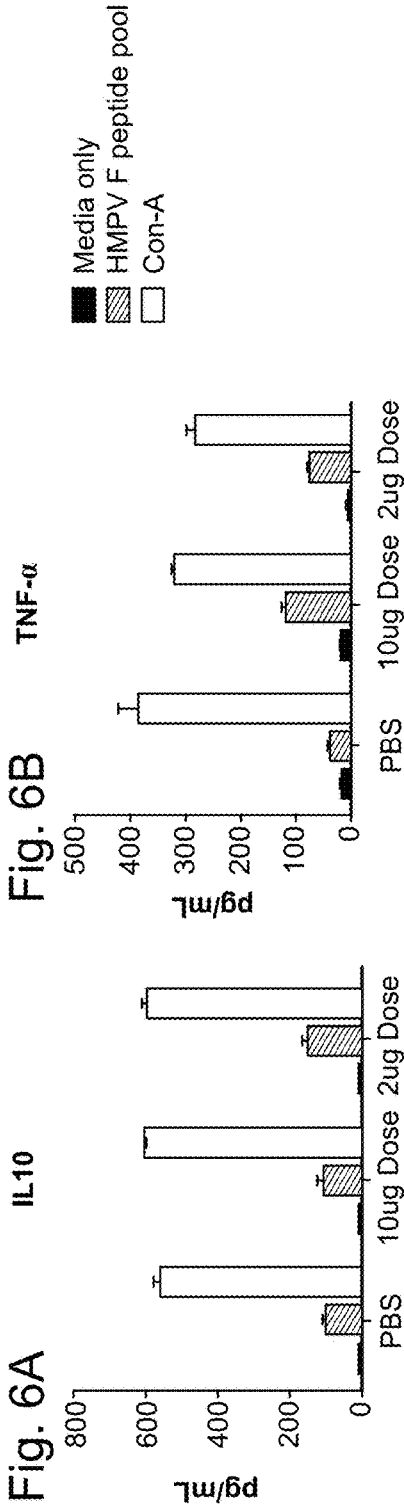
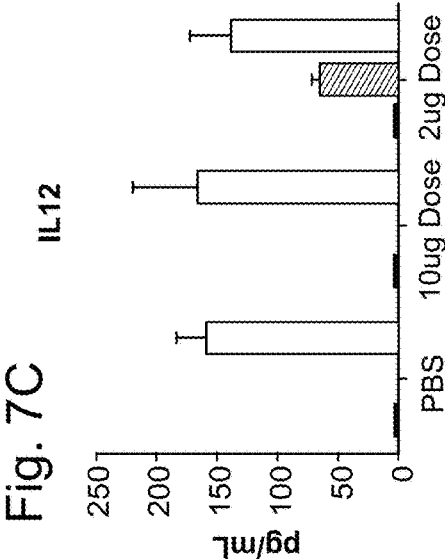
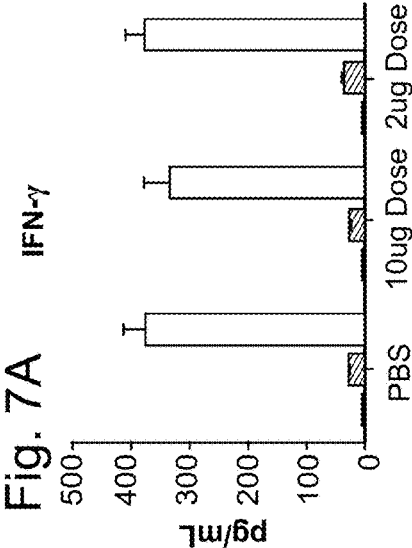
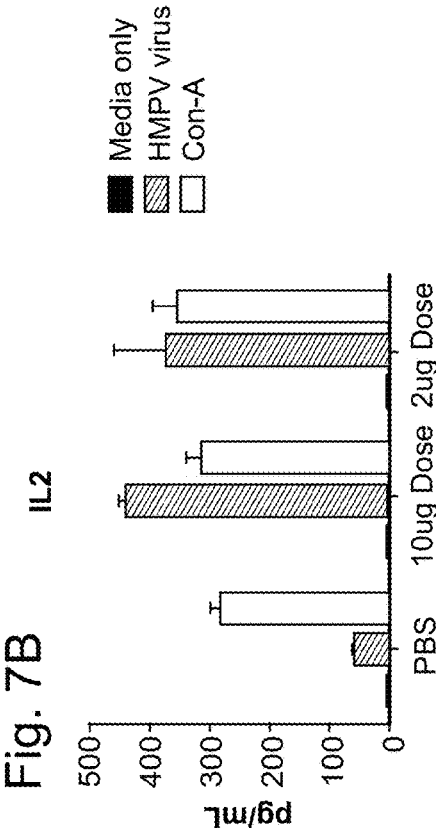


Fig. 4









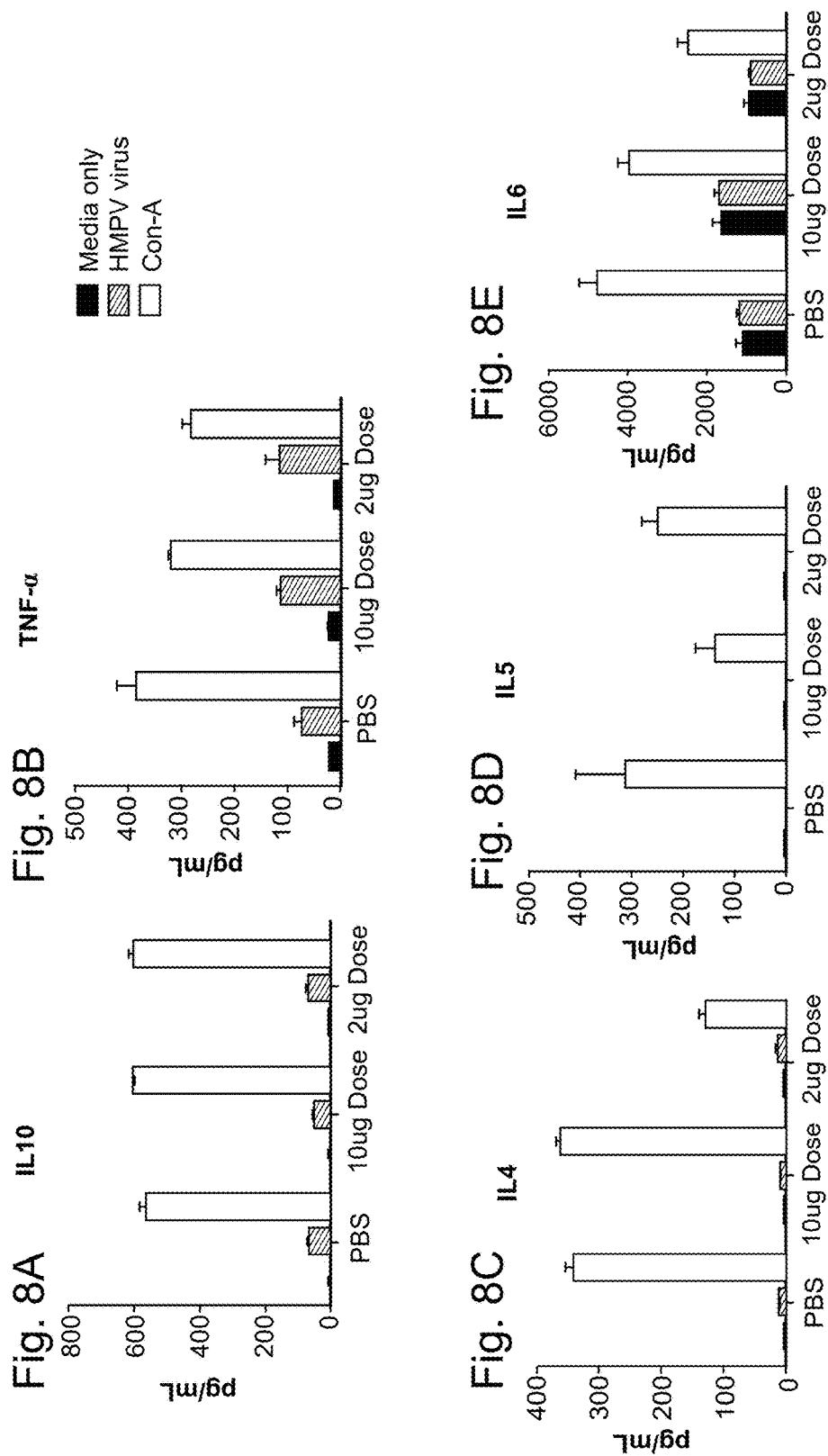


Fig. 9A

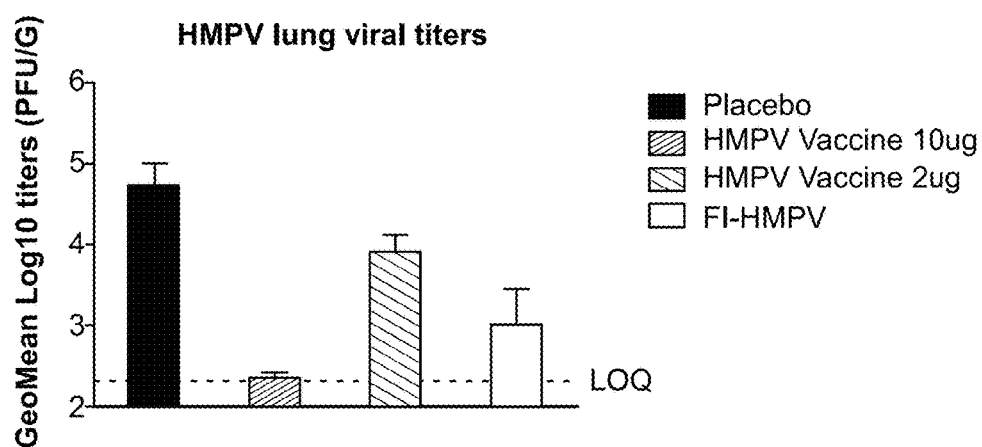


Fig. 9B

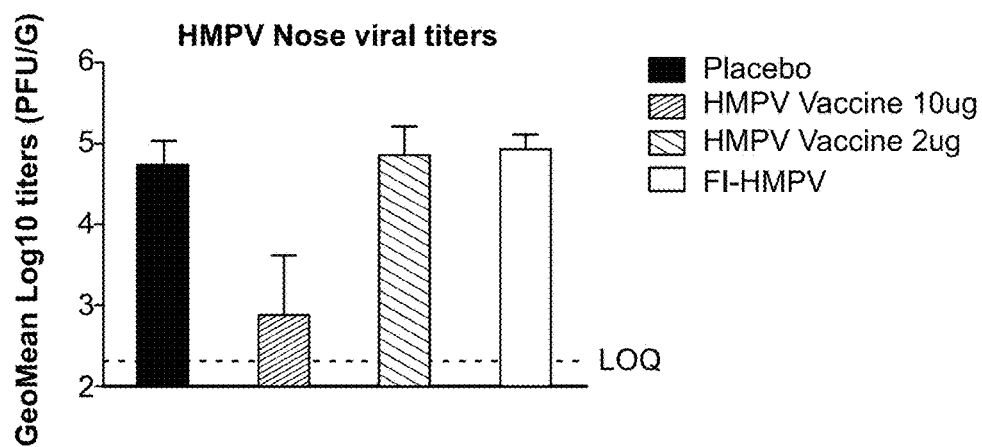


Fig. 10

HMPV vaccine lung Histopathology

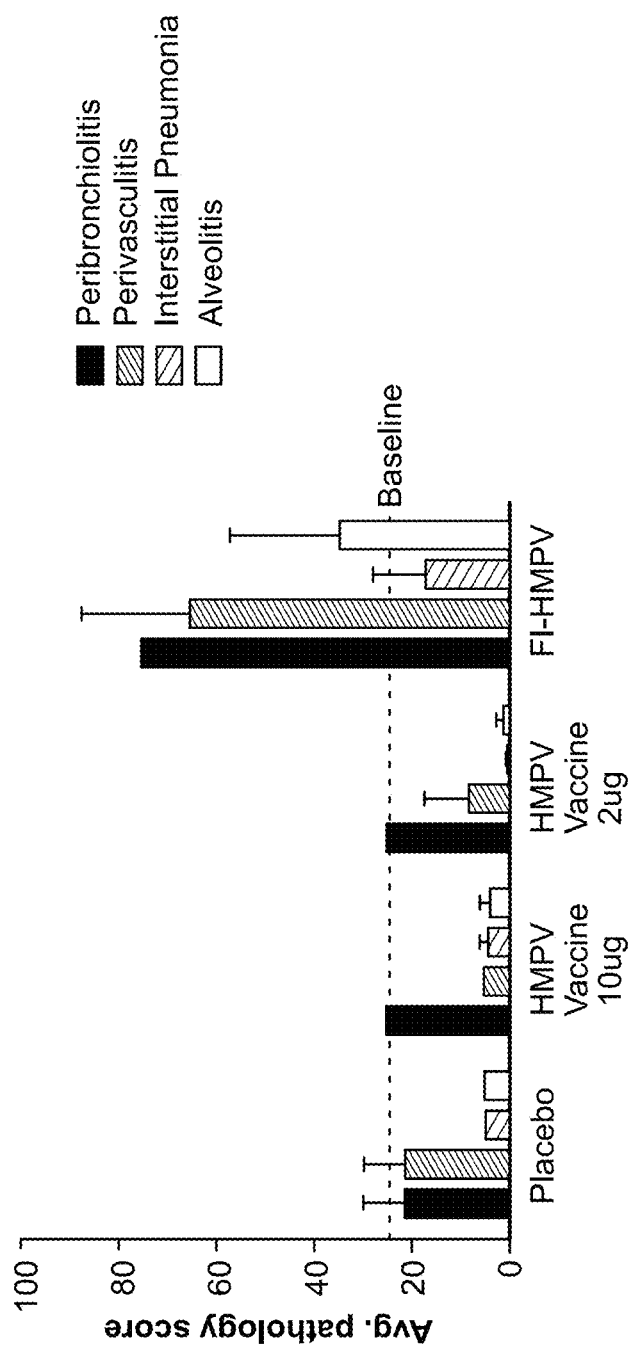
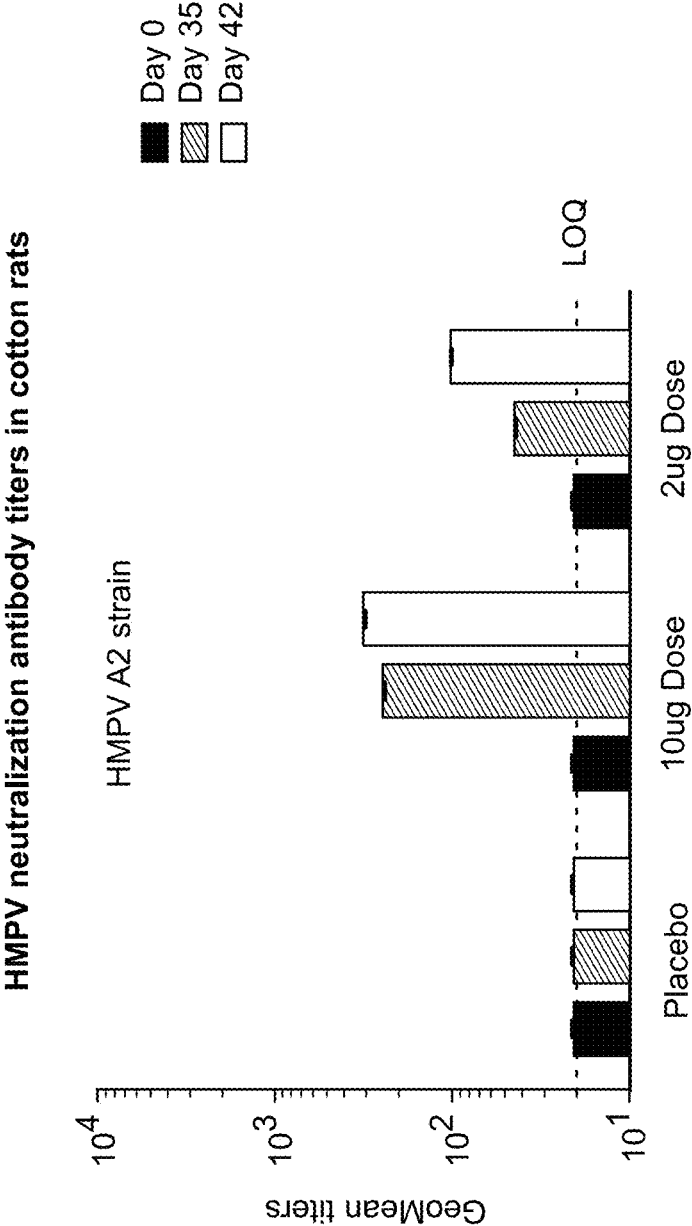
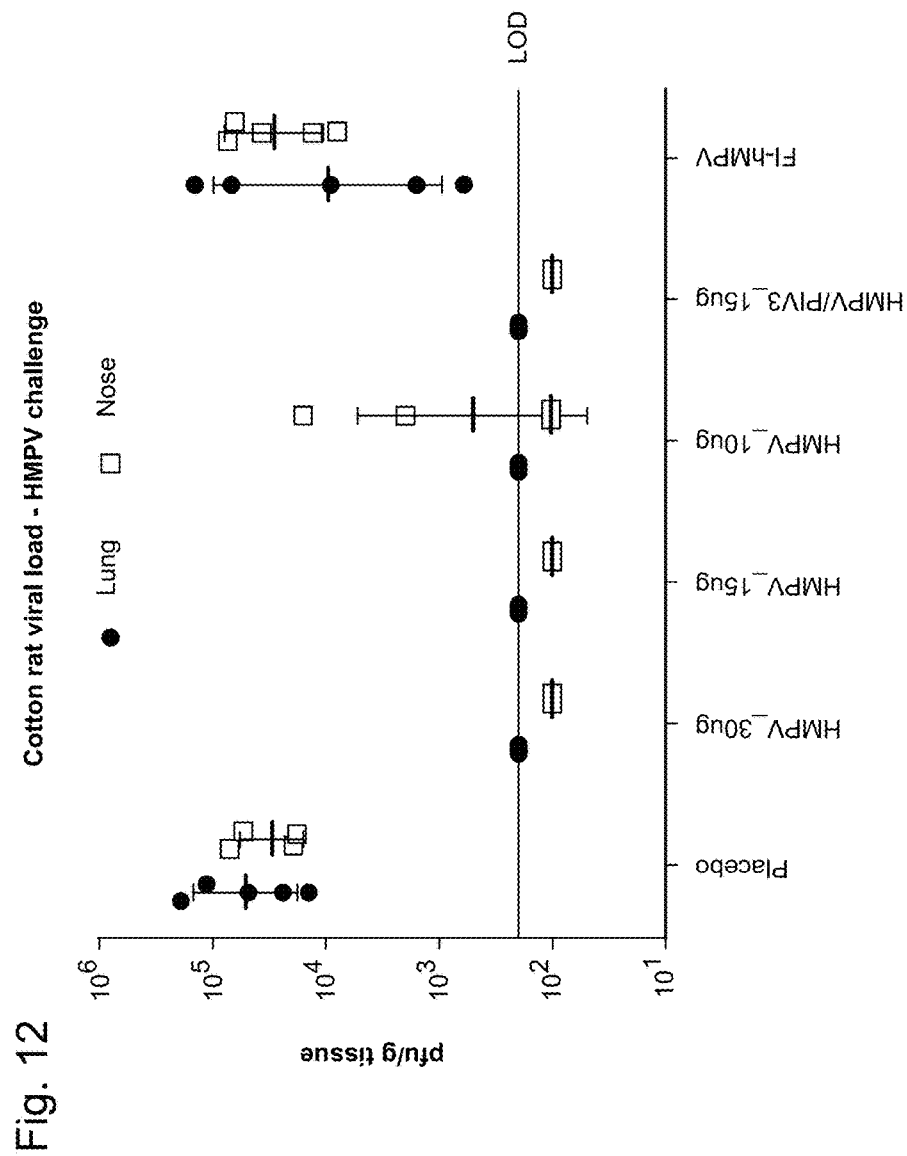


Fig. 11





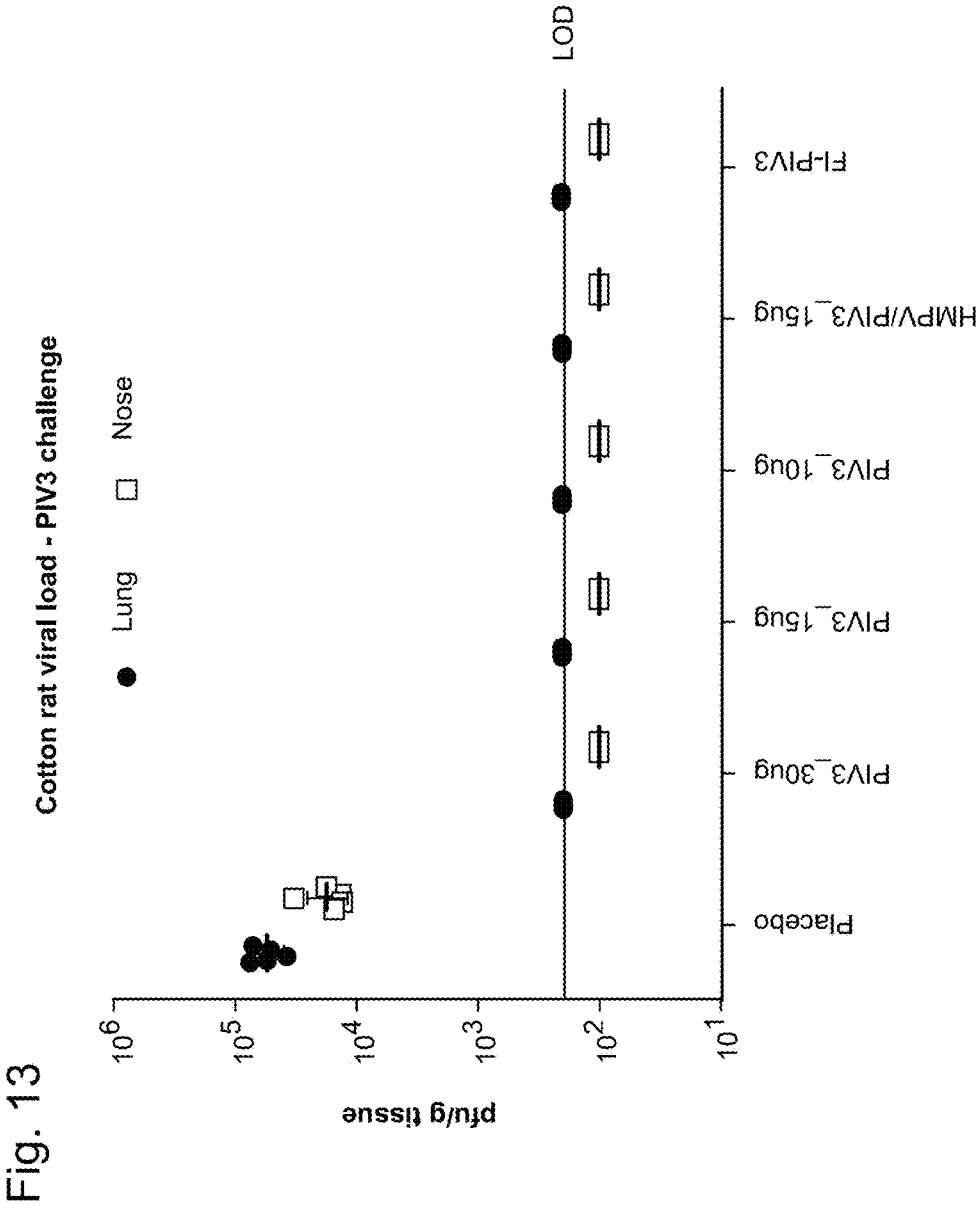


Fig. 14

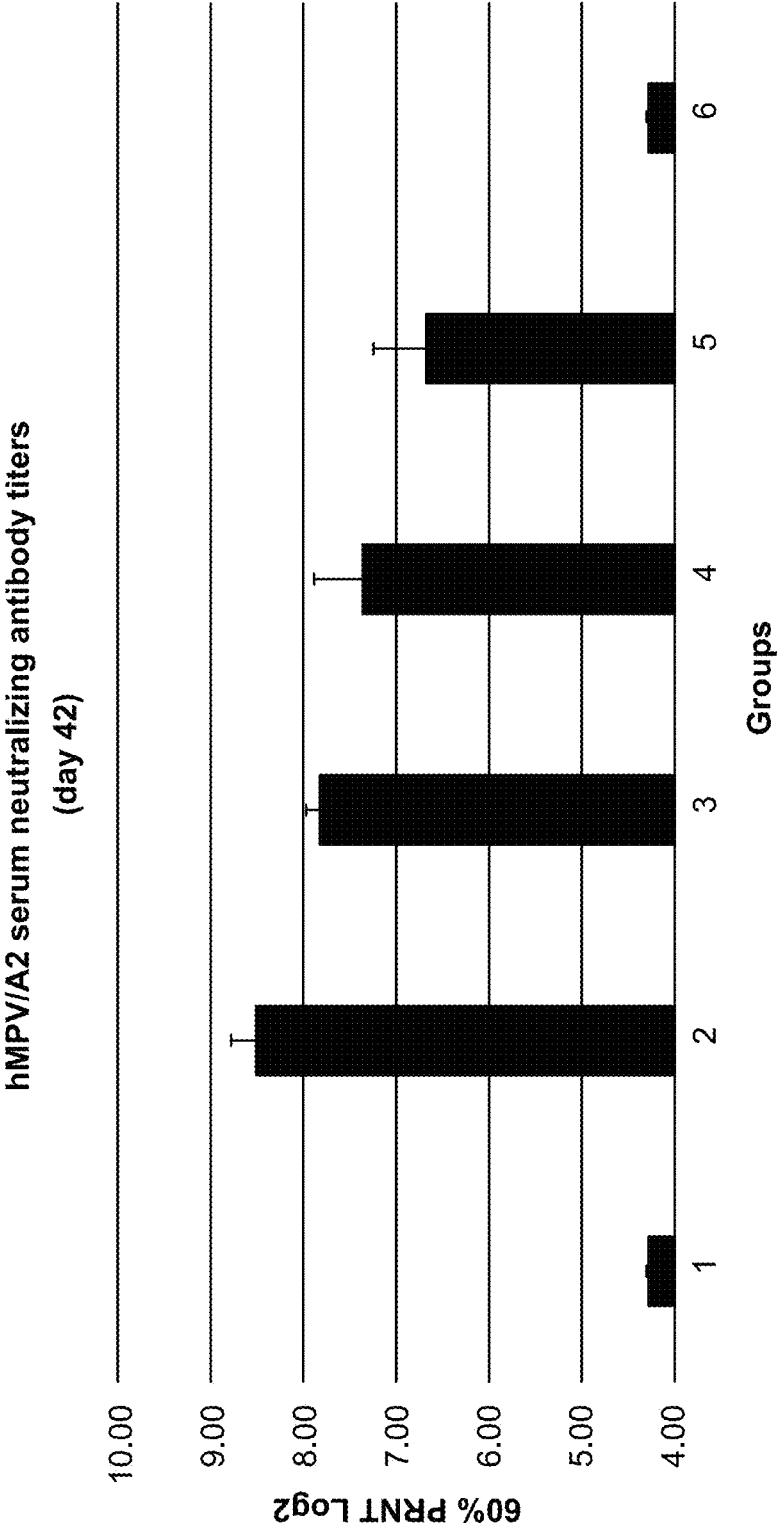


Fig. 15

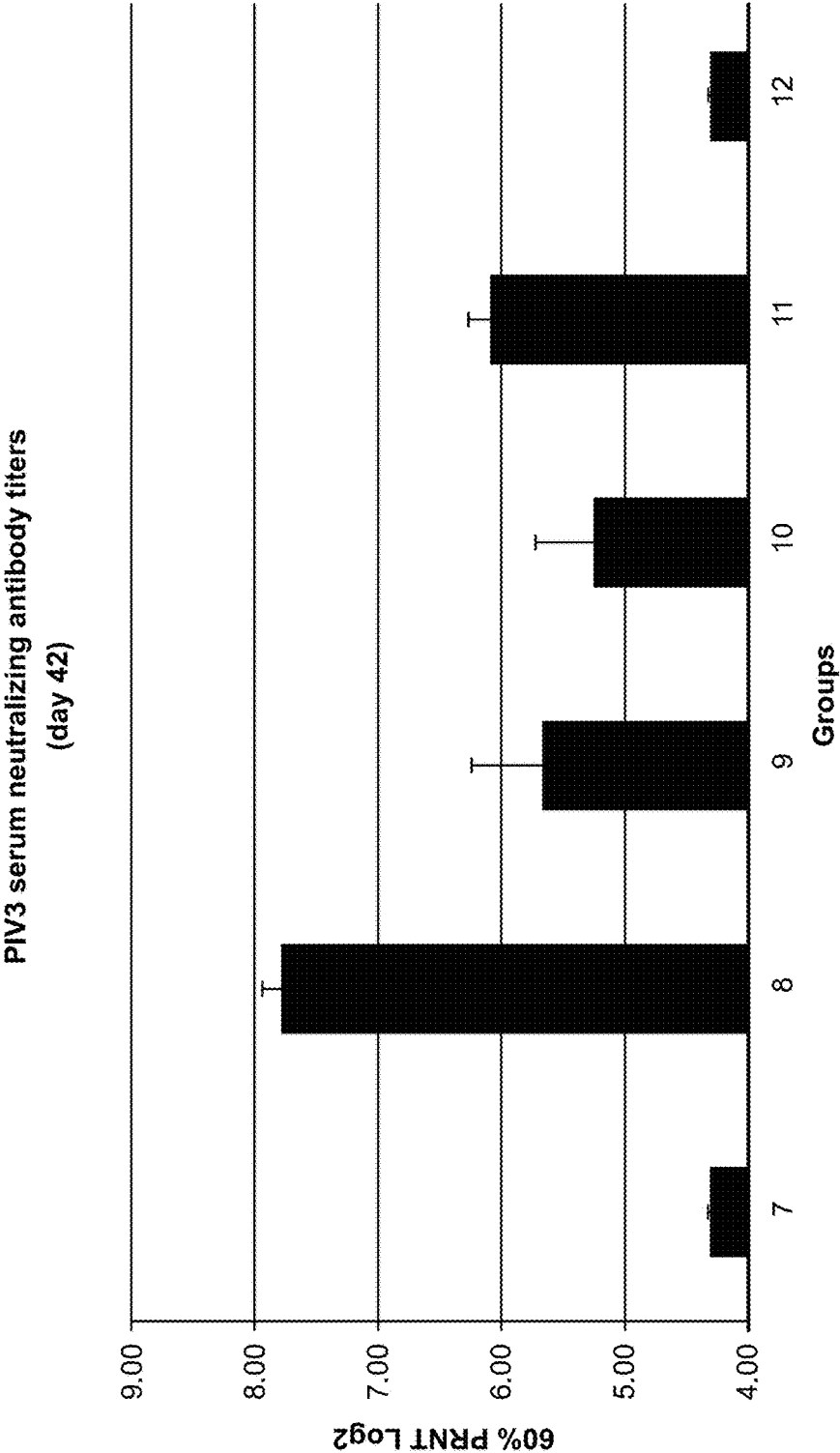


Fig. 16
Cotton rat lung histopathology

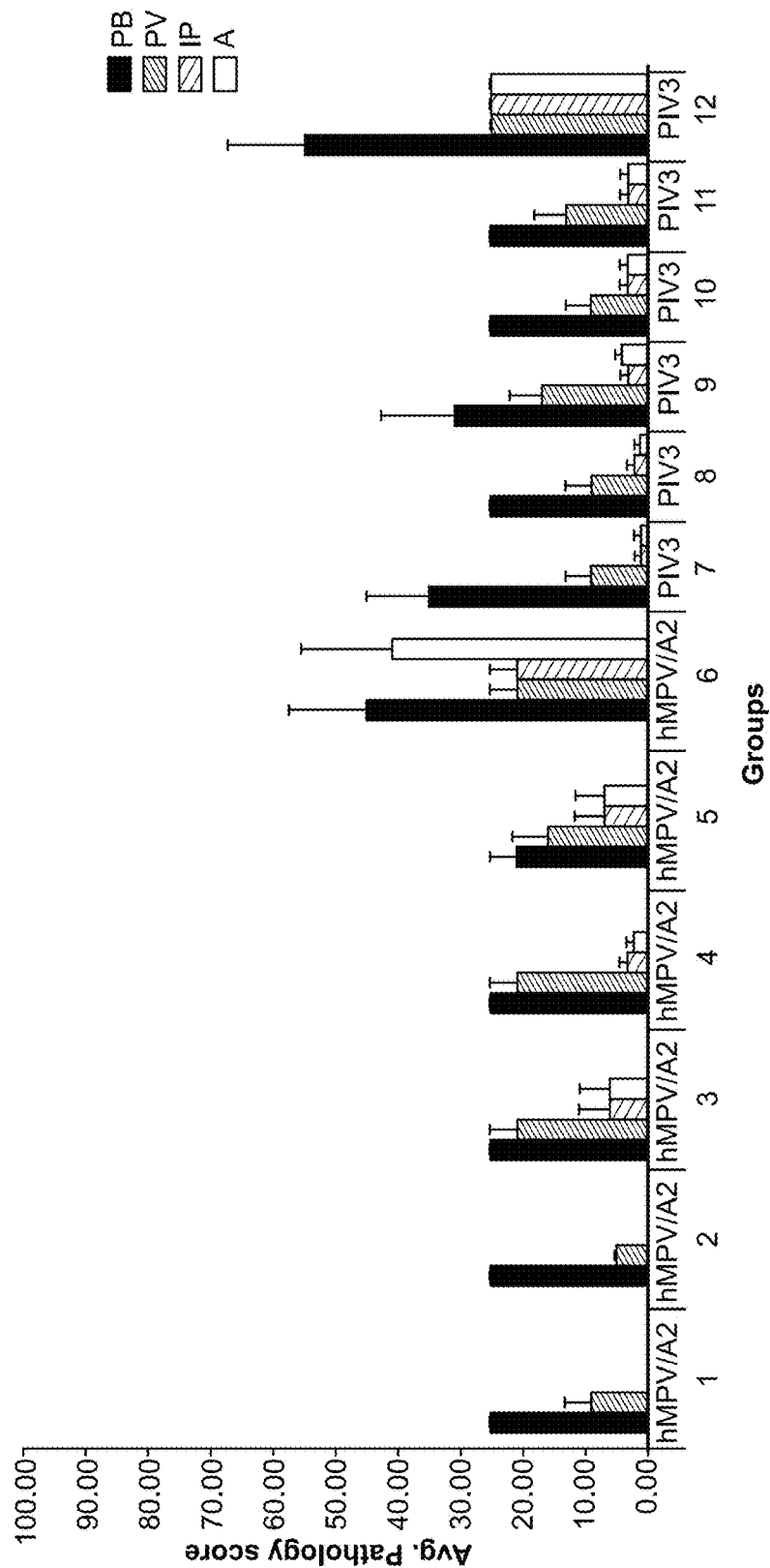


Fig. 17

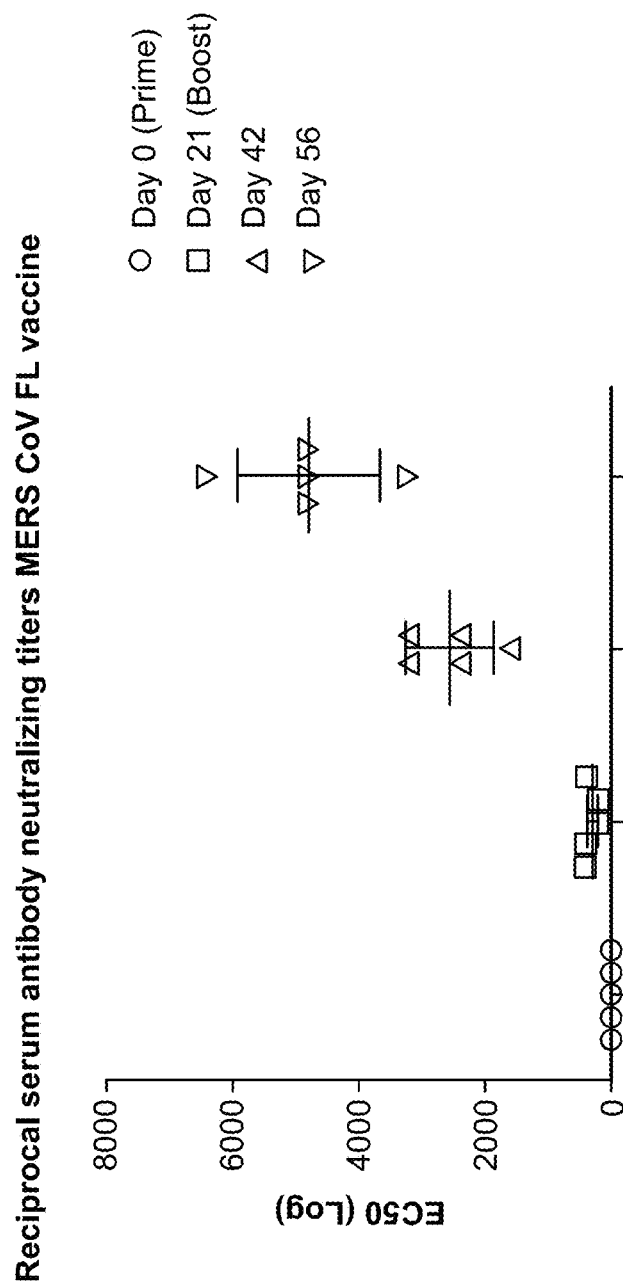


Fig. 18

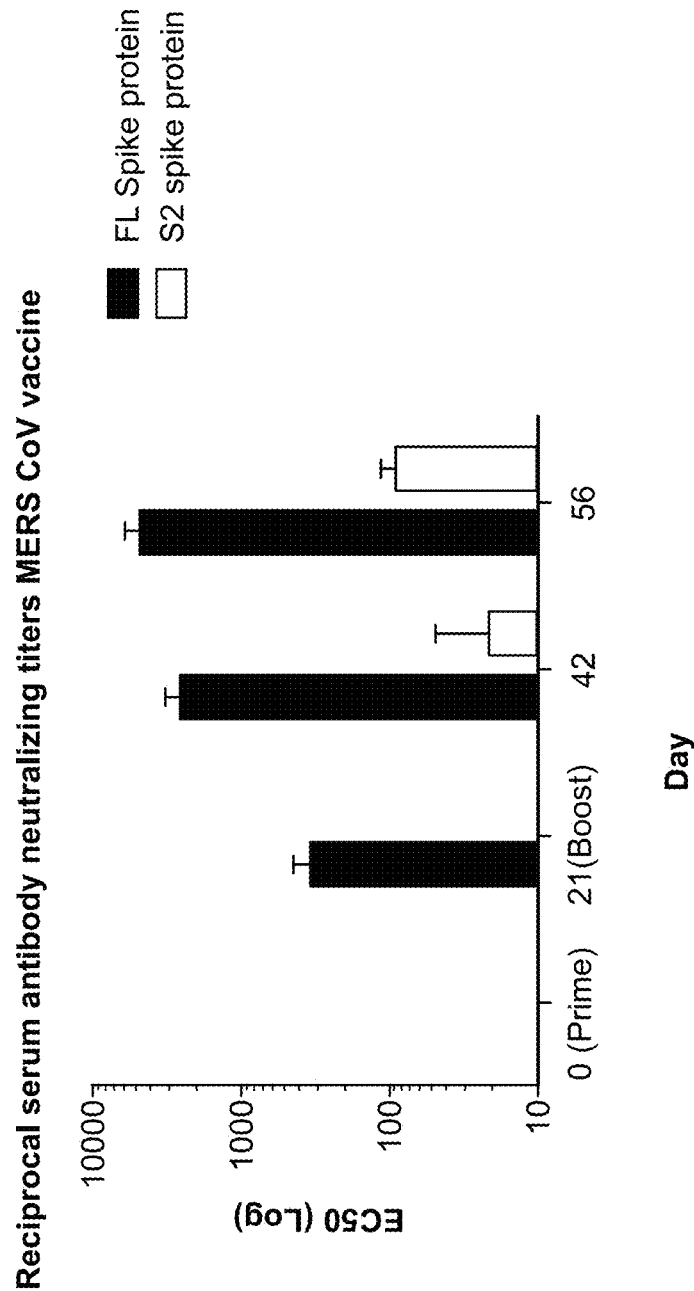


Fig. 19A

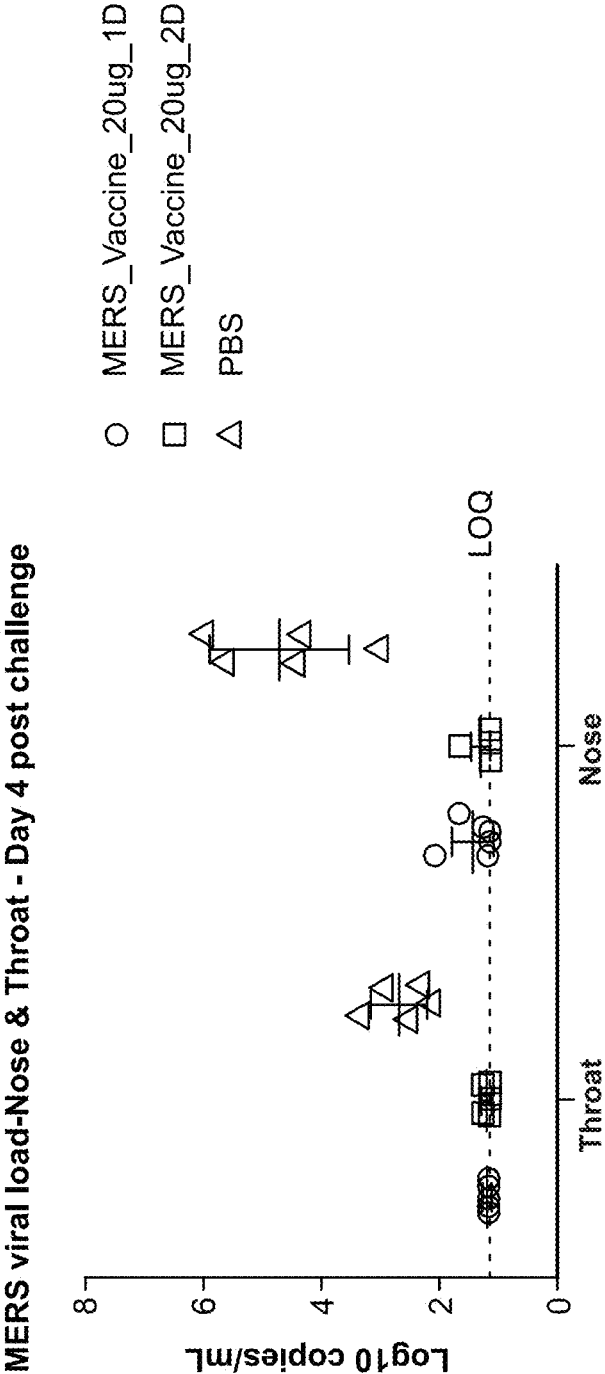


Fig. 19B

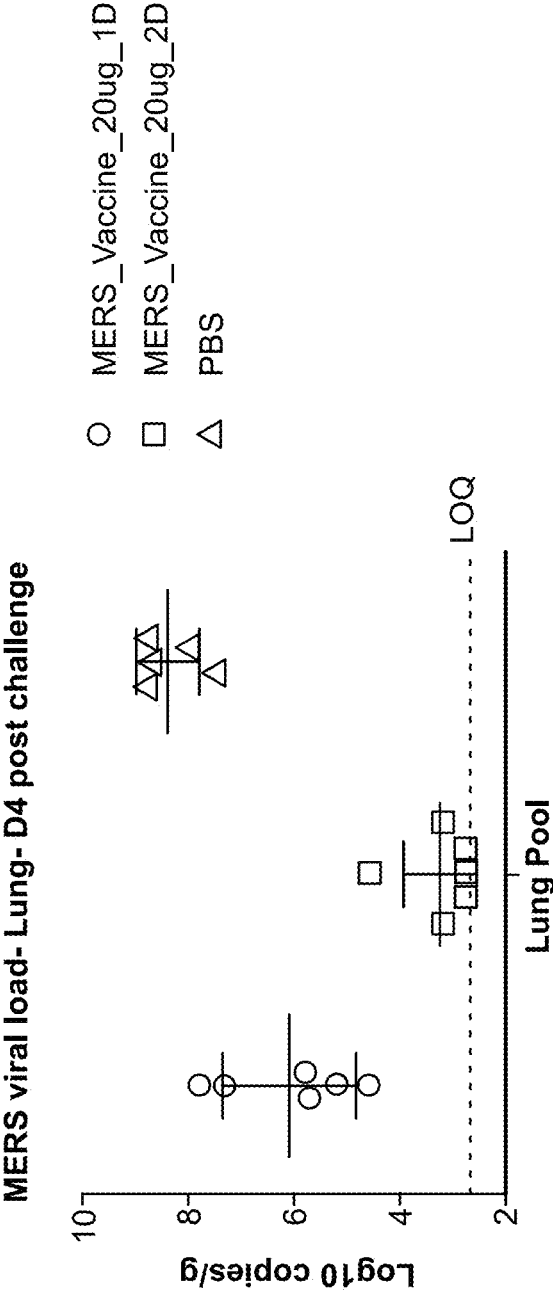


Fig. 19C

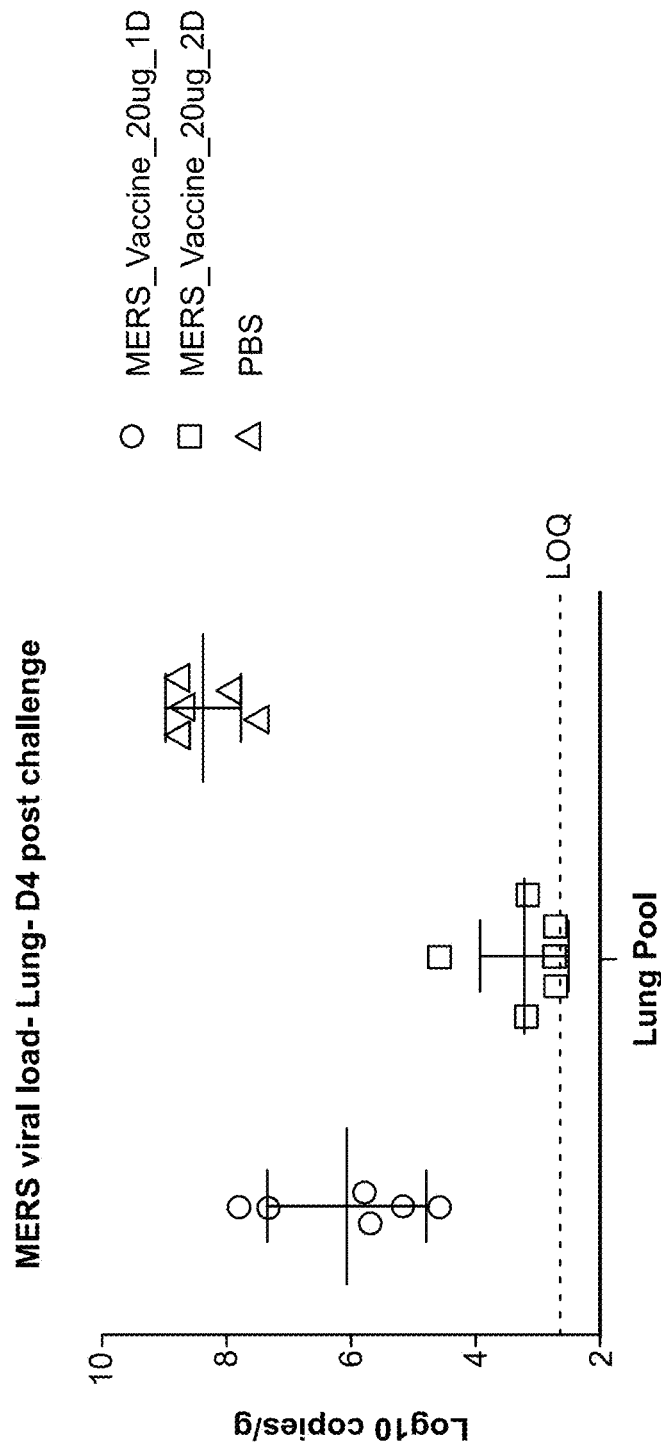


Fig. 20A

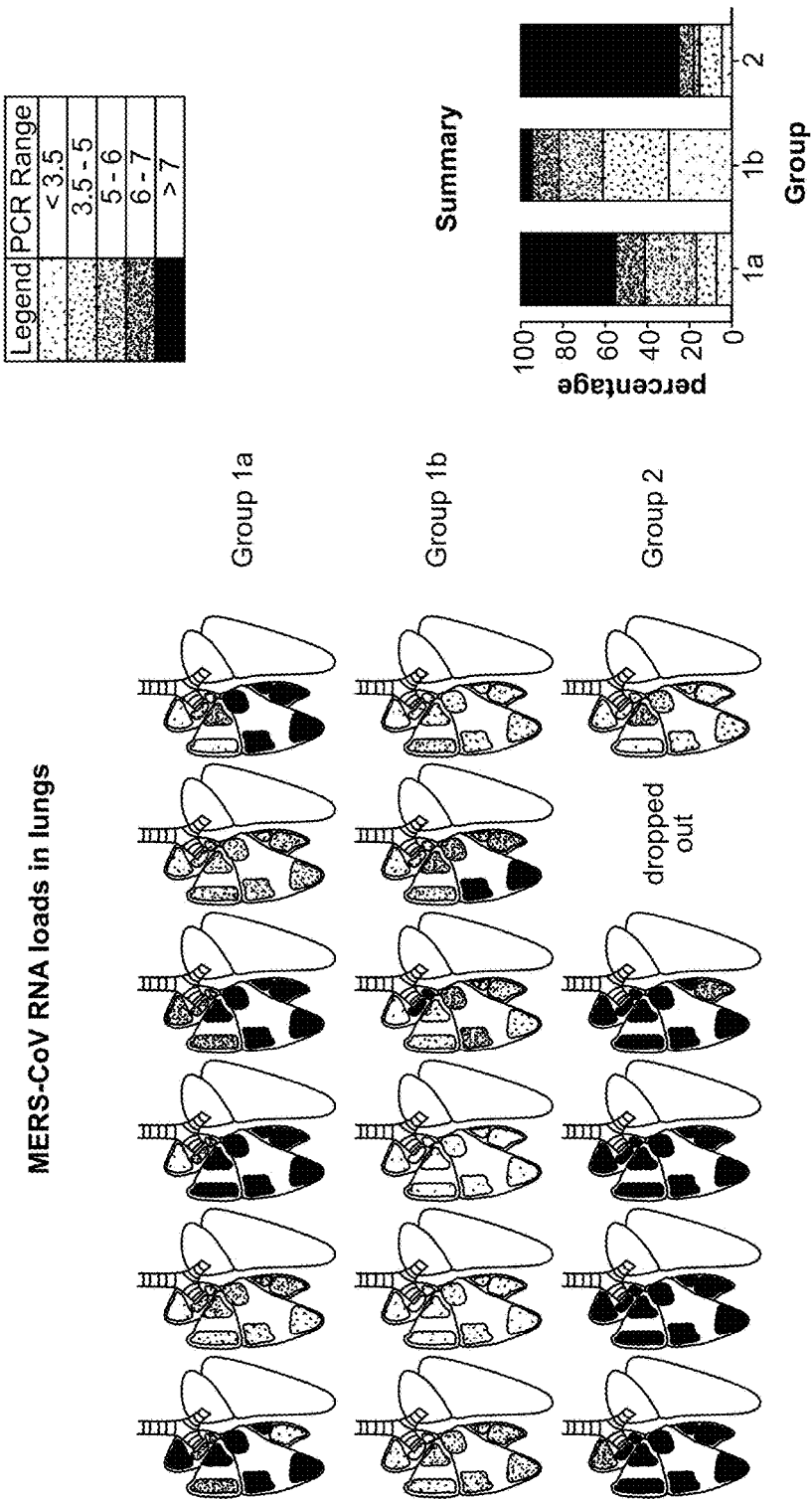


Fig. 20B

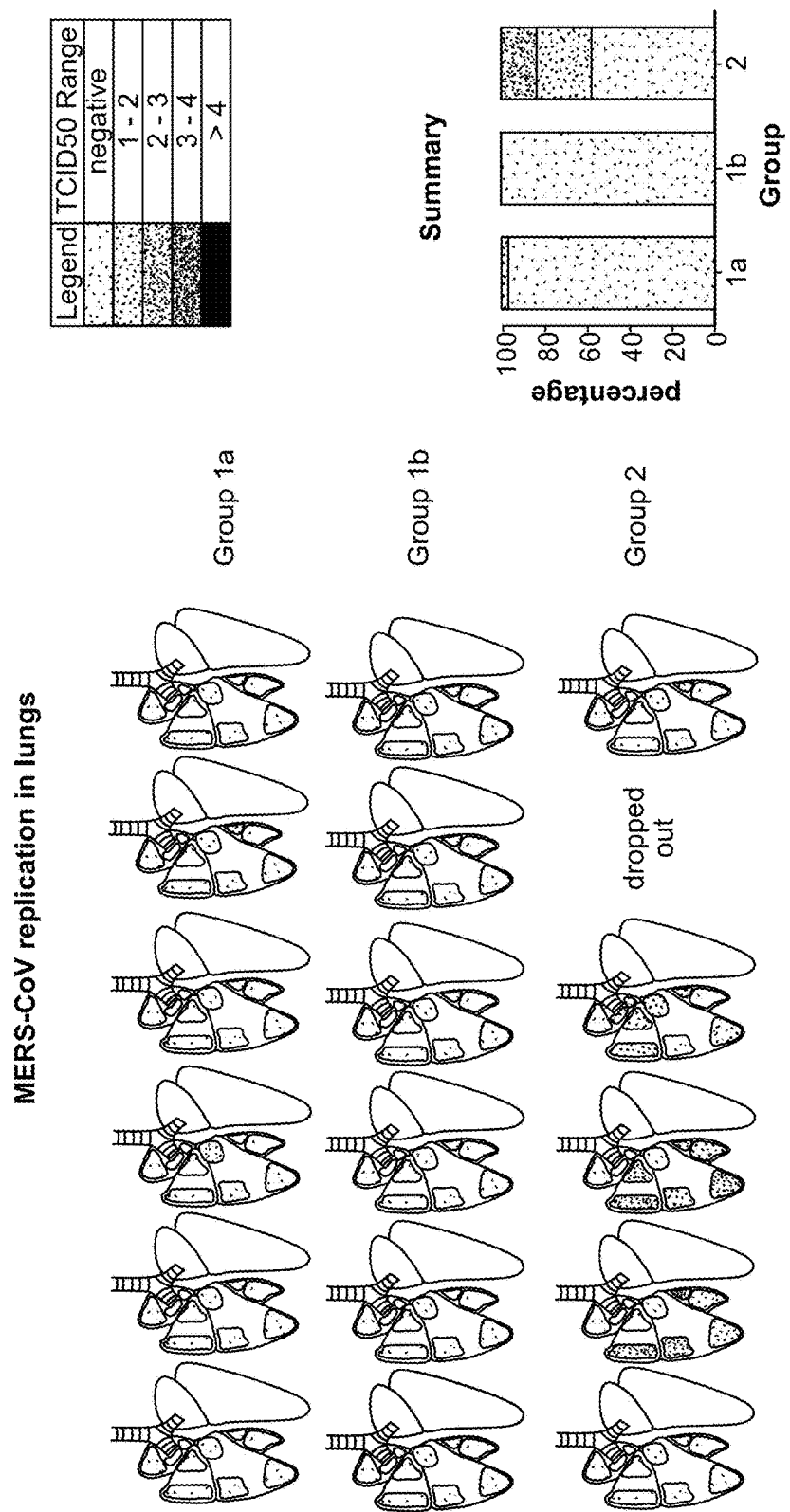
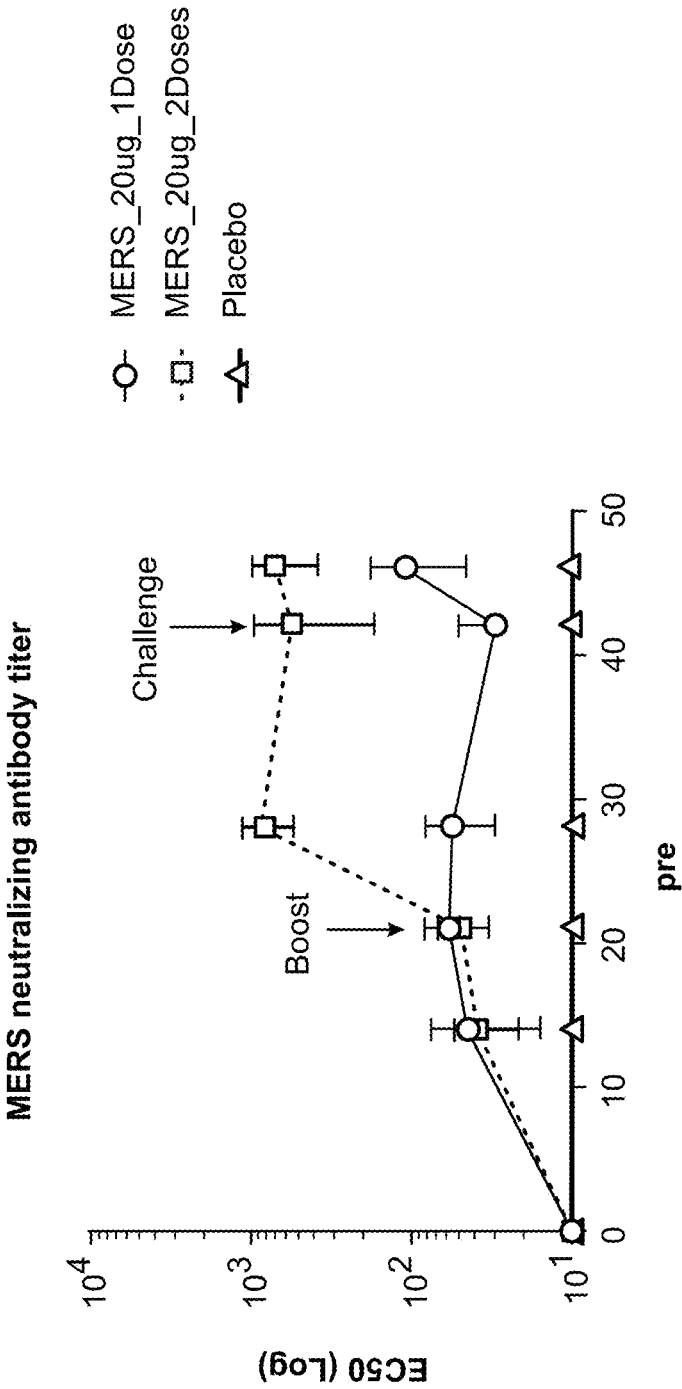


Fig. 21



HPIV3 RNA VACCINES**RELATED APPLICATIONS**

[0001] This application is a continuation of U.S. application Ser. No. 16/040,981, filed Jul. 20, 2018, which is a continuation of U.S. application Ser. No. 15/674,599, now U.S. Pat. No. 10,064,934, filed Aug. 11, 2017, which is a continuation of international application number PCT/US2016/058327, which claims the benefit under 35 U.S.C. § 119(e) of U.S. provisional application No. 62/244,802, filed Oct. 22, 2015, U.S. provisional application No. 62/247,297, filed Oct. 28, 2015, U.S. provisional application No. 62/244,946, filed Oct. 22, 2015, U.S. provisional application No. 62/247,362, filed Oct. 28, 2015, U.S. provisional application No. 62/244,813, filed Oct. 22, 2015, U.S. provisional application No. 62/247,394, filed Oct. 28, 2015, U.S. provisional application No. 62/244,837, filed Oct. 22, 2015, U.S. provisional application No. 62/247,483, filed Oct. 28, 2015, and U.S. provisional application No. 62/245,031, filed Oct. 22, 2015, each of which is incorporated by reference herein in its entirety.

BACKGROUND

[0002] Respiratory disease is a medical term that encompasses pathological conditions affecting the organs and tissues that make gas exchange possible in higher organisms, and includes conditions of the upper respiratory tract, trachea, bronchi, bronchioles, alveoli, pleura and pleural cavity, and the nerves and muscles of breathing. Respiratory diseases range from mild and self-limiting, such as the common cold, to life-threatening entities like bacterial pneumonia, pulmonary embolism, acute asthma and lung cancer. Respiratory disease is a common and significant cause of illness and death around the world. In the US, approximately 1 billion “common colds” occur each year. Respiratory conditions are among the most frequent reasons for hospital stays among children.

[0003] The human metapneumovirus (hMPV) is a negative-sense, single-stranded RNA virus of the genus *Pneumovirinae* and of the family Paramyxoviridae and is closely related to the avian metapneumovirus (AMPV) subgroup C. It was isolated for the first time in 2001 in the Netherlands by using the RAP-PCR (RNA arbitrarily primed PCR) technique for identification of unknown viruses growing in cultured cells. hMPV is second only to RSV as an important cause of viral lower respiratory tract illness (LRI) in young children. The seasonal epidemiology of hMPV appears to be similar to that of RSV, but the incidence of infection and illness appears to be substantially lower.

[0004] Parainfluenza virus type 3 (PIV3), like hMPV, is also a negative-sense, single-stranded sense RNA virus of the genus *Pneumovirinae* and of the family Paramyxoviridae and is a major cause of ubiquitous acute respiratory infections of infancy and early childhood. Its incidence peaks around 4-12 months of age, and the virus is responsible for 3-10% of hospitalizations, mainly for bronchiolitis and pneumonia. PIV3 can be fatal, and in some instances is associated with neurologic diseases, such as febrile seizures. It can also result in airway remodeling, a significant cause of morbidity. In developing regions of the world, infants and young children are at the highest risk of mortality, either from primary PIV3 viral infection or a secondary consequences, such as bacterial infections. Human parainfluenza

viruses (hPIV) types 1, 2 and 3 (hPIV1, hPIV2 and hPIV3, respectively), also like hMPV, are second only to RSV as important causes of viral LRI in young children.

[0005] RSV, too, is a negative-sense, single-stranded RNA virus of the genus *Pneumovirinae* and of the family Paramyxoviridae. Symptoms in adults typically resemble a sinus infection or the common cold, although the infection may be asymptomatic. In older adults (e.g., >60 years), RSV infection may progress to bronchiolitis or pneumonia. Symptoms in children are often more severe, including bronchiolitis and pneumonia. It is estimated that in the United States, most children are infected with RSV by the age of three. The RSV virion consists of an internal nucleocapsid comprised of the viral RNA bound to nucleoprotein (N), phosphoprotein (P), and large polymerase protein (L). The nucleocapsid is surrounded by matrix protein (M) and is encapsulated by a lipid bilayer into which the viral fusion (F) and attachment (G) proteins as well as the small hydrophobic protein (SH) are incorporated. The viral genome also encodes two nonstructural proteins (NS1 and NS2), which inhibit type I interferon activity as well as the M-2 protein.

[0006] The continuing health problems associated with hMPV, PIV3 and RSV are of concern internationally, reinforcing the importance of developing effective and safe vaccine candidates against these virus.

[0007] Despite decades of research, no vaccines currently exist (Sato and Wright, *Pediatr. Infect. Dis. J.* 2008; 27(10 Suppl):S123-5). Recombinant technology, however, has been used to target the formation of vaccines for hPIV-1, 2 and 3 serotypes, for example, and has taken the form of several live-attenuated intranasal vaccines. Two vaccines in particular were found to be immunogenic and well tolerated against hPIV-3 in phase I trials. hPIV1 and hPIV2 vaccine candidates remain less advanced (Durbin and Karron, *Clinical infectious diseases: an official publication of the Infectious Diseases Society of America* 2003; 37(12):1668-77).

[0008] Measles virus (MeV), like hMPV, PIV3 and RSV, is a negative-sense, single-stranded RNA virus that is the cause of measles, an infection of the respiratory system. MeV is of the genus *Morbillivirus* within the family Paramyxoviridae. Humans are the natural hosts of the virus; no animal reservoirs are known to exist. Symptoms of measles include fever, cough, runny nose, red eyes and a generalized, maculopapular, erythematous rash. The virus is highly contagious and is spread by coughing

[0009] In addition to hMPV, PIV, RSV and MeV, beta-coronaviruses are known to cause respiratory illnesses. Betacoronaviruses (BetaCoVs) are one of four genera of coronaviruses of the subfamily Coronavirinae in the family Coronaviridae, of the order Nidovirales. They are enveloped, positive-sense, single-stranded RNA viruses of zoonotic origin. The coronavirus genera are each composed of varying viral lineages, with the *betacoronavirus* genus containing four such lineages. The BetaCoVs of the greatest clinical importance concerning humans are OC43 and HKU1 of the A lineage, SARS-CoV of the B lineage, and MERS-CoV of the C lineage. MERS-CoV is the first betacoronavirus belonging to lineage C that is known to infect humans.

[0010] The Middle East respiratory syndrome coronavirus (MERS-CoV), or EMC/2012 (HCoV-EMC/2012), initially referred to as novel coronavirus 2012 or simply novel coronavirus, was first reported in 2012 after genome sequencing of a virus isolated from sputum samples from a

person who fell ill during a 2012 outbreak of a new flu. As of July 2015, MERS-CoV cases have been reported in over 21 countries. The outbreaks of MERS-CoV have raised serious concerns world-wide, reinforcing the importance of developing effective and safe vaccine candidates against MERS-CoV.

[0011] Severe acute respiratory syndrome (SARS) emerged in China in 2002 and spread to other countries before brought under control. Because of a concern for reemergence or a deliberate release of the SARS coronavirus, vaccine development was initiated.

[0012] Deoxyribonucleic acid (DNA) vaccination is one technique used to stimulate humoral and cellular immune responses to foreign antigens, such as hMPV antigens and/or PIV antigens and/or RSV antigens. The direct injection of genetically engineered DNA (e.g., naked plasmid DNA) into a living host results in a small number of its cells directly producing an antigen, resulting in a protective immunological response. With this technique, however, comes potential problems, including the possibility of insertional mutagenesis, which could lead to the activation of oncogenes or the inhibition of tumor suppressor genes.

SUMMARY

[0013] Provided herein are ribonucleic acid (RNA) vaccines that build on the knowledge that RNA (e.g., messenger RNA (mRNA)) can safely direct the body's cellular machinery to produce nearly any protein of interest, from native proteins to antibodies and other entirely novel protein constructs that can have therapeutic activity inside and outside of cells. The RNA (e.g., mRNA) vaccines of the present disclosure may be used to induce a balanced immune response against hMPV, PIV, RSV, MeV, and/or BetaCoV (e.g., MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1), or any combination of two or more of the foregoing viruses, comprising both cellular and humoral immunity, without risking the possibility of insertional mutagenesis, for example, hMPV, PIV, RSV, MeV, BetaCoV (e.g., MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1) and combinations thereof are referred to herein as "respiratory viruses." Thus, the term "respiratory virus RNA vaccines" encompasses hMPV RNA vaccines, PIV RNA vaccines, RSV RNA vaccines, MeV RNA vaccines, BetaCoV RNA vaccines, and any combination of two or more of hMPV RNA vaccines, PIV RNA vaccines, RSV RNA vaccines, MeV RNA vaccines, and BetaCoV RNA vaccines.

[0014] The RNA (e.g., mRNA) vaccines may be utilized in various settings depending on the prevalence of the infection or the degree or level of unmet medical need. The RNA (e.g., mRNA) vaccines may be utilized to treat and/or prevent a hMPV, PIV, RSV, MeV, a BetaCoV (e.g., MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH, HCoV-HKU1), or any combination of two or more of the foregoing viruses, of various genotypes, strains, and isolates. The RNA (e.g., mRNA) vaccines have superior properties in that they produce much larger antibody titers and produce responses earlier than commercially available anti-viral therapeutic treatments. While not wishing to be bound by theory, it is believed that the RNA (e.g., mRNA) vaccines, as mRNA polynucleotides, are better designed to produce the appropriate protein conformation upon translation as the RNA (e.g., mRNA) vaccines

co-opt natural cellular machinery. Unlike traditional vaccines, which are manufactured ex vivo and may trigger unwanted cellular responses, RNA (e.g., mRNA) vaccines are presented to the cellular system in a more native fashion.

[0015] In some aspects the invention is a respiratory virus vaccine, comprising at least one RNA polynucleotide having an open reading frame encoding at least one respiratory virus antigenic polypeptide, formulated in a cationic lipid nanoparticle.

[0016] Surprisingly, in some aspects—it has also been shown that efficacy of mRNA vaccines can be significantly enhanced when combined with a flagellin adjuvant, in particular, when one or more antigen-encoding mRNAs is combined with an mRNA encoding flagellin.

[0017] RNA (e.g., mRNA) vaccines combined with the flagellin adjuvant (e.g., mRNA-encoded flagellin adjuvant) have superior properties in that they may produce much larger antibody titers and produce responses earlier than commercially available vaccine formulations. While not wishing to be bound by theory, it is believed that the RNA (e.g., mRNA) vaccines, for example, as mRNA polynucleotides, are better designed to produce the appropriate protein conformation upon translation, for both the antigen and the adjuvant, as the RNA (e.g., mRNA) vaccines co-opt natural cellular machinery. Unlike traditional vaccines, which are manufactured ex vivo and may trigger unwanted cellular responses, RNA (e.g., mRNA) vaccines are presented to the cellular system in a more native fashion.

[0018] Some embodiments of the present disclosure provide RNA (e.g., mRNA) vaccines that include at least one RNA (e.g., mRNA) polynucleotide having an open reading frame encoding at least one antigenic polypeptide or an immunogenic fragment thereof (e.g., an immunogenic fragment capable of inducing an immune response to the antigenic polypeptide) and at least one RNA (e.g., mRNA polynucleotide) having an open reading frame encoding a flagellin adjuvant.

[0019] In some embodiments, at least one flagellin polypeptide (e.g., encoded flagellin polypeptide) is a flagellin protein. In some embodiments, at least one flagellin polypeptide (e.g., encoded flagellin polypeptide) is an immunogenic flagellin fragment. In some embodiments, at least one flagellin polypeptide and at least one antigenic polypeptide are encoded by a single RNA (e.g., mRNA) polynucleotide. In other embodiments, at least one flagellin polypeptide and at least one antigenic polypeptide are each encoded by a different RNA polynucleotide.

[0020] In some embodiments at least one flagellin polypeptide has at least 80%, at least 85%, at least 90%, or at least 95% identity to a flagellin polypeptide having a sequence identified by any one of SEQ ID NO: 54-56.

[0021] Provided herein, in some embodiments, is a ribonucleic acid (RNA) (e.g., mRNA) vaccine, comprising at least one (e.g., at least 2, 3, 4 or 5) RNA (e.g., mRNA) polynucleotide having an open reading frame encoding at least one (e.g., at least 2, 3, 4 or 5) hMPV, PIV, RSV, MeV, or a BetaCoV (e.g., MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH, HCoV-HKU1) antigenic polypeptide, or any combination of two or more of the foregoing antigenic polypeptides. Herein, use of the term "antigenic polypeptide" encompasses immunogenic fragments of the antigenic polypeptide (an immuno-

genic fragment that induces (or is capable of inducing) an immune response to hMPV, PIV, RSV, MeV, or a BetaCoV), unless otherwise stated.

[0022] Also provided herein, in some embodiments, is a RNA (e.g., mRNA) vaccine comprising at least one (e.g., at least 2, 3, 4 or 5) RNA polynucleotide having an open reading frame encoding at least one (e.g., at least 2, 3, 4 or 5) hMPV, PIV, RSV, MeV, and/or a BetaCoV (e.g., MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH, HCoV-HKU1) antigenic polypeptide or an immunogenic fragment thereof, linked to a signal peptide.

[0023] Further provided herein, in some embodiments, is a nucleic acid (e.g., DNA) encoding at least one (e.g., at least 2, 3, 4 or 5) hMPV, PIV, RSV, MeV, and/or a BetaCoV (e.g., MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH, HCoV-HKU1) RNA (e.g., mRNA) polynucleotide.

[0024] Further still, provided herein, in some embodiments, is a method of inducing an immune response in a subject, the method comprising administering to the subject a vaccine comprising at least one (e.g., at least 2, 3, 4 or 5) RNA (e.g., mRNA) polynucleotide having an open reading frame encoding at least one (e.g., at least 2, 3, 4 or 5) hMPV, PIV, RSV, MeV, and/or a BetaCoV (e.g., MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH, HCoV-HKU1) antigenic polypeptide, or any combination of two or more of the foregoing antigenic polypeptides.

[0025] hMPV/PIV3/RSV

[0026] In some embodiments, a RNA (e.g., mRNA) vaccine comprises at least one RNA (e.g., mRNA) polynucleotide having an open reading frame encoding at least one hMPV, PIV3 or RSV antigenic polypeptide. In some embodiments, at least one antigenic polypeptide is a hMPV, PIV3 or RSV polypeptide. In some embodiments, at least one antigenic polypeptide is major surface glycoprotein G or an immunogenic fragment thereof. In some embodiments, at least one antigenic polypeptide is Fusion (F) glycoprotein (e.g., Fusion glycoprotein F0, F1 or F2) or an immunogenic fragment thereof. In some embodiments, at least one antigenic polypeptide is major surface glycoprotein G or an immunogenic fragment thereof and F glycoprotein or an immunogenic fragment thereof. In some embodiments, the antigenic polypeptide is nucleoprotein (N) or an immunogenic fragment thereof, phosphoprotein (P) or an immunogenic fragment thereof, large polymerase protein (L) or an immunogenic fragment thereof, matrix protein (M) or an immunogenic fragment thereof, small hydrophobic protein (SH) or an immunogenic fragment thereof nonstructural protein1(NS1) or an immunogenic fragment thereof, or nonstructural protein 2 (NS2) and an immunogenic fragment thereof. In some embodiments, at least one hMPV antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 5-8 (Table 3; see also amino acid sequences of Table 4). In some embodiments, the amino acid sequence of the hMPV antigenic polypeptide is, or is a fragment of, or is a homolog or variant having at least 80% (e.g., 85%, 90%, 95%, 98%, 99%) identity to, the amino acid sequence identified by any one of SEQ ID NO: 5-8 (Table 3; see also amino acid sequences of Table 4).

[0027] In some embodiments, at least one hMPV antigenic polypeptide is encoded by a nucleic acid sequence identified by any one of SEQ ID NO: 1-4 (Table 2).

[0028] In some embodiments, at least one hMPV RNA (e.g., mRNA) polynucleotide is encoded by a nucleic acid sequence, or a fragment of a nucleotide sequence, identified by any one of SEQ ID NO: 1-4 (Table 2). In some embodiments, at least one hMPV RNA (e.g., mRNA) polynucleotide comprises a nucleic acid sequence, or a fragment of a nucleotide sequence, identified by any one of SEQ ID NO: 57-60 (Table 2).

[0029] In some embodiments, at least one antigenic polypeptide is obtained from hMPV strain CAN98-75 (CAN75) or the hMPV strain CAN97-83 (CAN83).

[0030] In some embodiments, at least one PIV3 antigenic polypeptide comprises hemagglutinin-neuraminidase, Fusion (F) glycoprotein, matrix protein (M), nucleocapsid protein (N), viral replicase (L), non-structural V protein, or an immunogenic fragment thereof.

[0031] In some embodiments, at least one PIV3 antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 12-13 (Table 6; see also amino acid sequences of Table 7). In some embodiments, the amino acid sequence of the PIV3 antigenic polypeptide is, or is a fragment of, or is a homolog or variant having at least 80% (e.g., 85%, 90%, 95%, 98%, 99%) identity to, the amino acid sequence identified by any one of SEQ ID NO: 12-13 (Table 6; see also amino acid sequences of Table 7).

[0032] In some embodiments, at least one PIV3 antigenic polypeptide is encoded by a nucleic acid sequence identified by any one of SEQ ID NO: 9-12 (Table 5; see also nucleic acid sequences of Table 7).

[0033] In some embodiments, at least one PIV3 RNA (e.g., mRNA) polynucleotide is encoded by a nucleic acid sequence, or a fragment of a nucleotide sequence, identified by any one of SEQ ID NO: 9-12 (Table 5; see also nucleic acid sequences of Table 7). In some embodiments, at least one PIV3 RNA (e.g., mRNA) polynucleotide comprises a nucleic acid sequence, or a fragment of a nucleotide sequence, identified by any one of SEQ ID NO: 61-64 (Table 5).

[0034] In some embodiments, at least one antigenic polypeptide is obtained from PIV3 strain HPIV3/Homo sapiens/PER/FLA4815/2008.

[0035] In some embodiments, at least one RSV antigenic polypeptide comprises at least one antigenic polypeptide that comprises glycoprotein G, glycoprotein F, or an immunogenic fragment thereof. In some embodiments, at least one RSV antigenic polypeptide comprises at least one antigenic polypeptide that comprises glycoprotein F and at least one or at least two antigenic polypeptide selected from G, M, N, P, L, SH, M2, NS1 and NS2.

[0036] MeV

[0037] In some embodiments, a RNA (e.g., mRNA) vaccine comprises at least one RNA (e.g., mRNA) polynucleotide having an open reading frame encoding at least one MeV antigenic polypeptide. In some embodiments, at least one antigenic polypeptide is a hemagglutinin (HA) protein or an immunogenic fragment thereof. The HA protein may be from MeV strain D3 or B8, for example. In some embodiments, at least one antigenic polypeptide is a Fusion (F) protein or an immunogenic fragment thereof. The F protein may be from MeV strain D3 or B8, for example. In some embodiments, a MeV RNA (e.g., mRNA) vaccine comprises at least one RNA polynucleotide encoding a HA protein and a F protein. The HA and F proteins may be from MeV strain D3 or B8, for example.

[0038] In some embodiments, at least one MeV antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 47-50 (Table 14). In some embodiments, the amino acid sequence of the MeV antigenic polypeptide is, or is a fragment of, or is a homolog or variant having at least 80% (e.g., 85%, 90%, 95%, 98%, 99%) identity to, the amino acid sequence identified by any one of SEQ ID NO: 47-50 (Table 14).

[0039] In some embodiments, at least one MeV antigenic polypeptide is encoded by a nucleic acid sequence of SEQ ID NO: 35-46 (Table 13).

[0040] In some embodiments, at least one MeV RNA (e.g., mRNA) polynucleotide is encoded by a nucleic acid sequence, or a fragment of a nucleotide sequence, identified by any one of SEQ ID NO: 35-46 (Table 13). In some embodiments, at least one MeV RNA (e.g., mRNA) polynucleotide comprises a nucleic acid sequence, or a fragment of a nucleotide sequence, identified by any one of SEQ ID NO: 69-80 (Table 13).

[0041] In some embodiments, at least one antigenic polypeptide is obtained from MeV strain B3/B3.1, C2, D4, D6, D7, D8, G3, H1, Moraten, Rubeovax, MVi/New Jersey. USA/45.05, MVi/Texas.USA/4.07, AIK-C, MVi/New York. USA/26.09/3, MVi/California.USA/16.03, MVi/Virginia. USA/15.09, MVi/California.USA/8.04, or MVi/Pennsylvania.USA/20.09.

[0042] BetaCoV

[0043] In some embodiments, a RNA (e.g., mRNA) vaccine comprises at least one RNA (e.g., mRNA) polynucleotide having an open reading frame encoding at least one BetaCoV antigenic polypeptide. In some embodiments, the BetaCoV is MERS-CoV. In some embodiments, the BetaCoV is SARS-CoV. In some embodiments, the BetaCoV is HCoV-OC43. In some embodiments, the BetaCoV is HCoV-229E. In some embodiments, the BetaCoV is HCoV-NL63. In some embodiments, the BetaCoV is HCoV-HKU1. In some embodiments, at least one antigenic polypeptide is a betacoronavirus structural protein. For example, a betacoronavirus structural protein may be spike protein (S), envelope protein (E), nucleocapsid protein (N), membrane protein (M) or an immunogenic fragment thereof. In some embodiments, a betacoronavirus structural protein is a spike protein (S). In some embodiments, a betacoronavirus structural protein is a S1 subunit or a S2 subunit of spike protein (S) or an immunogenic fragment thereof.

[0044] BetaCoV RNA (e.g., mRNA) polynucleotides of the vaccines provided herein may encode viral protein components of betacoronaviruses, for example, accessory proteins, replicase proteins and the like are encompassed by the present disclosure. RNA (e.g., mRNA) vaccines may include RNA polynucleotides encoding at least one accessory protein (e.g., protein 3, protein 4a, protein 4b, protein 5), at least one replicase protein (e.g., protein 1a, protein 1b), or a combination of at least one accessory protein and at least one replicase protein. The present disclosure also encompasses RNA (e.g., mRNA) vaccines comprising RNA (e.g., mRNA) polynucleotides encoding an accessory protein and/or a replicase protein in combination with at least one structural protein. Due to their surface expression properties, vaccines featuring RNA polynucleotides encoding structural proteins are believed to have preferred immunogenic activity and, hence, may be most suitable for use in the vaccines of the present disclosure.

[0045] Some embodiments of the present disclosure provide betacoronavirus (e.g., MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH, HCoV-HKU1 or a combination thereof) vaccines that include at least one RNA (e.g., mRNA) polynucleotide having an open reading frame encoding at least one betacoronavirus (e.g., MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH, HCoV-HKU1) antigenic polypeptide. Also provided herein are pan-betacoronavirus vaccines. Thus, a betacoronavirus vaccine comprising a RNA (e.g., mRNA) polynucleotide having an open reading frame encoding any one, two, three or four of MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, and HCoV-HKU1, for example, may be effective against any one of, any combination of, or all of, MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1. Other betacoronaviruses are encompassed by the present disclosure.

[0046] In some embodiments, at least one antigenic polypeptide is a MERS-CoV structural protein. For example, a MERS-CoV structural protein may be spike protein (S), envelope protein (E), nucleocapsid protein (N), membrane protein (M) or an immunogenic fragment thereof. In some embodiments, the MERS-CoV structural protein is a spike protein (S) (see, e.g., Coleman C M et al. *Vaccine* 2014; 32:3169-74, incorporated herein by reference). In some embodiments, the MERS-CoV structural protein is a S1 subunit or a S2 subunit of spike protein (S) or an immunogenic fragment thereof (Li J et al. *Viral Immunol* 2013; 26(2):126-32; He Y et al. *Biochem Biophys Res Commun* 2004; 324(2):773-81, each of which is incorporated herein by reference).

[0047] In some embodiments, at least one MERS-CoV antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 24-28 or 33 (Table 11). In some embodiments, the amino acid sequence of the MERS-CoV antigenic polypeptide is, or is a fragment of, or is a homolog or variant having at least 80% (e.g., 85%, 90%, 95%, 98%, 99%) identity to, the amino acid sequence identified by any one of SEQ ID NO: 24-28 or 33 (Table 11).

[0048] In some embodiments, at least one MERS-CoV antigenic polypeptide is encoded by a nucleic acid sequence identified by any one of SEQ ID NO: 20-23 (Table 10).

[0049] In some embodiments, at least one MERS-CoV RNA (e.g., mRNA) polynucleotide is encoded by a nucleic acid sequence, or a fragment of a nucleotide sequence, identified by any one of SEQ ID NO: 20-23 (Table 10). In some embodiments, at least one MERS-CoV RNA (e.g., mRNA) polynucleotide comprises a nucleic acid sequence, or a fragment of a nucleotide sequence, identified by any one of SEQ ID NO: 65-68 (Table 10).

[0050] In some embodiments, at least one antigenic polypeptide is obtained from MERS-CoV strain Riyadh_14_2013, 2cEMC/2012, or Hasa_1_2013.

[0051] In some embodiments, at least one antigenic polypeptide is a SARS-CoV structural protein. For example, a SARS-CoV structural protein may be spike protein (S), envelope protein (E), nucleocapsid protein (N), membrane protein (M) or an immunogenic fragment thereof. In some embodiments, the SARS-CoV structural protein is a spike protein (S). In some embodiments, the SARS-CoV structural protein is a S1 subunit or a S2 subunit of spike protein (S) or an immunogenic fragment thereof.

[0052] In some embodiments, at least one SARS-CoV antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 29, 32 or 34 (Table 11). In some embodiments, the amino acid sequence of the SARS-CoV antigenic polypeptide is, or is a fragment of, or is a homolog or variant having at least 80% (e.g., 85%, 90%, 95%, 98%, 99%) identity to, the amino acid sequence identified by any one of SEQ ID NO: 29, 32 or 34 (Table 11).

[0053] In some embodiments, at least one antigenic polypeptide is a HCoV-OC43 structural protein. For example, a HCoV-OC43 structural protein may be spike protein (S), envelope protein (E), nucleocapsid protein (N), membrane protein (M) or an immunogenic fragment thereof. In some embodiments, the HCoV-OC43 structural protein is a spike protein (S). In some embodiments, the HCoV-OC43 structural protein is a S1 subunit or a S2 subunit of spike protein (S) or an immunogenic fragment thereof.

[0054] In some embodiments, at least one HCoV-OC43 antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 30 (Table 11). In some embodiments, the amino acid sequence of the HCoV-OC43 antigenic polypeptide is, or is a fragment of, or is a homolog or variant having at least 80% (e.g., 85%, 90%, 95%, 98%, 99%) identity to, the amino acid sequence identified by any one of SEQ ID NO: 30 (Table 11).

[0055] In some embodiments, an antigenic polypeptide is a HCoV-HKU1 structural protein. For example, a HCoV-HKU1 structural protein may be spike protein (S), envelope protein (E), nucleocapsid protein (N), membrane protein (M) or an immunogenic fragment thereof. In some embodiments, the HCoV-HKU1 structural protein is a spike protein (S). In some embodiments, the HCoV-HKU1 structural protein is a S1 subunit or a S2 subunit of spike protein (S) or an immunogenic fragment thereof.

[0056] In some embodiments, at least one HCoV-HKU1 antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 31 (Table 11). In some embodiments, the amino acid sequence of the HCoV-HKU1 antigenic polypeptide is, or is a fragment of, or is a homolog or variant having at least 80% (e.g., 85%, 90%, 95%, 98%, 99%) identity to, the amino acid sequence identified by any one of SEQ ID NO: 31 (Table 11).

[0057] In some embodiments, an open reading frame of a RNA (e.g., mRNA) vaccine is codon-optimized. In some embodiments, at least one RNA polynucleotide encodes at least one antigenic polypeptide having an amino acid sequence identified by any one of SEQ ID NO: 5-8, 12-13, 24-34, or 47-50 (Tables 3, 6, 11 and 14; see also amino acid sequences of Tables 4, 7, 12 and 15) and is codon optimized mRNA.

[0058] In some embodiments, a RNA (e.g., mRNA) vaccine further comprising an adjuvant.

[0059] Tables 4, 7, 12 and 15 provide National Center for Biotechnology Information (NCBI) accession numbers of interest. It should be understood that the phrase “an amino acid sequence of Tables 4, 7, 12 and 15” refers to an amino acid sequence identified by one or more NCBI accession numbers listed in Tables 4, 7, 12 and 15. Each of the amino acid sequences, and variants having greater than 95% identity or greater than 98% identity to each of the amino acid sequences encompassed by the accession numbers of Tables 4, 7, 12 and 15 are included within the constructs (polynucleotides/polypeptides) of the present disclosure.

[0060] In some embodiments, at least one mRNA polynucleotide is encoded by a nucleic acid having a sequence identified by any one of SEQ ID NO: 1-4, 9-12, 20-23, or 35-46 (Tables 2, 5, 10 and 13; see also nucleic acid sequences of Table 7) and having less than 80% identity to wild-type mRNA sequence. In some embodiments, at least one mRNA polynucleotide is encoded by a nucleic acid having a sequence identified by any one of SEQ ID NO: 1-4, 9-12, 20-23, or 35-46 (Tables 2, 5, 10 and 13; see also nucleic acid sequences of Table 7) and having less than 75%, 85% or 95% identity to a wild-type mRNA sequence. In some embodiments, at least one mRNA polynucleotide is encoded by a nucleic acid having a sequence identified by any one of SEQ ID NO: 1-4, 9-12, 20-23, or 35-46 (Tables 2, 5, 10 and 13; see also nucleic acid sequences of Table 7) and having less than 50-80%, 60-80%, 40-80%, 30-80%, 70-80%, 75-80% or 78-80% identity to wild-type mRNA sequence. In some embodiments, at least one mRNA polynucleotide is encoded by a nucleic acid having a sequence identified by any one of SEQ ID NO: 1-4, 9-12, 20-23, or 35-46 (Tables 2, 5, 10 and 13; see also nucleic acid sequences of Table 7) and having less than 40-85%, 50-85%, 60-85%, 30-85%, 70-85%, 75-85% or 80-85% identity to wild-type mRNA sequence. In some embodiments, at least one mRNA polynucleotide is encoded by a nucleic acid having a sequence identified by any one of SEQ ID NO: 1-4, 9-12, 20-23, or 35-46 (Tables 2, 5, 10 and 13; see also nucleic acid sequences of Table 7) and having less than 40-90%, 50-90%, 60-90%, 30-90%, 70-90%, 75-90%, 80-90%, or 85-90% identity to wild-type mRNA sequence.

[0061] In some embodiments, at least one RNA polynucleotide encodes at least one antigenic polypeptide having an amino acid sequence identified by any one of SEQ ID NO: 5-8, 12-13, 24-34, or 47-50 (Tables 3, 6, 11 and 14; see also amino acid sequences of Tables 4, 7, 12 and 15) and having at least 80% (e.g., 85%, 90%, 95%, 98%, 99%) identity to wild-type mRNA sequence, but does not include wild-type mRNA sequence.

[0062] In some embodiments, at least one RNA polynucleotide encodes at least one antigenic polypeptide having an amino acid sequence identified by any one of SEQ ID NO: 5-8, 12-13, 24-34, or 47-50 (Tables 3, 6, 11 and 14; see also amino acid sequences of Tables 4, 7, 12 and 15) and has less than 95%, 90%, 85%, 80% or 75% identity to wild-type mRNA sequence. In some embodiments, at least one RNA polynucleotide encodes at least one antigenic polypeptide having an amino acid sequence identified by any one of SEQ ID NO: 5-8, 12-13, 24-34, or 47-50 (Tables 3, 6, 11 and 14; see also amino acid sequences of Tables 4, 7, 12 and 15) and has 30-80%, 40-80%, 50-80%, 60-80%, 70-80%, 75-80% or 78-80%, 30-85%, 40-85%, 50-85%, 60-85%, 70-85%, 75-85% or 78-85%, 30-90%, 40-90%, 50-90%, 60-90%, 70-90%, 75-90%, 80-90% or 85-90% identity to wild-type mRNA sequence.

[0063] In some embodiments, at least one RNA polynucleotide encodes at least one antigenic polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identity to an amino acid sequence identified by any one of SEQ ID NO: 5-8, 12-13, 24-34, or 47-50 (Tables 3, 6, 11 and 14; see also amino acid sequences of Tables 4, 7, 12 and 15). In some embodiments, at least one RNA polynucleotide encodes at least one antigenic polypeptide having 95%-99% identity to an amino acid sequence

identified by any one of SEQ ID NO: 5-8, 12-13, 24-34, or 47-50 (Tables 3, 6, 11 and 14; see also amino acid sequences of Tables 4, 7, 12 and 15).

[0064] In some embodiments, at least one RNA polynucleotide encodes at least one antigenic polypeptide having at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identity to an amino acid sequence identified by any one of SEQ ID NO: 5-8, 12-13, 24-34, or 47-50 (Tables 3, 6, 11 and 14; see also amino acid sequences of Tables 4, 7, 12 and 15) and having membrane fusion activity. In some embodiments, at least one RNA polynucleotide encodes at least one antigenic polypeptide having 95%-99% identity to an amino acid sequence identified by any one of SEQ ID NO: 5-8, 12-13, 24-34, or 47-50 (Tables 3, 6, 11 and 14; see also amino acid sequences of Tables 4, 7, 12 and 15) and having membrane fusion activity.

[0065] In some embodiments, at least one RNA polynucleotide encodes at least one antigenic polypeptide (e.g., at least one hMPV antigenic polypeptide, at least one PIV3 antigenic polypeptide, at least one RSV antigenic polypeptide, at least one MeV antigenic polypeptide, or at least one BetaCoV antigenic polypeptide, e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1, or any combination of two or more of the foregoing antigenic polypeptides) that attaches to cell receptors.

[0066] In some embodiments, at least one RNA polynucleotide encodes at least one antigenic polypeptide (e.g., at least one hMPV antigenic polypeptide, at least one PIV3 antigenic polypeptide, at least one RSV antigenic polypeptide, at least one MeV antigenic polypeptide, or at least one BetaCoV antigenic polypeptide, e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1, or any combination of two or more of the foregoing antigenic polypeptides) that causes fusion of viral and cellular membranes.

[0067] In some embodiments, at least one RNA polynucleotide encodes at least one antigenic polypeptide (e.g., at least one hMPV antigenic polypeptide, at least one PIV3 antigenic polypeptide, at least one RSV antigenic polypeptide,

at least one RSV antigenic polypeptide, at least one MeV antigenic polypeptide, or at least one BetaCoV antigenic polypeptide, e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1, or any combination of two or more of the foregoing antigenic polypeptides), at least one 5' terminal cap and at least one chemical modification, formulated within a lipid nanoparticle.

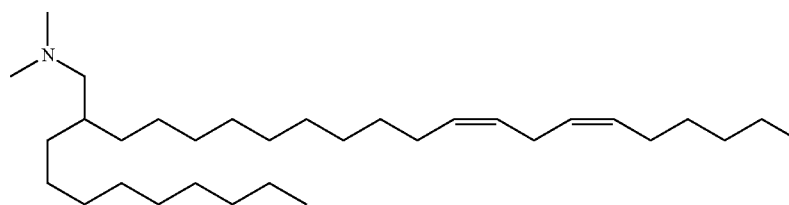
[0069] In some embodiments, a 5' terminal cap is 7mG (5')ppp(5')NlmpNp.

[0070] In some embodiments, at least one chemical modification is selected from pseudouridine, N1-methylpseudouridine, N1-ethylpseudouridine, 2-thiouridine, 4'-thiouridine, 5-methylcytosine, 5-methyluridine, 2-thio-1-methyl-1-deaza-pseudouridine, 2-thio-1-methyl-pseudouridine, 2-thio-5-aza-uridine, 2-thio-dihydropseudouridine, 2-thio-dihydrouridine, 2-thio-pseudouridine, 4-methoxy-2-thio-pseudouridine, 4-methoxy-pseudouridine, 4-thio-1-methyl-pseudouridine, 4-thio-pseudouridine, 5-aza-uridine, dihydropseudouridine, 5-methoxyuridine and 2'-O-methyluridine. In some embodiments, the chemical modification is in the 5-position of the uracil. In some embodiments, the chemical modification is a N1-methylpseudouridine. In some embodiments, the chemical modification is a N1-ethylpseudouridine.

[0071] In some embodiments, a lipid nanoparticle comprises a cationic lipid, a PEG-modified lipid, a sterol and a non-cationic lipid. In some embodiments, a cationic lipid is an ionizable cationic lipid and the non-cationic lipid is a neutral lipid, and the sterol is a cholesterol. In some embodiments, a cationic lipid is selected from the group consisting of 2,2-dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoleyl-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319), (12Z,15Z)-N,N-dimethyl-2-nonylhenicosa-12,15-dien-1-amine (L608), and N,N-dimethyl-1-[(1S,2R)-2-octylcyclopropyl]heptadecan-8-amine (L530).

[0072] In some embodiments, the lipid is

(L608)

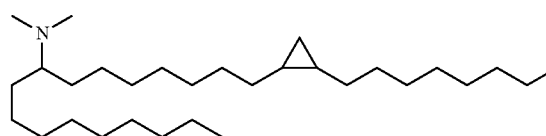


at least one MeV antigenic polypeptide, or at least one BetaCoV antigenic polypeptide, e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1, or any combination of two or more of the foregoing antigenic polypeptides) that is responsible for binding of the virus to a cell being infected.

[0068] Some embodiments of the present disclosure provide a vaccine that includes at least one ribonucleic acid (RNA) (e.g., mRNA) polynucleotide having an open reading frame encoding at least one antigenic polypeptide (e.g., at least one hMPV antigenic polypeptide, at least one PIV3

[0073] In some embodiments, the lipid is

(L530)



[0074] In some embodiments, a lipid nanoparticle comprises compounds of Formula (I) and/or Formula (II), discussed below.

[0075] In some embodiments, a respiratory virus RNA (e.g., mRNA) vaccine is formulated in a lipid nanoparticle that comprises a compound selected from Compounds 3, 18, 20, 25, 26, 29, 30, 60, 108-112 and 122, described below.

[0076] Some embodiments of the present disclosure provide a vaccine that includes at least one RNA (e.g., mRNA) polynucleotide having an open reading frame encoding at least one antigenic polypeptide (e.g., at least one hMPV antigenic polypeptide, at least one PIV3 antigenic polypeptide, at least one RSV antigenic polypeptide, at least one MeV antigenic polypeptide, or at least one BetaCoV antigenic polypeptide, e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1, or any combination of two or more of the foregoing antigenic polypeptides), wherein at least 80% (e.g., 85%, 90%, 95%, 98%, 99%) of the uracil in the open reading frame have a chemical modification, optionally wherein the vaccine is formulated in a lipid nanoparticle (e.g., a lipid nanoparticle comprises a cationic lipid, a PEG-modified lipid, a sterol and a non-cationic lipid).

[0077] In some embodiments, 100% of the uracil in the open reading frame have a chemical modification. In some embodiments, a chemical modification is in the 5-position of the uracil. In some embodiments, a chemical modification is a N1-methyl pseudouridine. In some embodiments, 100% of the uracil in the open reading frame have a N1-methyl pseudouridine in the 5-position of the uracil.

[0078] In some embodiments, an open reading frame of a RNA (e.g., mRNA) polynucleotide encodes at least two antigenic polypeptides (e.g., at least two hMPV antigenic polypeptides, at least two PIV3 antigenic polypeptides, at least two RSV antigenic polypeptides, at least two MeV antigenic polypeptides, or at least two BetaCoV antigenic polypeptides, e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1, or any combination of two or more of the foregoing antigenic polypeptides). In some embodiments, the open reading frame encodes at least five or at least ten antigenic polypeptides. In some embodiments, the open reading frame encodes at least 100 antigenic polypeptides. In some embodiments, the open reading frame encodes 2-100 antigenic polypeptides.

[0079] In some embodiments, a vaccine comprises at least two RNA (e.g., mRNA) polynucleotides, each having an open reading frame encoding at least one antigenic polypeptide (e.g., at least one hMPV antigenic polypeptide, at least one PIV3 antigenic polypeptide, at least one RSV antigenic polypeptide, at least one MeV antigenic polypeptide, or at least one BetaCoV antigenic polypeptide, e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1, or any combination of two or more of the foregoing antigenic polypeptides). In some embodiments, the vaccine comprises at least five or at least ten RNA (e.g., mRNA) polynucleotides, each having an open reading frame encoding at least one antigenic polypeptide or an immunogenic fragment thereof. In some embodiments, the vaccine comprises at least 100 RNA (e.g., mRNA) polynucleotides, each having an open reading frame encoding at least one antigenic polypeptide. In some embodiments, the vaccine

comprises 2-100 RNA (e.g., mRNA) polynucleotides, each having an open reading frame encoding at least one antigenic polypeptide.

[0080] In some embodiments, at least one antigenic polypeptide (e.g., at least one hMPV antigenic polypeptide, at least one PIV3 antigenic polypeptide, at least one RSV antigenic polypeptide, at least one MeV antigenic polypeptide, or at least one BetaCoV antigenic polypeptide, e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1, or any combination of two or more of the foregoing antigenic polypeptides) is fused to a signal peptide. In some embodiments, the signal peptide is selected from: a HulgGk signal peptide (METPAQLLFLLLLWLP-DTTG; SEQ ID NO: 15); IgE heavy chain epsilon-1 signal peptide (MDWTWILFLVAAATRVHS; SEQ ID NO: 16); Japanese encephalitis PRM signal sequence (MLGSNSGQRVVFITILLLLVAPAYS; SEQ ID NO: 17); VSVg protein signal sequence (MKCLLYLAFLFIGVNCA; SEQ ID NO: 18) and Japanese encephalitis JEV signal sequence (MWLVSLAIVTACAGA; SEQ ID NO: 19).

[0081] In some embodiments, the signal peptide is fused to the N-terminus of at least one antigenic polypeptide. In some embodiments, a signal peptide is fused to the C-terminus of at least one antigenic polypeptide.

[0082] In some embodiments, at least one antigenic polypeptide (e.g., at least one hMPV antigenic polypeptide, at least one PIV3 antigenic polypeptide, at least one RSV antigenic polypeptide, at least one MeV antigenic polypeptide, or at least one BetaCoV antigenic polypeptide, e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1, or any combination of two or more of the foregoing antigenic polypeptides) comprises a mutated N-linked glycosylation site.

[0083] Also provided herein is a RNA (e.g., mRNA) vaccine of any one of the foregoing paragraphs (e.g., a hMPV vaccine, a PIV3 vaccine, a RSV vaccine, a MeV vaccine, or a BetaCoV vaccine, e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1, or any combination of two or more of the foregoing vaccines), formulated in a nanoparticle (e.g., a lipid nanoparticle).

[0084] In some embodiments, the nanoparticle has a mean diameter of 50-200 nm. In some embodiments, the nanoparticle is a lipid nanoparticle. In some embodiments, the lipid nanoparticle comprises a cationic lipid, a PEG-modified lipid, a sterol and a non-cationic lipid. In some embodiments, the lipid nanoparticle comprises a molar ratio of about 20-60% cationic lipid, 0.5-15% PEG-modified lipid, 25-55% sterol, and 25% non-cationic lipid. In some embodiments, the cationic lipid is an ionizable cationic lipid and the non-cationic lipid is a neutral lipid, and the sterol is a cholesterol. In some embodiments, the cationic lipid is selected from 2,2-dilinoleyl-4-dimethylaminoethyl-[1,3]-dioleane (DLin-KC2-DMA), dilinoleyl-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319).

[0085] In some embodiments, a lipid nanoparticle comprises compounds of Formula (I) and/or Formula (II), as discussed below.

[0086] In some embodiments, a lipid nanoparticle comprises Compounds 3, 18, 20, 25, 26, 29, 30, 60, 108-112, or 122, as discussed below.

[0087] In some embodiments, the nanoparticle has a polydispersity value of less than 0.4 (e.g., less than 0.3, 0.2 or 0.1).

[0088] In some embodiments, the nanoparticle has a net neutral charge at a neutral pH value.

[0089] In some embodiments, the respiratory virus vaccine is multivalent.

[0090] Some embodiments of the present disclosure provide methods of inducing an antigen specific immune response in a subject, comprising administering to the subject any of the RNA (e.g., mRNA) vaccine as provided herein in an amount effective to produce an antigen-specific immune response. In some embodiments, the RNA (e.g., mRNA) vaccine is a hMPV vaccine, a PIV3 vaccine, a RSV vaccine, a MeV vaccine, or a BetaCoV vaccine, e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1 vaccines. In some embodiments, the RNA (e.g., mRNA) vaccine is a combination vaccine comprising a combination of any two or more of the foregoing vaccines.

[0091] In some embodiments, an antigen-specific immune response comprises a T cell response or a B cell response.

[0092] In some embodiments, a method of producing an antigen-specific immune response comprises administering to a subject a single dose (no booster dose) of a RNA (e.g., mRNA) vaccine of the present disclosure. In some embodiments, the RNA (e.g., mRNA) vaccine is a hMPV vaccine, a PIV3 vaccine, a RSV vaccine, a MeV vaccine, or a BetaCoV vaccine, e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1 vaccines. In some embodiments, the RNA (e.g., mRNA) vaccine is a combination vaccine comprising a combination of any two or more of the foregoing vaccines.

[0093] In some embodiments, a method further comprises administering to the subject a second (booster) dose of a RNA (e.g., mRNA) vaccine. Additional doses of a RNA (e.g., mRNA) vaccine may be administered.

[0094] In some embodiments, the subjects exhibit a seroconversion rate of at least 80% (e.g., at least 85%, at least 90%, or at least 95%) following the first dose or the second (booster) dose of the vaccine. Seroconversion is the time period during which a specific antibody develops and becomes detectable in the blood. After seroconversion has occurred, a virus can be detected in blood tests for the antibody. During an infection or immunization, antigens enter the blood, and the immune system begins to produce antibodies in response. Before seroconversion, the antigen itself may or may not be detectable, but antibodies are considered absent. During seroconversion, antibodies are present but not yet detectable. Any time after seroconversion, the antibodies can be detected in the blood, indicating a prior or current infection.

[0095] In some embodiments, a RNA (e.g., mRNA) vaccine is administered to a subject by intradermal or intramuscular injection.

[0096] Some embodiments of the present disclosure provide methods of inducing an antigen specific immune response in a subject, including administering to a subject a RNA (e.g., mRNA) vaccine in an effective amount to produce an antigen specific immune response in a subject.

Antigen-specific immune responses in a subject may be determined, in some embodiments, by assaying for antibody titer (for titer of an antibody that binds to a hMPV, PIV3, RSV, MeV and/or BetaCoV antigenic polypeptide) following administration to the subject of any of the RNA (e.g., mRNA) vaccines of the present disclosure. In some embodiments, the anti-antigenic polypeptide antibody titer produced in the subject is increased by at least 1 log relative to a control. In some embodiments, the anti-antigenic polypeptide antibody titer produced in the subject is increased by 1-3 log relative to a control.

[0097] In some embodiments, the anti-antigenic polypeptide antibody titer produced in a subject is increased at least 2 times relative to a control. In some embodiments, the anti-antigenic polypeptide antibody titer produced in the subject is increased at least 5 times relative to a control. In some embodiments, the anti-antigenic polypeptide antibody titer produced in the subject is increased at least 10 times relative to a control. In some embodiments, the anti-antigenic polypeptide antibody titer produced in the subject is increased 2-10 times relative to a control.

[0098] In some embodiments, the control is an anti-antigenic polypeptide antibody titer produced in a subject who has not been administered a RNA (e.g., mRNA) vaccine of the present disclosure. In some embodiments, the control is an anti-antigenic polypeptide antibody titer produced in a subject who has been administered a live attenuated or inactivated hMPV, PIV3, RSV, MeV and/or BetaCoV vaccine (see, e.g., Ren J. et al. *J of Gen. Virol.* 2015; 96: 1515-1520), or wherein the control is an anti-antigenic polypeptide antibody titer produced in a subject who has been administered a recombinant or purified hMPV, PIV3, RSV, MeV and/or BetaCoV protein vaccine. In some embodiments, the control is an anti-antigenic polypeptide antibody titer produced in a subject who has been administered a hMPV, PIV3, RSV, MeV and/or BetaCoV virus-like particle (VLP) vaccine (see, e.g., Cox R G et al., *J Virol.* 2014 June; 88(11): 6368-6379).

[0099] A RNA (e.g., mRNA) vaccine of the present disclosure is administered to a subject in an effective amount (an amount effective to induce an immune response). In some embodiments, the effective amount is a dose equivalent to an at least 2-fold, at least 4-fold, at least 10-fold, at least 100-fold, at least 1000-fold reduction in the standard of care dose of a recombinant hMPV, PIV3, RSV, MeV and/or BetaCoV protein vaccine, wherein the anti-antigenic polypeptide antibody titer produced in the subject is equivalent to an anti-antigenic polypeptide antibody titer produced in a control subject administered the standard of care dose of a recombinant hMPV, PIV3, RSV, MeV and/or BetaCoV protein vaccine, a purified hMPV, PIV3, RSV, MeV and/or BetaCoV protein vaccine, a live attenuated hMPV, PIV3, RSV, MeV and/or BetaCoV vaccine, an inactivated hMPV, PIV3, RSV, MeV and/or BetaCoV vaccine, or a hMPV, PIV3, RSV, MeV and/or BetaCoV VLP vaccine. In some embodiments, the effective amount is a dose equivalent to 2-1000-fold reduction in the standard of care dose of a recombinant hMPV, PIV3, RSV, MeV and/or BetaCoV protein vaccine, wherein the anti-antigenic polypeptide antibody titer produced in the subject is equivalent to an anti-antigenic polypeptide antibody titer produced in a control subject administered the standard of care dose of a recombinant hMPV, PIV3, RSV, MeV and/or BetaCoV protein vaccine, a purified hMPV, PIV3, RSV, MeV and/or

BetaCoV protein vaccine, a live attenuated hMPV, PIV3, RSV, MeV and/or BetaCoV vaccine, an inactivated hMPV, PIV3, RSV, MeV and/or BetaCoV vaccine, or a hMPV, PIV3, RSV, MeV and/or BetaCoV VLP vaccine.

[0100] In some embodiments, the control is an anti-antigenic polypeptide antibody titer produced in a subject who has been administered a virus-like particle (VLP) vaccine comprising structural proteins of hMPV, PIV3, RSV, MeV and/or BetaCoV.

[0101] In some embodiments, the RNA (e.g., mRNA) vaccine is formulated in an effective amount to produce an antigen specific immune response in a subject.

[0102] In some embodiments, the effective amount is a total dose of 25 µg to 1000 µg, or 50 µg to 1000 µg. In some embodiments, the effective amount is a total dose of 100 µg. In some embodiments, the effective amount is a dose of 25 µg administered to the subject a total of two times. In some embodiments, the effective amount is a dose of 100 µg administered to the subject a total of two times. In some embodiments, the effective amount is a dose of 400 µg administered to the subject a total of two times. In some embodiments, the effective amount is a dose of 500 µg administered to the subject a total of two times.

[0103] In some embodiments, the efficacy (or effectiveness) of a RNA (e.g., mRNA) vaccine is greater than 60%. In some embodiments, the RNA (e.g., mRNA) polynucleotide of the vaccine at least one hMPV antigenic polypeptide, at least one PIV3 antigenic polypeptide, at least one RSV antigenic polypeptide, at least one MeV antigenic polypeptide, at least one BetaCoV antigenic polypeptide, e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1, or any combination of two or more of the foregoing antigenic polypeptides.

[0104] Vaccine efficacy may be assessed using standard analyses (see, e.g., Weinberg et al., *J Infect Dis.* 2010 Jun. 1; 201(11):1607-10). For example, vaccine efficacy may be measured by double-blind, randomized, clinical controlled trials. Vaccine efficacy may be expressed as a proportionate reduction in disease attack rate (AR) between the unvaccinated (ARU) and vaccinated (ARV) study cohorts and can be calculated from the relative risk (RR) of disease among the vaccinated group with use of the following formulas:

$$\text{Efficacy} = (\text{ARU} - \text{ARV}) / \text{ARU} \times 100; \text{ and}$$

$$\text{Efficacy} = (1 - \text{RR}) \times 100.$$

[0105] Likewise, vaccine effectiveness may be assessed using standard analyses (see, e.g., Weinberg et al., *J Infect Dis.* 2010 Jun. 1; 201(11):1607-10). Vaccine effectiveness is an assessment of how a vaccine (which may have already proven to have high vaccine efficacy) reduces disease in a population. This measure can assess the net balance of benefits and adverse effects of a vaccination program, not just the vaccine itself, under natural field conditions rather than in a controlled clinical trial. Vaccine effectiveness is proportional to vaccine efficacy (potency) but is also affected by how well target groups in the population are immunized, as well as by other non-vaccine-related factors that influence the 'real-world' outcomes of hospitalizations, ambulatory visits, or costs. For example, a retrospective case control analysis may be used, in which the rates of vaccination among a set of infected cases and appropriate controls are compared. Vaccine effectiveness may be expressed as a

rate difference, with use of the odds ratio (OR) for developing infection despite vaccination:

$$\text{Effectiveness} = (1 - \text{OR}) \times 100.$$

[0106] In some embodiments, the efficacy (or effectiveness) of a RNA (e.g., mRNA) vaccine is at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, or at least 90%.

[0107] In some embodiments, the vaccine immunizes the subject against hMPV, PIV3, RSV, MeV, BetaCoV (e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1), or any combination of two or more of the foregoing viruses for up to 2 years. In some embodiments, the vaccine immunizes the subject against hMPV, PIV3, RSV, MeV, BetaCoV (e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1), or any combination of two or more of the foregoing viruses for more than 2 years, more than 3 years, more than 4 years, or for 5-10 years.

[0108] In some embodiments, the subject is about 5 years old or younger. For example, the subject may be between the ages of about 1 year and about 5 years (e.g., about 1, 2, 3, 5 or 5 years), or between the ages of about 6 months and about 1 year (e.g., about 6, 7, 8, 9, 10, 11 or 12 months). In some embodiments, the subject is about 12 months or younger (e.g., 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2 months or 1 month). In some embodiments, the subject is about 6 months or younger. In some embodiments, the subject was born full term (e.g., about 37-42 weeks). In some embodiments, the subject was born prematurely, for example, at about 36 weeks of gestation or earlier (e.g., about 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26 or 25 weeks). For example, the subject may have been born at about 32 weeks of gestation or earlier. In some embodiments, the subject was born prematurely between about 32 weeks and about 36 weeks of gestation. In such subjects, a RNA (e.g., mRNA) vaccine may be administered later in life, for example, at the age of about 6 months to about 5 years, or older.

[0109] In some embodiments, the subject is pregnant (e.g., in the first, second or third trimester) when administered an RNA (e.g., mRNA) vaccine. Viruses such as hMPV, PIV3 and RSV causes infections of the lower respiratory tract, mainly in infants and young children. One-third of RSV related deaths, for example, occur in the first year of life, with 99 percent of these deaths occurring in low-resource countries. It's so widespread in the United States that nearly all children become infected with the virus before their second birthdays. Thus, the present disclosure provides RNA (e.g., mRNA) vaccines for maternal immunization to improve mother-to-child transmission of protection against the virus.

[0110] In some embodiments, the subject is a young adult between the ages of about 20 years and about 50 years (e.g., about 20, 25, 30, 35, 40, 45 or 50 years old).

[0111] In some embodiments, the subject is an elderly subject about 60 years old, about 70 years old, or older (e.g., about 60, 65, 70, 75, 80, 85 or 90 years old).

[0112] In some embodiments, the subject is has a chronic pulmonary disease (e.g., chronic obstructive pulmonary disease (COPD) or asthma). Two forms of COPD include chronic bronchitis, which involves a long-term cough with mucus, and emphysema, which involves damage to the

lungs over time. Thus, a subject administered a RNA (e.g., mRNA) vaccine may have chronic bronchitis or emphysema.

[0113] In some embodiments, the subject has been exposed to hMPV, PIV3, RSV, MeV, BetaCoV (e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1), or any combination of two or more of the foregoing viruses; the subject is infected with hMPV, PIV3, RSV, MeV, BetaCoV (e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1), or any combination of two or more of the foregoing viruses; or subject is at risk of infection by hMPV, PIV3, RSV, MeV, BetaCoV (e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1), or any combination of two or more of the foregoing viruses.

[0114] In some embodiments, the subject is immunocompromised (has an impaired immune system, e.g., has an immune disorder or autoimmune disorder).

[0115] In some embodiments the nucleic acid vaccines described herein are chemically modified. In other embodiments the nucleic acid vaccines are unmodified.

[0116] Yet other aspects provide compositions for and methods of vaccinating a subject comprising administering to the subject a nucleic acid vaccine comprising one or more RNA polynucleotides having an open reading frame encoding a first respiratory virus antigenic polypeptide, wherein the RNA polynucleotide does not include a stabilization element, and wherein an adjuvant is not coformulated or co-administered with the vaccine.

[0117] In other aspects the invention is a composition for or method of vaccinating a subject comprising administering to the subject a nucleic acid vaccine comprising one or more RNA polynucleotides having an open reading frame encoding a first antigenic polypeptide wherein a dosage of between 10 µg/kg and 400 µg/kg of the nucleic acid vaccine is administered to the subject. In some embodiments the dosage of the RNA polynucleotide is 1-5 µg, 5-10 µg, 10-15 µg, 15-20 µg, 10-25 µg, 20-25 µg, 20-50 µg, 30-50 µg, 40-50 µg, 40-60 µg, 60-80 µg, 60-100 µg, 50-100 µg, 80-120 µg, 40-120 µg, 40-150 µg, 50-150 µg, 50-200 µg, 80-200 µg, 100-200 µg, 120-250 µg, 150-250 µg, 180-280 µg, 200-300 µg, 50-300 µg, 80-300 µg, 100-300 µg, 40-300 µg, 50-350 µg, 100-350 µg, 200-350 µg, 300-350 µg, 320-400 µg, 40-380 µg, 40-100 µg, 100-400 µg, 200-400 µg, or 300-400 µg per dose. In some embodiments, the nucleic acid vaccine is administered to the subject by intradermal or intramuscular injection. In some embodiments, the nucleic acid vaccine is administered to the subject on day zero. In some embodiments, a second dose of the nucleic acid vaccine is administered to the subject on day twenty one.

[0118] In some embodiments, a dosage of 25 micrograms of the RNA polynucleotide is included in the nucleic acid vaccine administered to the subject. In some embodiments, a dosage of 100 micrograms of the RNA polynucleotide is included in the nucleic acid vaccine administered to the subject. In some embodiments, a dosage of 50 micrograms of the RNA polynucleotide is included in the nucleic acid vaccine administered to the subject. In some embodiments, a dosage of 75 micrograms of the RNA polynucleotide is included in the nucleic acid vaccine administered to the subject. In some embodiments, a dosage of 150 micrograms of the RNA polynucleotide is included in the nucleic acid

vaccine administered to the subject. In some embodiments, a dosage of 400 micrograms of the RNA polynucleotide is included in the nucleic acid vaccine administered to the subject. In some embodiments, a dosage of 200 micrograms of the RNA polynucleotide is included in the nucleic acid vaccine administered to the subject. In some embodiments, the RNA polynucleotide accumulates at a 100 fold higher level in the local lymph node in comparison with the distal lymph node. In other embodiments the nucleic acid vaccine is chemically modified and in other embodiments the nucleic acid vaccine is not chemically modified.

[0119] Aspects of the invention provide a nucleic acid vaccine comprising one or more RNA polynucleotides having an open reading frame encoding a first antigenic polypeptide, wherein the RNA polynucleotide does not include a stabilization element, and a pharmaceutically acceptable carrier or excipient, wherein an adjuvant is not included in the vaccine. In some embodiments, the stabilization element is a histone stem-loop. In some embodiments, the stabilization element is a nucleic acid sequence having increased GC content relative to wild type sequence.

[0120] Aspects of the invention provide nucleic acid vaccines comprising one or more RNA polynucleotides having an open reading frame encoding a first antigenic polypeptide, wherein the RNA polynucleotide is present in the formulation for in vivo administration to a host, which confers an antibody titer superior to the criterion for seroprotection for the first antigen for an acceptable percentage of human subjects. In some embodiments, the antibody titer produced by the mRNA vaccines of the invention is a neutralizing antibody titer. In some embodiments the neutralizing antibody titer is greater than a protein vaccine. In other embodiments the neutralizing antibody titer produced by the mRNA vaccines of the invention is greater than an adjuvanted protein vaccine. In yet other embodiments the neutralizing antibody titer produced by the mRNA vaccines of the invention is 1,000-10,000, 1,200-10,000, 1,400-10,000, 1,500-10,000, 1,000-5,000, 1,000-4,000, 1,800-10,000, 2,000-10,000, 2,000-5,000, 2,000-3,000, 2,000-4,000, 3,000-5,000, 3,000-4,000, or 2,000-2,500. A neutralization titer is typically expressed as the highest serum dilution required to achieve a 50% reduction in the number of plaques.

[0121] Also provided are nucleic acid vaccines comprising one or more RNA polynucleotides having an open reading frame encoding a first antigenic polypeptide, wherein the RNA polynucleotide is present in a formulation for in vivo administration to a host for eliciting a longer lasting high antibody titer than an antibody titer elicited by an mRNA vaccine having a stabilizing element or formulated with an adjuvant and encoding the first antigenic polypeptide. In some embodiments, the RNA polynucleotide is formulated to produce a neutralizing antibodies within one week of a single administration. In some embodiments, the adjuvant is selected from a cationic peptide and an immunostimulatory nucleic acid. In some embodiments, the cationic peptide is protamine.

[0122] Aspects provide nucleic acid vaccines comprising one or more RNA polynucleotides having an open reading frame comprising at least one chemical modification or optionally no nucleotide modification, the open reading frame encoding a first antigenic polypeptide, wherein the RNA polynucleotide is present in the formulation for in vivo administration to a host such that the level of antigen expression in the host significantly exceeds a level of

antigen expression produced by an mRNA vaccine having a stabilizing element or formulated with an adjuvant and encoding the first antigenic polypeptide.

[0123] Other aspects provide nucleic acid vaccines comprising one or more RNA polynucleotides having an open reading frame comprising at least one chemical modification or optionally no nucleotide modification, the open reading frame encoding a first antigenic polypeptide, wherein the vaccine has at least 10 fold less RNA polynucleotide than is required for an unmodified mRNA vaccine to produce an equivalent antibody titer. In some embodiments, the RNA polynucleotide is present in a dosage of 25-100 micrograms.

[0124] Aspects of the invention also provide a unit of use vaccine, comprising between 10 ug and 400 ug of one or more RNA polynucleotides having an open reading frame comprising at least one chemical modification or optionally no nucleotide modification, the open reading frame encoding a first antigenic polypeptide, and a pharmaceutically acceptable carrier or excipient, formulated for delivery to a human subject. In some embodiments, the vaccine further comprises a cationic lipid nanoparticle.

[0125] Aspects of the invention provide methods of creating, maintaining or restoring antigenic memory to a respiratory virus strain in an individual or population of individuals comprising administering to said individual or population an antigenic memory booster nucleic acid vaccine comprising (a) at least one RNA polynucleotide, said polynucleotide comprising at least one chemical modification or optionally no nucleotide modification and two or more codon-optimized open reading frames, said open reading frames encoding a set of reference antigenic polypeptides, and (b) optionally a pharmaceutically acceptable carrier or excipient. In some embodiments, the vaccine is administered to the individual via a route selected from the group consisting of intramuscular administration, intradermal administration and subcutaneous administration. In some embodiments, the administering step comprises contacting a muscle tissue of the subject with a device suitable for injection of the composition. In some embodiments, the administering step comprises contacting a muscle tissue of the subject with a device suitable for injection of the composition in combination with electroporation.

[0126] Aspects of the invention provide methods of vaccinating a subject comprising administering to the subject a single dosage of between 25 ug/kg and 400 ug/kg of a nucleic acid vaccine comprising one or more RNA polynucleotides having an open reading frame encoding a first antigenic polypeptide in an effective amount to vaccinate the subject.

[0127] Other aspects provide nucleic acid vaccines comprising one or more RNA polynucleotides having an open reading frame comprising at least one chemical modification, the open reading frame encoding a first antigenic polypeptide, wherein the vaccine has at least 10 fold less RNA polynucleotide than is required for an unmodified mRNA vaccine to produce an equivalent antibody titer. In some embodiments, the RNA polynucleotide is present in a dosage of 25-100 micrograms.

[0128] Other aspects provide nucleic acid vaccines comprising an LNP formulated RNA polynucleotide having an open reading frame comprising no nucleotide modifications (unmodified), the open reading frame encoding a first antigenic polypeptide, wherein the vaccine has at least 10 fold less RNA polynucleotide than is required for an unmodified

mRNA vaccine not formulated in a LNP to produce an equivalent antibody titer. In some embodiments, the RNA polynucleotide is present in a dosage of 25-100 micrograms.

[0129] The data presented in the Examples demonstrate significant enhanced immune responses using the formulations of the invention. Both chemically modified and unmodified RNA vaccines are useful according to the invention. Surprisingly, in contrast to prior art reports that it was preferable to use chemically unmodified mRNA formulated in a carrier for the production of vaccines, it is described herein that chemically modified mRNA-LNP vaccines required a much lower effective mRNA dose than unmodified mRNA, i.e., tenfold less than unmodified mRNA when formulated in carriers other than LNP. Both the chemically modified and unmodified RNA vaccines of the invention produce better immune responses than mRNA vaccines formulated in a different lipid carrier.

[0130] In other aspects the invention encompasses a method of treating an elderly subject age 60 years or older comprising administering to the subject a nucleic acid vaccine comprising one or more RNA polynucleotides having an open reading frame encoding a respiratory virus antigenic polypeptide in an effective amount to vaccinate the subject.

[0131] In other aspects the invention encompasses a method of treating a young subject age 17 years or younger comprising administering to the subject a nucleic acid vaccine comprising one or more RNA polynucleotides having an open reading frame encoding a respiratory virus antigenic polypeptide in an effective amount to vaccinate the subject.

[0132] In other aspects the invention encompasses a method of treating an adult subject comprising administering to the subject a nucleic acid vaccine comprising one or more RNA polynucleotides having an open reading frame encoding a respiratory virus antigenic polypeptide in an effective amount to vaccinate the subject.

[0133] In some aspects the invention is a method of vaccinating a subject with a combination vaccine including at least two nucleic acid sequences encoding respiratory antigens wherein the dosage for the vaccine is a combined therapeutic dosage wherein the dosage of each individual nucleic acid encoding an antigen is a sub therapeutic dosage. In some embodiments, the combined dosage is 25 micrograms of the RNA polynucleotide in the nucleic acid vaccine administered to the subject. In some embodiments, the combined dosage is 100 micrograms of the RNA polynucleotide in the nucleic acid vaccine administered to the subject. In some embodiments the combined dosage is 50 micrograms of the RNA polynucleotide in the nucleic acid vaccine administered to the subject. In some embodiments, the combined dosage is 75 micrograms of the RNA polynucleotide in the nucleic acid vaccine administered to the subject. In some embodiments, the combined dosage is 150 micrograms of the RNA polynucleotide in the nucleic acid vaccine administered to the subject. In some embodiments, the combined dosage is 400 micrograms of the RNA polynucleotide in the nucleic acid vaccine administered to the subject. In some embodiments, the sub therapeutic dosage of each individual nucleic acid encoding an antigen is 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 micrograms. In other embodiments the nucleic acid vaccine is chemically modified and in other embodiments the nucleic acid vaccine is not chemically modified.

[0134] The RNA polynucleotide is one of SEQ ID NO: 1-4, 9-12, 20-23, 35-46, 57-61, and 64-80 and includes at least one chemical modification. In other embodiments the RNA polynucleotide is one of SEQ ID NO: 1-4, 9-12, 20-23, 35-46, 57-61, and 64-80 and does not include any nucleotide modifications, or is unmodified. In yet other embodiments the at least one RNA polynucleotide encodes an antigenic protein of any of SEQ ID NO: 5-8, 12-13, 24-34, and 47-50 and includes at least one chemical modification. In other embodiments the RNA polynucleotide encodes an antigenic protein of any of SEQ ID NO: 5-8, 12-13, 24-34, and 47-50 and does not include any nucleotide modifications, or is unmodified.

[0135] In preferred aspects, vaccines of the invention (e.g., LNP-encapsulated mRNA vaccines) produce prophylactically- and/or therapeutically-efficacious levels, concentrations and/or titers of antigen-specific antibodies in the blood or serum of a vaccinated subject. As defined herein, the term antibody titer refers to the amount of antigen-specific antibody produced in a subject, e.g., a human subject. In exemplary embodiments, antibody titer is expressed as the inverse of the greatest dilution (in a serial dilution) that still gives a positive result. In exemplary embodiments, antibody titer is determined or measured by enzyme-linked immunosorbent assay (ELISA). In exemplary embodiments, antibody titer is determined or measured by neutralization assay, e.g., by microneutralization assay. In certain aspects, antibody titer measurement is expressed as a ratio, such as 1:40, 1:100, etc.

[0136] In exemplary embodiments of the invention, an efficacious vaccine produces an antibody titer of greater than 1:40, greater than 1:100, greater than 1:400, greater than 1:1000, greater than 1:2000, greater than 1:3000, greater than 1:4000, greater than 1:500, greater than 1:6000, greater than 1:7500, greater than 1:10000. In exemplary embodiments, the antibody titer is produced or reached by 10 days following vaccination, by 20 days following vaccination, by 30 days following vaccination, by 40 days following vaccination, or by 50 or more days following vaccination. In exemplary embodiments, the titer is produced or reached following a single dose of vaccine administered to the subject. In other embodiments, the titer is produced or reached following multiple doses, e.g., following a first and a second dose (e.g., a booster dose.)

[0137] In exemplary aspects of the invention, antigen-specific antibodies are measured in units of $\mu\text{g/ml}$ or are measured in units of IU/L (International Units per liter) or mIU/ml (milli International Units per ml). In exemplary embodiments of the invention, an efficacious vaccine produces $>0.5 \mu\text{g/ml}$, $>0.1 \mu\text{g/ml}$, $>0.2 \mu\text{g/ml}$, $>0.35 \mu\text{g/ml}$, $>0.5 \mu\text{g/ml}$, $>1 \mu\text{g/ml}$, $>2 \mu\text{g/ml}$, $>5 \mu\text{g/ml}$ or $>10 \mu\text{g/ml}$. In exemplary embodiments of the invention, an efficacious vaccine produces $>10 \text{ mIU/ml}$, $>20 \text{ mIU/ml}$, $>50 \text{ mIU/ml}$, $>100 \text{ mIU/ml}$, $>200 \text{ mIU/ml}$, $>500 \text{ mIU/ml}$ or $>1000 \text{ mIU/ml}$. In exemplary embodiments, the antibody level or concentration is produced or reached by 10 days following vaccination, by 20 days following vaccination, by 30 days following vaccination, by 40 days following vaccination, or by 50 or more days following vaccination. In exemplary embodiments, the level or concentration is produced or reached following a single dose of vaccine administered to the subject. In other embodiments, the level or concentration is produced or reached following multiple doses, e.g., following a first and a second dose (e.g., a booster dose.) In

exemplary embodiments, antibody level or concentration is determined or measured by enzyme-linked immunosorbent assay (ELISA). In exemplary embodiments, antibody level or concentration is determined or measured by neutralization assay, e.g., by microneutralization assay.

[0138] The details of various embodiments of the disclosure are set forth in the description below. Other features, objects, and advantages of the disclosure will be apparent from the description and from the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

[0139] The foregoing and other objects, features and advantages will be apparent from the following description of particular embodiments of the disclosure, as illustrated in the accompanying drawings in which like reference characters refer to the same parts throughout the different views. The drawings are not necessarily to scale, emphasis instead being placed upon illustrating the principles of various embodiments of the disclosure.

[0140] FIG. 1 shows a schematic of one example of a RNA (e.g. mRNA) vaccine construct of the present disclosure. The construct depicts a human metapneumovirus and human respiratory syncytial virus full length fusion protein obtained from wild-type strains (*The Journal of General Virology*. 2008; 89(Pt 12):3113-3118, incorporated herein by reference).

[0141] FIGS. 2A-2C are graphs showing the levels of anti-hMPV fusion protein-specific antibodies in the serum of mice immunized with hMPV mRNA vaccines on day 0 (FIG. 2A), day 14 (FIG. 2B) and day 35 (FIG. 2C) post immunization. The mice were immunized with a single dose ($2 \mu\text{g}$ or $10 \mu\text{g}$) on day 0 and were given a boost dose ($2 \mu\text{g}$ or $10 \mu\text{g}$) on day 21, hMPV fusion protein-specific antibodies were detected at up to 1:10000 dilution of serum on day 35 for both doses.

[0142] FIGS. 3A-3C are graphs showing the result of IgG isotyping in the serum of mice immunized with hMPV mRNA vaccines. The levels of hMPV fusion protein-specific IgG2a (FIG. 3A) and IgG1 (FIG. 3B) antibodies in the serum are measured by ELISA. FIG. 3C shows that hMPV fusion protein mRNA vaccine induced a mixed Th1/Th2 cytokine response with a Th1 bias.

[0143] FIG. 4 is a graph showing in vitro neutralization of a hMPV B2 strain (TN/91-316) using the sera of mice immunized with a mRNA vaccine encoding hMPV fusion protein. Mouse serum obtained from mice receiving a $10 \mu\text{g}$ or a $2 \mu\text{g}$ dose contained hMPV-neutralizing antibodies.

[0144] FIGS. 5A-5C are graphs showing a Th1 cytokine response induced by a hMPV fusion peptide pool (15-mers-50 (overlap)) in splenocytes isolated from mice immunized with the hMPV mRNA vaccines. Virus-free media was used as a negative control and Concanavalin A (ConA, a positive control for splenocyte stimulation) was included. The cytokines tested included IFN- γ (FIG. 5A), IL-2 (FIG. 5B) and IL12 (FIG. 5C).

[0145] FIGS. 6A-6E are graphs showing the Th2 cytokine response induced by a hMPV fusion peptide pool (15-mers-50) in splenocytes isolated from mice immunized with the hMPV mRNA vaccines. Virus-free media was used as a negative control and Concanavalin A was also included. The cytokines tested included IL-10 (FIG. 6A), TNF- α (FIG. 6B), IL4 (FIG. 6C), IL-5 (FIG. 6D) and IL-6 (FIG. 6E).

[0146] FIGS. 7A-7C are graphs showing the Th1 response induced by inactivated hMPV virus in splenocytes isolated

from mice immunized with hMPV mRNA vaccines. Virus-free media was used as a negative control and Concanavalin A was included. The cytokines tested included IFN- γ (FIG. 7A), IL-2 (FIG. 7B) and IL12 (FIG. 7C).

[0147] FIGS. 8A-8E are graphs showing the Th2 response induced by inactivated hMPV virus in splenocytes isolated from mice immunized with the hMPV mRNA vaccines. Virus-free media was used as a negative control and Concanavalin A was included. The cytokines tested include IL-10 (FIG. 8A), TNF- α (FIG. 8B), IL4 (FIG. 8C), IL-5 (FIG. 8D) and IL-6 (FIG. 8E).

[0148] FIGS. 9A-9B are graphs showing the results of cotton rat challenge experiments. Two different doses of the hMPV mRNA vaccines were used (2 μ g or 10 μ g doses) to immunize the cotton rats before challenge. The hMPV mRNA vaccines reduced the viral titer in the lung and nose of the cotton rat, with the 10 μ g dose being more effective in reducing viral titer. Use of a 10 μ g dose resulted in 100% protection in the lung and a ~2 log reduction in nose viral titer. Use of a 2 μ g dose resulted in a 1 log reduction in lung viral titer and no reduction in nose viral titer. The vaccine was administered on Day 0, and a boost was administered on Day 21.

[0149] FIG. 10 is a graph showing the lung histopathology of cotton rats that received hMPV mRNA vaccines. Pathology associated with vaccine-enhanced disease was not observed in immunized groups.

[0150] FIG. 11 is a graph showing hMPV neutralization antibody titers in cotton rats that received hMPV mRNA vaccines (2 μ g or 10 μ g doses) on days 35 and 42 post immunization.

[0151] FIG. 12 is a graph showing the lung and nose viral load in cotton rats challenged with a hMPV/A2 strain after immunization with the indicated mRNA vaccines (hMPV mRNA vaccine or hMPV/PIV mRNA combination vaccine). Vaccinated cotton rats showed reduced lung and nose viral loads after challenge, compared to control.

[0152] FIG. 13 is a graph showing the lung and nose viral load in cotton rats challenged with PIV3 strain after immunization with indicated mRNA vaccines (PIV mRNA vaccine or hMPV/PIV combination vaccine). Vaccinated cotton rats showed reduced lung and nose viral loads after challenge, compared to control.

[0153] FIG. 14 is a graph showing hMPV neutralizing antibody titers in cotton rats that received different dosages of hMPV mRNA vaccines or hMPV/PIV combination mRNA vaccines on day 42 post immunization. The dosages of the vaccine are indicated in Table 9.

[0154] FIG. 15 is a graph showing PIV3 neutralizing antibody titers in cotton rats that received different dosages of PIV mRNA vaccines or hMPV/PIV combination mRNA vaccines on day 42 post immunization. The dosages of the vaccine are indicated in Table 9.

[0155] FIG. 16 is a graph showing the lung histopathology score of cotton rats immunized with hMPV mRNA vaccines, PIV mRNA vaccines or hMPV/PIV combination mRNA vaccines as indicated in Table 9. Low occurrence of alveolitis and interstitial pneumonia was observed, indicating no antibody-dependent enhancement (ADE) of hMPV associated diseases.

[0156] FIG. 17 is a graph showing the reciprocal MERS-CoV neutralizing antibody titers in mice immunized with

betacoronavirus mRNA vaccine encoding the MERS-CoV full-length Spike protein, on days 0, 21, 42, and 56 post immunization.

[0157] FIG. 18 is a graph showing the reciprocal MERS-CoV neutralizing antibody titers in mice immunized with betacoronavirus mRNA vaccine encoding either the MERS-CoV full-length Spike protein, or the S2 subunit of the Spike protein. The full length spike protein induced a stronger immune response compared to the S2 subunit alone.

[0158] FIGS. 19A-19C are graphs showing the viral load in the nose and throat, the bronchoalveolar lavage (BAL), or the lungs of New Zealand white rabbits 4 days post challenge with MERS-CoV. The New Zealand white rabbits were immunized with one 20 μ g-dose (on day 0) or two 20 μ g-doses (on day 0 and 21) of MERS-CoV mRNA vaccine encoding the full-length Spike protein before challenge. FIG. 19A shows that two doses of MERS-CoV mRNA vaccine resulted in a 3 log reduction of viral load in the nose and led to complete protection in the throat of the New Zealand white rabbits. FIG. 19B shows that two doses of MERS-CoV mRNA vaccine resulted in a 4 log reduction of viral load in the BAL of the New Zealand white rabbits. FIG. 19C shows one dose of MERS-CoV mRNA vaccine resulted in a 2 log reduction of viral load, while two doses of MERS-CoV mRNA vaccine resulted in an over 4 log reduction of viral load in the lungs of the New Zealand white rabbits.

[0159] FIGS. 20A-20B are images and graphs showing viral load or replicating virus detected by PCR in the lungs of New Zealand white rabbits 4 days post challenge with MERS-CoV. The New Zealand white rabbits were immunized with a single 20 μ g dose (on day 0, Group 1a) of MERS-CoV mRNA vaccine encoding the full-length Spike protein, two 20 μ g doses (on day 0 and 21, Group 1b) of MERS-CoV mRNA vaccine encoding the full-length Spike protein, or placebo (Group 2) before challenge. FIG. 20A shows that two doses of 20 μ g a MERS-CoV mRNA vaccine reduced over 99% (2 log) of viruses in the lungs of New Zealand white rabbits. FIG. 20B shows that the group of New Zealand white rabbits that received 2 doses of 20 μ g MERS-CoV mRNA vaccine did not have any detectable replicating MERS-CoV virus in their lungs.

[0160] FIG. 21 is a graph showing the MERS-CoV neutralizing antibody titers in New Zealand white rabbits immunized with MERS-CoV mRNA vaccine encoding the full-length Spike protein. The results show that two doses of 20 μ g MERS-CoV mRNA vaccine induced a significant amount of neutralizing antibodies against MERS-CoV (EC_{50} between 500-1000). The MERS-CoV mRNA vaccine induced antibody titer is 3-5 fold better than any other vaccines tested in the same model.

DETAILED DESCRIPTION

[0161] The present disclosure provides, in some embodiments, vaccines that comprise RNA (e.g., mRNA) polynucleotides encoding a human metapneumovirus (hMPV) antigenic polypeptide, a parainfluenza virus type 3 (PIV3) antigenic polypeptide, a respiratory syncytial virus (RSV) antigenic polypeptide, a measles virus (MeV) antigenic polypeptide, or a betacoronavirus antigenic polypeptide (e.g., Middle East respiratory syndrome coronavirus (MERS-CoV), SARS-CoV, human coronavirus (HCoV)-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH (New Haven) and HCoV-HKU1) (see, e.g., Esper F. et al.

Emerging Infectious Diseases, 12(5), 2006; and Pyrc K. et al. *Journal of Virology*, 81(7):3051-57, 2007, the contents of each of which is here incorporated by reference in their entirety). The present disclosure also provides, in some embodiments, combination vaccines that comprise at least one RNA (e.g., mRNA) polynucleotide encoding at least two antigenic polypeptides selected from hMPV antigenic polypeptides, PIV3 antigenic polypeptides, RSV antigenic polypeptides, MeV antigenic polypeptides and BetaCoV antigenic polypeptides. Also provided herein are methods of administering the RNA (e.g., mRNA) vaccines, methods of producing the RNA (e.g., mRNA) vaccines, compositions (e.g., pharmaceutical compositions) comprising the RNA (e.g., mRNA) vaccines, and nucleic acids (e.g., DNA) encoding the RNA (e.g., mRNA) vaccines. In some embodiments, a RNA (e.g., mRNA) vaccine comprises an adjuvant, such as a flagellin adjuvant, as provided herein.

[0162] The RNA (e.g., mRNA) vaccines (e.g., hMPV, PIV3, RSV, MeV, BetaCoV RNA vaccines and combinations thereof), in some embodiments, may be used to induce a balanced immune response, comprising both cellular and humoral immunity, without many of the risks associated with DNA vaccination.

[0163] The entire contents of International Application No. PCT/US2015/02740 is incorporated herein by reference.

Human Metapneumovirus (hMPV)

[0164] hMPV shares substantial homology with respiratory syncytial virus (RSV) in its surface glycoproteins. hMPV fusion protein (F) is related to other paramyxovirus fusion proteins and appears to have homologous regions that may have similar functions. The hMPV fusion protein amino acid sequence contains features characteristic of other paramyxovirus F proteins, including a putative cleavage site and potential N-linked glycosylation sites. Paramyxovirus fusion proteins are synthesized as inactive precursors (F0) that are cleaved by host cell proteases into the biologically fusion-active F1 and F2 domains (see, e.g., Cseke G. et al. *Journal of Virology* 2007; 81(2):698-707, incorporated herein by reference). hMPV has one putative cleavage site, in contrast to the two sites established for RSV F, and only shares 34% amino acid sequence identity with RSV F. F2 is extracellular and disulfide linked to F1. Fusion proteins are type I glycoproteins existing as trimers, with two 4-3 heptad repeat domains at the N- and C-terminal regions of the protein (HR1 and HR2), which form coiled-coil alpha-helices. These coiled coils become apposed in an antiparallel fashion when the protein undergoes a conformational change into the fusogenic state. There is a hydrophobic fusion peptide N proximal to the N-terminal heptad repeat, which is thought to insert into the target cell membrane, while the association of the heptad repeats brings the trans-membrane domain into close proximity, inducing membrane fusion (see, e.g., Baker, K A et al. *Mol. Cell* 1999; 3:309-319). This mechanism has been proposed for a number of different viruses, including RSV, influenza virus, and human immunodeficiency virus. Fusion proteins are major antigenic determinants for all known paramyxoviruses and for other viruses that possess similar fusion proteins such as human immunodeficiency virus, influenza virus, and Ebola virus.

[0165] In some embodiments, a hMPV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding hMPV fusion protein (F). In some

embodiments, a hMPV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding a F1 or F2 subunit of a hMPV F protein. In some embodiments, a hMPV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding hMPV glycoprotein (G). In some embodiments, a hMPV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding hMPV matrix protein (M). In some embodiments, a hMPV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding hMPV phosphoprotein (P). In some embodiments, a hMPV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding hMPV nucleoprotein (N). In some embodiments, a hMPV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding hMPV SH protein (SH).

[0166] In some embodiments, a hMPV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein, G protein, M protein, P protein, N protein and SH protein.

[0167] In some embodiments, a hMPV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein and G protein. In some embodiments, a hMPV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein and M protein. In some embodiments, a hMPV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein and P protein. In some embodiments, a hMPV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein and N protein. In some embodiments, a hMPV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein and SH protein.

[0168] In some embodiments, a hMPV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding G protein and M protein. In some embodiments, a hMPV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding G protein and P protein. In some embodiments, a hMPV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding G protein and N protein. In some embodiments, a hMPV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding G protein and SH protein.

[0169] In some embodiments, a hMPV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein, G protein and M protein. In some embodiments, a hMPV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein, G protein and P protein. In some embodiments, a hMPV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein, G protein and N protein. In some embodiments, a hMPV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein, G protein and SH protein.

[0170] A hMPV vaccine may comprise, for example, at least one RNA (e.g., mRNA) polynucleotide having an open reading frame encoding at least one hMPV antigenic polypeptide identified by any one of SEQ ID NO: 5-8 (Table 3; see also amino acid sequences of Table 4).

[0171] A hMPV vaccine may comprise, for example, at least one RNA (e.g., mRNA) polynucleotide encoded by a nucleic acid (e.g., DNA) identified by any one of SEQ ID NO: 1-4 (Table 2).

[0172] The present disclosure is not limited by a particular strain of hMPV. The strain of hMPV used in a vaccine may be any strain of hMPV. Non-limiting examples of strains of hMPV for use as provide herein include the CAN98-75 (CAN75) and the CAN97-83 (CAN83) hMPV strains (Skidopoulos M H et al. *J Virol.* 20014; 78(13):6927-37, incorporated herein by reference), a hMPV A1, A2, B1 or B2 strain (see, e.g., de Graaf M et al. *The Journal of General Virology* 2008; 89:975-83; Peret TCT et al. *The Journal of Infectious Disease* 2002; 185:1660-63, incorporated herein by reference), a hMPV isolate TN/92-4 (e.g., SEQ ID NO: 1 and 5), a hMPV isolate NL/1/99 (e.g., SEQ ID NO: 2 and 6), or a hMPV isolate PER/CFI0497/2010/B (e.g., SEQ ID NO: 3 and 7).

[0173] In some embodiments, at least one hMPV antigenic polypeptide is obtained from a hMPV A1, A2, B1 or B2 strain (see, e.g., de Graaf M et al. *The Journal of General Virology* 2008; 89:975-83; Peret T C T et al. *The Journal of Infectious Disease* 2002; 185:1660-63, incorporated herein by reference). In some embodiments, at least one antigenic polypeptide is obtained from the CAN98-75 (CAN75) hMPV strain. In some embodiments, at least one antigenic polypeptide is obtained from the CAN97-83 (CAN83) hMPV strain. In some embodiments, at least one antigenic polypeptide is obtained from hMPV isolate TN/92-4 (e.g., SEQ ID NO: 1 and 5). In some embodiments, at least one antigenic polypeptide is obtained from hMPV isolate NL/1/99 (e.g., SEQ ID NO: 2 and 6). In some embodiments, at least one antigenic polypeptide is obtained from hMPV isolate PER/CFI0497/2010/B (e.g., SEQ ID NO: 3 and 7).

[0174] In some embodiments, hMPV vaccines comprise RNA (e.g., mRNA) polynucleotides encoding a hMPV antigenic polypeptides having at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identity with hMPV F protein and having F protein activity.

[0175] A protein is considered to have F protein activity if, for example, the protein acts to fuse the viral envelope and host cell plasma membrane, mediates viral entry into a host cell via an interaction with arginine-glycine-aspartate RGD-binding integrins, or a combination thereof (see, e.g., Cox R G et al. *J Virol.* 2012; 88(22):12148-60, incorporated herein by reference).

[0176] In some embodiments, hMPV vaccines comprise RNA (e.g., mRNA) polynucleotides encoding hMPV antigenic polypeptides having at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identity with hMPV G protein and having G protein activity.

[0177] A protein is considered to have G protein activity if, for example, the protein acts to modulate (e.g., inhibit) hMPV-induced cellular (immune) responses (see, e.g., Bao X et al. *PLoS Pathog.* 2008; 4(5):e1000077, incorporated herein by reference).

Human Parainfluenza Virus Type 3 (PIV3)

[0178] Parainfluenza viruses belong to the family Paramyxoviridae. These are enveloped viruses with a negative-sense single-stranded RNA genome. Parainfluenza viruses belong to the subfamily Paramyxoviridae, which is subdivided into three genera: Respirovirus (PIV-1, PIV-3, and Sendai virus (SeV)), Rubulavirus (PIV-2, PIV-4 and

mumps virus) and Morbillivirus (measles virus, rinderpest virus and canine distemper virus (CDV)). Their genome, a ~15 500 nucleotide-long negative-sense RNA molecule, encodes two envelope glycoproteins, the hemagglutinin-neuraminidase (HN), the fusion protein (F or F0), which is cleaved into F1 and F2 subunits, a matrix protein (M), a nucleocapsid protein (N) and several nonstructural proteins including the viral replicase (L). All parainfluenza viruses, except for PIV-1, express a non-structural V protein that blocks IFN signaling in the infected cell and acts therefore as a virulence factor (see, e.g., Nishio M et al. *J Virol.* 2008; 82(13):6130-38).

[0179] PIV3 hemagglutinin-neuraminidase (HN), a structural protein, is found on the viral envelope, where it is necessary for attachment and cell entry. It recognizes and binds to sialic acid-containing receptors on the host cell's surface. As a neuraminidase, HN removes sialic acid from virus particles, preventing self-aggregation of the virus, and promoting the efficient spread of the virus. Furthermore, HN promotes the activity of the fusion (F or F0) protein, contributing to the penetration of the host cell's surface.

[0180] PIV3 fusion protein (PIV3 F) is located on the viral envelope, where it facilitates the viral fusion and cell entry. The F protein is initially inactive, but proteolytic cleavage leads to its active forms, F1 and F2, which are linked by disulfide bonds. This occurs when the HN protein binds its receptor on the host cell's surface. During early phases of infection, the F glycoprotein mediates penetration of the host cell by fusion of the viral envelope to the plasma membrane. In later stages of the infection, the F protein facilitates the fusion of the infected cells with neighboring uninfected cells, which leads to the formation of a syncytium and spread of the infection.

[0181] PIV3 matrix protein (M) is found within the viral envelope and assists with viral assembly. It interacts with the nucleocapsid and envelope glycoproteins, where it facilitates the budding of progeny viruses through its interactions with specific sites on the cytoplasmic tail of the viral glycoproteins and nucleocapsid. It also plays a role in transporting viral components to the budding site.

[0182] PIV3 phosphoprotein (P) and PIV3 large polymerase protein (L) are found in the nucleocapsid where they form part of the RNA polymerase complex. The L protein, a viral RNA-dependent RNA polymerase, facilitates genomic transcription, while the host cell's ribosomes translate the viral mRNA into viral proteins.

[0183] PIV3 V is a non-structural protein that blocks IFN signaling in the infected cell, therefore acting as a virulence factor.

[0184] PIV3 nucleoprotein (N) encapsidates the genome in a ratio of 1 N per 6 ribonucleotides, protecting it from nucleases. The nucleocapsid (NC) has a helical structure. The encapsidated genomic RNA is termed the NC and serves as template for transcription and replication. During replication, encapsidation by PIV3 N is coupled to RNA synthesis and all replicative products are resistant to nucleases. PIV3 N homo-multimerizes to form the nucleocapsid and binds to viral genomic RNA. PIV3 N binds the P protein and thereby positions the polymerase on the template.

[0185] In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding PIV3 fusion protein (F). In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding a

F1 or F2 subunit of a PIV3 F protein. In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding PIV3 hemagglutinin-neuraminidase (HN) (see, e.g., van Wyke Coelingh K L et al. *J Virol.* 1987; 61(5):1473-77, incorporated herein by reference). In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding PIV3 matrix protein (M). In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding PIV3 phosphoprotein (P). In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding PIV3 nucleoprotein (N).

[0186] In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein, HN protein, M protein, P protein, and N protein.

[0187] In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein and HN protein. In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein and M protein. In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein and P protein. In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein and N protein.

[0188] In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding HN protein and M protein. In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding HN protein and P protein. In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding HN protein and N protein.

[0189] In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein, HN protein and M protein. In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein, HN protein and P protein. In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein, HN protein and N protein.

[0190] A PIV3 vaccine may comprise, for example, at least one RNA (e.g., mRNA) polynucleotide having an open reading frame encoding at least one PIV3 antigenic polypeptide identified by any one of SEQ ID NO: 12-13 (Table 6; see also amino acid sequences of Table 7).

[0191] A PIV3 vaccine may comprise, for example, at least one RNA (e.g., mRNA) polynucleotide encoded by a nucleic acid (e.g., DNA) identified by any one of SEQ ID NO: 9-12 (Table 5; see also nucleic acid sequences of Table 7).

[0192] The present disclosure is not limited by a particular strain of PIV3. The strain of PIV3 used in a vaccine may be any strain of PIV3. A non-limiting example of a strain of PIV3 for use as provide herein includes HPIV3/Homo sapiens/PER/FLA4815/2008.

[0193] In some embodiments, PIV3 vaccines comprise RNA (e.g., mRNA) polynucleotides encoding a PIV3 antigenic polypeptides having at least 95%, at least 96%, at least

97%, at least 98% or at least 99% identity with PIV3 F protein and having F protein activity.

[0194] In some embodiments, PIV3 vaccines comprise RNA (e.g., mRNA) polynucleotides encoding PIV3 antigenic polypeptides having at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identity with PIV3 hemagglutinin-neuraminidase (HN) and having hemagglutinin-neuraminidase activity.

[0195] A protein is considered to have hemagglutinin-neuraminidase activity if, for example, it is capable of both receptor binding and receptor cleaving. Such proteins are major surface glycoproteins that have functional sites for cell attachment and for neuraminidase activity. They are able to cause red blood cells to agglutinate and to cleave the glycosidic linkages of neuraminic acids, so they have the potential to both bind a potential host cell and then release the cell if necessary, for example, to prevent self-aggregation of the virus.

[0196] In some embodiments, PIV3 vaccines comprise RNA (e.g., mRNA) polynucleotides encoding PIV3 antigenic polypeptides having at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identity with PIV3 HN, F (e.g., F, F1 or F2), M, N, L or V and having HN, F (e.g., F, F1 or F2), M, N, L or V activity, respectively.

Respiratory Syncytial Virus (RSV)

[0197] RSV is a negative-sense, single-stranded RNA virus of the genus *Pneumovirinae*. The virus is present in at least two antigenic subgroups, known as Group A and Group B, primarily resulting from differences in the surface G glycoproteins. Two RSV surface glycoproteins—G and F—mediate attachment with and attachment to cells of the respiratory epithelium. F surface glycoproteins mediate coalescence of neighboring cells. This results in the formation of syncytial cells. RSV is the most common cause of bronchiolitis. Most infected adults develop mild cold-like symptoms such as congestion, low-grade fever, and wheezing. Infants and small children may suffer more severe symptoms such as bronchiolitis and pneumonia. The disease may be transmitted among humans via contact with respiratory secretions.

[0198] The genome of RSV encodes at least three surface glycoproteins, including F, G, and SH, four nucleocapsid proteins, including L, P, N, and M2, and one matrix protein, M. Glycoprotein F directs viral penetration by fusion between the virion and the host membrane. Glycoprotein G is a type II transmembrane glycoprotein and is the major attachment protein. SH is a short integral membrane protein. Matrix protein M is found in the inner layer of the lipid bilayer and assists virion formation. Nucleocapsid proteins L, P, N, and M2 modulate replication and transcription of the RSV genome. It is thought that glycoprotein G tethers and stabilizes the virus particle at the surface of bronchial epithelial cells, while glycoprotein F interacts with cellular glycosaminoglycans to mediate fusion and delivery of the RSV virion contents into the host cell (Krzyszaniak M A et al. *PLoS Pathog* 2013; 9(4)).

[0199] In some embodiments, a RSV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein. In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding G protein. In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding L

protein. In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding P protein. In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding N protein. In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding M2 protein. In some embodiments, a PIV3 vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding M protein.

[0200] In some embodiments, a RSV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein, G protein, L protein, P protein, N protein, M2 protein and M protein.

[0201] In some embodiments, a RSV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein and G protein. In some embodiments, a RSV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein and L protein. In some embodiments, a RSV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein and P protein. In some embodiments, a RSV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein and N protein. In some embodiments, a RSV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein and M2 protein. In some embodiments, a RSV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein and M protein.

[0202] In some embodiments, a RSV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding G protein and L protein. In some embodiments, a RSV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding G protein and P protein. In some embodiments, a RSV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding G protein and N protein. In some embodiments, a RSV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding G protein and M2 protein. In some embodiments, a RSV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding G protein and M protein.

[0203] In some embodiments, a RSV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein, G protein and L protein. In some embodiments, a RSV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein, G protein and P protein. In some embodiments, a RSV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein, G protein and N protein. In some embodiments, a RSV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein, G protein and M2 protein. In some embodiments, a RSV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein, G protein and M protein.

[0204] The present disclosure is not limited by a particular strain of RSV. The strain of RSV used in a vaccine may be any strain of RSV.

[0205] In some embodiments, RSV vaccines comprise RNA (e.g., mRNA) polynucleotides encoding a RSV antigenic polypeptides having at least 95%, at least 96%, at least

97%, at least 98% or at least 99% identity with RSV F protein and having F protein activity.

[0206] In some embodiments, RSV vaccines comprise RNA (e.g., mRNA) polynucleotides encoding RSV antigenic polypeptides having at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identity with RSV G protein and having G protein activity.

[0207] A protein is considered to have G protein activity if, for example, the protein acts to modulate (e.g., inhibit) hMPV-induced cellular (immune) responses (see, e.g., Bao X et al. *PLoS Pathog.* 2008; 4(5):e1000077, incorporated herein by reference).

Measles Virus (MeV)

[0208] Molecular epidemiologic investigations and virologic surveillance contribute notably to the control and prevention of measles. Nearly half of measles-related deaths worldwide occur in India, yet virologic surveillance data are incomplete for many regions of the country. Previous studies have documented the presence of measles virus genotypes D4, D7, and D8 in India, and genotypes D5, D9, D11, H1, and G3 have been detected in neighboring countries. Recently, MeV genotype B3 was detected in India (Kuttiatt V S et al. *Emerg Infect Dis.* 2014; 20(10): 1764-66).

[0209] The glycoprotein complex of paramyxoviruses mediates receptor binding and membrane fusion. In particular, the MeV fusion (F) protein executes membrane fusion, after receptor binding by the hemagglutinin (HA) protein (Muhlebach M D et al. *Journal of Virology* 2008; 82(22): 11437-45). The MeV P gene codes for three proteins: P, an essential polymerase cofactor, and V and C, which have multiple functions but are not strictly required for viral propagation in cultured cells. V shares the amino-terminal domain with P but has a zinc-binding carboxyl-terminal domain, whereas C is translated from an overlapping reading frame. The MeV C protein is an infectivity factor. During replication, the P protein binds incoming monomeric nucleocapsid (N) proteins with its amino-terminal domain and positions them for assembly into the nascent ribonucleocapsid. The P protein amino-terminal domain is natively unfolded (Deveaux P et al. *Journal of Virology* 2004; 78(21): 11632-40).

[0210] In some embodiments, a MeV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding HA protein. In some embodiments, a MeV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein. In some embodiments, a MeV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding P protein. In some embodiments, a MeV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding V protein. In some embodiments, a MeV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding C protein.

[0211] In some embodiments, a MeV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding HA protein, F protein, P protein, V protein and C protein.

[0212] In some embodiments, a MeV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding HA protein and F protein. In some embodiments, a MeV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding HA protein and P protein. In some embodiments, a MeV

vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding HA protein and V protein. In some embodiments, a MeV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding HA protein and C protein.

[0213] some embodiments, a MeV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein and P protein. In some embodiments, a MeV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein and V protein. In some embodiments, a MeV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding F protein and C protein.

[0214] In some embodiments, a MeV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding HA protein, F protein and P protein. In some embodiments, a MeV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding HA protein, F protein and V protein. In some embodiments, a MeV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding HA protein, F protein and C protein.

[0215] In some embodiments, MeV vaccines comprise RNA (e.g., mRNA) encoding a MeV antigenic polypeptide having at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identity with MeV HA protein and having MeV HA protein activity.

[0216] In some embodiments, MeV vaccines comprise RNA (e.g., mRNA) encoding a MeV antigenic polypeptide having at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identity with MeV F protein and having MeV F protein activity.

[0217] A protein is considered to have HA protein activity if the protein mediates receptor binding and/or membrane fusion. MeV F protein executes membrane fusion, after receptor binding by the MeV HA protein.

[0218] A MeV vaccine may comprise, for example, at least one RNA (e.g., mRNA) polynucleotide having an open reading frame encoding at least one MeV antigenic polypeptide identified by any one of SEQ ID NO: 47-50 (Table 14; see also amino acid sequences of Table 15).

[0219] A MeV vaccine may comprise, for example, at least one RNA (e.g., mRNA) polynucleotide identified by any one of SEQ ID NO: 37, 40, 43, 46 (Table 13).

[0220] A MeV vaccine may comprise, for example, at least one RNA (e.g., mRNA) polynucleotide encoded by a nucleic acid (e.g., DNA) identified by any one of SEQ ID NO: 35, 36, 38, 39, 41, 42, 44 and 45 (Table 13).

[0221] The present disclosure is not limited by a particular strain of MeV. The strain of MeV used in a vaccine may be any strain of MeV. Non-limiting examples of strains of MeV for use as provide herein include B3/B3.1, C2, D4, D6, D7, D8, G3, H1, Moraten, Rubeovax, MVi/New Jersey.USA/45.05, MVi/Texas.USA/4.07, AIK-C, MVi/New York.USA/26.09/3, MVi/California.USA/16.03, MVi/Virginia.USA/15.09, MVi/California.USA/8.04, and MVi/Pennsylvania.USA/20.09.

[0222] MeV proteins may be from MeV genotype D4, D5, D7, D8, D9, D11, H1, G3 or B3. In some embodiments, a MeV HA protein or a MeV F protein is from MeV genotype D8. In some embodiments, a MeV HA protein or a MeV F protein is from MeV genotype B3.

Betacoronaviruses (BetaCoV)

[0223] MERS-Co V. MERS-CoV is a positive-sense, single-stranded RNA virus of the genus *Betacoronavirus*. The genomes are phylogenetically classified into two clades, clade A and clade B. It has a strong tropism for non-ciliated bronchial epithelial cells, evades the innate immune response and antagonizes interferon (IFN) production in infected cells. Dipeptyl peptidase 4 (DDP4, also known as CD26) has been identified as a functional cellular receptor for MERS-CoV. Its enzymatic activity is not required for infection, although its amino acid sequence is highly conserved across species and is expressed in the human bronchial epithelium and kidneys. Most infected individuals develop severe acute respiratory illnesses, including fever, cough, and shortness of breath, and the virus can be fatal. The disease may be transmitted among humans, generally among those in close contact.

[0224] The genome of MERS-CoV encodes at least four unique accessory proteins, such as 3, 4a, 4b and 5, two replicase proteins (open reading frame 1a and 1b), and four major structural proteins, including spike (S), envelope (E), nucleocapsid (N), and membrane (M) proteins (Almazan F et al. *MBio* 2013; 4(5):e00650-13). The accessory proteins play nonessential roles in MERS-CoV replication, but they are likely structural proteins or interferon antagonists, modulating in vivo replication efficiency and/or pathogenesis, as in the case of SARS-CoV (Almazan F et al. *MBio* 2013; 4(5):e00650-13; Totura A L et al. *Curr Opin Virol* 2012; 2(3):264-75; Scobey T et al. *Proc Natl Acad Sci USA* 2013; 110(40):16157-62). The other proteins of MERS-CoV maintain different functions in virus replication. The E protein, for example, involves in virulence, and deleting the E-coding gene results in replication-competent and propagation-defective viruses or attenuated viruses (Almazan F et al. *MBio* 2013; 4(5):e00650-13). The S protein is particularly essential in mediating virus binding to cells expressing receptor dipeptidyl peptidase-4 (DPP4) through receptor-binding domain (RBD) in the S1 subunit, whereas the S2 subunit subsequently mediates virus entry via fusion of the virus and target cell membranes (Li F. *J Virol* 2015; 89(4): 1954-64; Raj V S et al. *Nature* 2013; 495(7440):251-4).

[0225] In some embodiments, a MERS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding S protein. In some embodiments, a MERS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding the S1 subunit of the S protein. In some embodiments, a MERS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding the S2 subunit of the S protein. In some embodiments, a MERS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding E protein. In some embodiments, a MERS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding N protein. In some embodiments, a MERS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding M protein.

[0226] In some embodiments, a MERS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding S protein (S, S1 and/or S2), E protein, N protein and M protein.

[0227] In some embodiments, a MERS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding S protein (S, S1 and/or S2) and E

protein. In some embodiments, a MERS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding S protein (S, S1 and/or S2) and N protein. In some embodiments, a MERS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding S protein (S, S1 and/or S2) and M protein.

[0228] In some embodiments, a MERS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding S protein (S, S1 and/or S2), E protein and M protein. In some embodiments, a MERS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding S protein (S, S1 and/or S2), E protein and N protein. In some embodiments, a MERS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding S protein (S, S1 and/or S2), M protein and N protein. In some embodiments, a MERS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding E protein, M protein and N protein.

[0229] A MERS-CoV vaccine may comprise, for example, at least one RNA (e.g., mRNA) polynucleotide having an open reading frame encoding at least one MERS-CoV antigenic polypeptide identified by any one of SEQ ID NO: 24-38 or 33 (Table 11; see also amino acid sequences of Table 12).

[0230] A MERS-CoV vaccine may comprise, for example, at least one RNA (e.g., mRNA) polynucleotide encoded by a nucleic acid (e.g., DNA) identified by any one of SEQ ID NO: 20-23 (Table 10).

[0231] The present disclosure is not limited by a particular strain of MERS-CoV. The strain of MERS-CoV used in a vaccine may be any strain of MERS-CoV. Non-limiting examples of strains of MERS-CoV for use as provide herein include Riyadh_14_2013, and 2cEMC/2012, Hasi_1_2013.

[0232] SARS-CoV. The genome of SARS-CoV includes of a single, positive-strand RNA that is approximately 29,700 nucleotides long. The overall genome organization of SARS-CoV is similar to that of other coronaviruses. The reference genome includes 13 genes, which encode at least 14 proteins. Two large overlapping reading frames (ORFs) encompass 71% of the genome. The remainder has 12 potential ORFs, including genes for structural proteins S (spike), E (small envelope), M (membrane), and N (nucleocapsid). Other potential ORFs code for unique putative SARS-CoV-specific polypeptides that lack obvious sequence similarity to known proteins. A detailed analysis of the SARS-CoV genome has been published in *J Mol Biol* 2003; 331: 991-1004.

[0233] In some embodiments, a SARS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding S protein (S, S1 and/or S2), E protein, N protein and M protein.

[0234] In some embodiments, a SARS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding S protein (S, S1 and/or S2) and E protein. In some embodiments, a SARS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding S protein (S, S1 and/or S2) and N protein. In some embodiments, a SARS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding S protein (S, S1 and/or S2) and M protein.

[0235] In some embodiments, a SARS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding S protein (S, S1 and/or S2), E protein and M protein. In some embodiments, a SARS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding S protein (S, S1 and/or S2), E protein and N protein. In some embodiments, a SARS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding S protein (S, S1 and/or S2), E protein and N protein. In some embodiments, a SARS-CoV vaccine of the present disclosure comprises a RNA (e.g., mRNA) polynucleotide encoding E protein, M protein and N protein.

[0236] A SARS-CoV vaccine may comprise, for example, at least one RNA (e.g., mRNA) polynucleotide having an open reading frame encoding at least one SARS-CoV antigenic polypeptide identified by any one of SEQ ID NO: 29, 32 or 34 (Table 11; see also amino acid sequences of Table 12).

[0237] The present disclosure is not limited by a particular strain of SARS-CoV. The strain of SARS-CoV used in a vaccine may be any strain of SARS-CoV.

[0238] HCoV-OC43. Human coronavirus OC43 is an enveloped, positive-sense, single-stranded RNA virus in the species *Betacoronavirus-1* (genus *Betacoronavirus*, subfamily Coronavirinae, family Coronaviridae, order Nidovirales). Four HCoV-OC43 genotypes (A to D), have been identified with genotype D most likely arising from recombination. The complete genome sequencing of two genotype C and D strains and bootscan analysis shows recombination events between genotypes B and C in the generation of genotype D. Of 29 strains identified, none belong to the more ancient genotype A. Along with HCoV-229E, a species in the *Alphacoronavirus* genus, HCoV-OC43 are among the known viruses that cause the common cold. Both viruses can cause severe lower respiratory tract infections, including pneumonia in infants, the elderly, and immunocompromised individuals such as those undergoing chemotherapy and those with HIV-AIDS.

[0239] HCoV-HKU1. Human coronavirus HKU1 (HCoV-HKU1) is a positive-sense, single-stranded RNA virus with the HE gene, which distinguishes it as a group 2, or betacoronavirus. It was discovered in January 2005 in two patients in Hong Kong. The genome of HCoV-HKU1 is a 29,926-nucleotide, polyadenylated RNA. The GC content is 32%, the lowest among all known coronaviruses. The genome organization is the same as that of other group II coronaviruses, with the characteristic gene order 1a, 1b, HE, S, E, M, and N. Furthermore, accessory protein genes are present between the S and E genes (ORF4) and at the position of the N gene (ORF5). The TRS is presumably located within the AAUCUAAAC sequence, which precedes each ORF except E. As in sialodacryoadenitis virus and mouse hepatitis virus (MHV), translation of the E protein possibly occurs via an internal ribosomal entry site. The 3' untranslated region contains a predicted stem-loop structure immediately downstream of the N ORF (nucleotide position 29647 to 29711). Further downstream, a pseudoknot structure is present at nucleotide position 29708 to 29760. Both RNA structures are conserved in group II coronaviruses and are critical for virus replication.

[0240] HCoV-NL63. The RNA genome of human coronavirus NL63 (HCoV-NL63) is 27,553 nucleotides, with a poly(A) tail (FIG. 1). With a GC content of 34%, HCoV-

NL63 has one of the lowest GC contents of the coronaviruses, for which GC content ranges from 32 to 42%. Untranslated regions of 286 and 287 nucleotides are present at the 5' and 3' termini, respectively. Genes predicted to encode the S, E, M, and N proteins are found in the 3' part of the HCoV-NL63 genome. The HE gene, which is present in some group II coronaviruses, is absent, and there is only a single, monocistronic accessory protein ORF (ORF3) located between the S and E genes. Subgenomic mRNAs are generated for all ORFs (S, ORF3, E, M, and N), and the core sequence of the TRS of HCoV-NL63 is defined as AAC-UAAA. This sequence is situated upstream of every ORF except for the E ORF, which contains the suboptimal core sequence AACUAAU. Interestingly, a 13-nucleotide sequence with perfect homology to the leader sequence is situated upstream of the suboptimal E TRS. Annealing of this 13-nucleotide sequence to the leader sequence may act as a compensatory mechanism for the disturbed leader-TRS/body-TRS interaction.

[0241] HCoV-229E. Human coronavirus 229E (HCoV-229E) is a single-stranded, positive-sense, RNA virus species in the *Alphacoronavirus* genus of the subfamily Coronavirinae, in the family Coronaviridae, of the order Nidovirales. Along with Human coronavirus OC43, it is responsible for the common cold. HCoV-NL63 and HCoV-229E are two of the four human coronaviruses that circulate worldwide. These two viruses are unique in their relationship towards each other. Phylogenetically, the viruses are more closely related to each other than to any other human coronavirus, yet they only share 65% sequence identity. Moreover, the viruses use different receptors to enter their target cell. HCoV-NL63 is associated with croup in children, whereas all signs suggest that the virus probably causes the common cold in healthy adults. HCoV-229E is a proven common cold virus in healthy adults, so it is probable that both viruses induce comparable symptoms in adults, even though their mode of infection differs (HCoV-NL63 and HCoV-229E are two of the four human coronaviruses that circulate worldwide. These two viruses are unique in their relationship towards each other. Phylogenetically, the viruses are more closely related to each other than to any other human coronavirus, yet they only share 65% sequence identity. Moreover, the viruses use different receptors to enter their target cell. HCoV-NL63 is associated with croup in children, whereas all signs suggest that the virus probably causes the common cold in healthy adults. HCoV-229E is a proven common cold virus in healthy adults, so it is probable that both viruses induce comparable symptoms in adults, even though their mode of infection differs (Dijkman R. et al. *J Formos Med Assoc.* 2009 April; 108(4):270-9, the contents of which is incorporated herein by reference in their entirety).

Combination Vaccines

[0242] Embodiments of the present disclosure also provide combination RNA (e.g., mRNA) vaccines. A “combination RNA (e.g., mRNA) vaccine” of the present disclosure refers to a vaccine comprising at least one (e.g., at least 2, 3, 4, or 5) RNA (e.g., mRNA) polynucleotide having an open reading frame encoding a combination of any two or more (or all of) antigenic polypeptides selected from hMPV antigenic polypeptides, PIV3 antigenic polypeptides, RSV antigenic polypeptides, MeV antigenic polypeptides, and BetaCoV antigenic polypeptides (e.g., selected from MERS-

CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1).

[0243] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a hMPV antigenic polypeptide, a PIV3 antigenic polypeptide, a RSV antigenic polypeptide, a MeV antigenic polypeptide, and a BetaCoV antigenic polypeptide (e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1).

[0244] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a hMPV antigenic polypeptide and a PIV3 antigenic polypeptide.

[0245] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a hMPV antigenic polypeptide and a RSV antigenic polypeptide.

[0246] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a hMPV antigenic polypeptide and a MeV antigenic polypeptide.

[0247] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a hMPV antigenic polypeptide and a BetaCoV antigenic polypeptide.

[0248] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a PIV3 antigenic polypeptide and a RSV antigenic polypeptide.

[0249] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a PIV3 antigenic polypeptide and a MeV antigenic polypeptide.

[0250] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a PIV3 antigenic polypeptide and a BetaCoV antigenic polypeptide (e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1).

[0251] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a RSV antigenic polypeptide and a MeV antigenic polypeptide.

[0252] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a RSV antigenic polypeptide and a BetaCoV antigenic polypeptide (e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1).

[0253] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a MeV antigenic polypeptide and a BetaCoV antigenic polypeptide (e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1).

[0254] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a hMPV antigenic polypeptide, a PIV3 antigenic polypeptide, a RSV antigenic polypeptide and a MeV antigenic polypeptide.

[0255] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a hMPV antigenic polypeptide, a PIV3

antigenic polypeptide, a RSV antigenic polypeptide and a BetaCoV antigenic polypeptide (e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1).

[0256] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a hMPV antigenic polypeptide, a PIV3 antigenic polypeptide, a MeV antigenic polypeptide and a BetaCoV antigenic polypeptide (e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1).

[0257] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a hMPV antigenic polypeptide, a RSV antigenic polypeptide, a MeV antigenic polypeptide and a BetaCoV antigenic polypeptide (e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1).

[0258] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a PIV3 antigenic polypeptide, a RSV antigenic polypeptide, a MeV antigenic polypeptide and a BetaCoV antigenic polypeptide (e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1).

[0259] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a hMPV antigenic polypeptide, a PIV3 antigenic polypeptide and a RSV antigenic polypeptide.

[0260] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a hMPV antigenic polypeptide, a PIV3 antigenic polypeptide and a MeV antigenic polypeptide.

[0261] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a hMPV antigenic polypeptide, a PIV3 antigenic polypeptide and a BetaCoV antigenic polypeptide (e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1).

[0262] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a hMPV antigenic polypeptide, a RSV antigenic polypeptide and a MeV antigenic polypeptide.

[0263] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a hMPV antigenic polypeptide, a RSV antigenic polypeptide and a BetaCoV antigenic polypeptide (e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1).

[0264] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a hMPV antigenic polypeptide, a MeV antigenic polypeptide and a BetaCoV antigenic polypeptide (e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1). In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a PIV3 antigenic polypeptide, a RSV antigenic polypeptide and a MeV antigenic polypeptide.

[0265] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucle-

otide encoding a PIV3 antigenic polypeptide, a RSV antigenic polypeptide and a BetaCoV antigenic polypeptide (e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1).

[0266] In some embodiments, a combination RNA (e.g., mRNA) vaccine comprises a RNA (e.g., mRNA) polynucleotide encoding a RSV antigenic polypeptide, a MeV antigenic polypeptide and a BetaCoV antigenic polypeptide (e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1).

[0267] Other combination respiratory virus RNA (e.g., mRNA) vaccines are encompassed by the present disclosure.

[0268] It has been discovered that the mRNA vaccines described herein are superior to current vaccines in several ways. First, the lipid nanoparticle (LNP) delivery is superior to other formulations including a protamine base approach described in the literature and no additional adjuvants are to be necessary. The use of LNPs enables the effective delivery of chemically modified or unmodified mRNA vaccines. Additionally it has been demonstrated herein that both modified and unmodified LNP formulated mRNA vaccines were superior to conventional vaccines by a significant degree. In some embodiments the mRNA vaccines of the invention are superior to conventional vaccines by a factor of at least 10 fold, 20 fold, 40 fold, 50 fold, 100 fold, 500 fold or 1,000 fold.

[0269] Although attempts have been made to produce functional RNA vaccines, including mRNA vaccines and self-replicating RNA vaccines, the therapeutic efficacy of these RNA vaccines have not yet been fully established. Quite surprisingly, the inventors have discovered, according to aspects of the invention a class of formulations for delivering mRNA vaccines in vivo that results in significantly enhanced, and in many respects synergistic, immune responses including enhanced antigen generation and functional antibody production with neutralization capability. These results can be achieved even when significantly lower doses of the mRNA are administered in comparison with mRNA doses used in other classes of lipid based formulations. The formulations of the invention have demonstrated significant unexpected in vivo immune responses sufficient to establish the efficacy of functional mRNA vaccines as prophylactic and therapeutic agents. Additionally, self-replicating RNA vaccines rely on viral replication pathways to deliver enough RNA to a cell to produce an immunogenic response. The formulations of the invention do not require viral replication to produce enough protein to result in a strong immune response. Thus, the mRNA of the invention are not self-replicating RNA and do not include components necessary for viral replication.

[0270] The invention involves, in some aspects, the surprising finding that lipid nanoparticle (LNP) formulations significantly enhance the effectiveness of mRNA vaccines, including chemically modified and unmodified mRNA vaccines. The efficacy of mRNA vaccines formulated in LNP was examined in vivo using several distinct antigens. The results presented herein demonstrate the unexpected superior efficacy of the mRNA vaccines formulated in LNP over other commercially available vaccines.

[0271] In addition to providing an enhanced immune response, the formulations of the invention generate a more

rapid immune response with fewer doses of antigen than other vaccines tested. The mRNA-LNP formulations of the invention also produce quantitatively and qualitatively better immune responses than vaccines formulated in a different carriers.

[0272] The data described herein demonstrate that the formulations of the invention produced significant unexpected improvements over existing antigen vaccines. Additionally, the mRNA-LNP formulations of the invention are superior to other vaccines even when the dose of mRNA is lower than other vaccines. Mice immunized with either 10 µg or 2 µg doses of an hMPV fusion protein mRNA LNP vaccine or a PIV3 mRNA LNP vaccine produced neutralizing antibodies which for instance, successfully neutralized the hMPV B2 virus. A 10 µg dose of mRNA vaccine protected 100% of mice from lethal challenge and drastically reduced the viral titer after challenge (~2 log reduction).

[0273] Two 20 µg doses of MERS-CoV mRNA LNP vaccine significantly reduced viral load and induced significant amount of neutralizing antibodies against MERS-CoV (EC₅₀ between 500-1000). The MERS-CoV mRNA vaccine induced antibody titer was 3-5 fold better than any other vaccines tested in the same model.

[0274] The LNP used in the studies described herein has been used previously to deliver siRNA in various animal models as well as in humans. In view of the observations made in association with the siRNA delivery of LNP formulations, the fact that LNP is useful in vaccines is quite surprising. It has been observed that therapeutic delivery of siRNA formulated in LNP causes an undesirable inflammatory response associated with a transient IgM response, typically leading to a reduction in antigen production and a compromised immune response. In contrast to the findings observed with siRNA, the LNP-mRNA formulations of the invention are demonstrated herein to generate enhanced IgG levels, sufficient for prophylactic and therapeutic methods rather than transient IgM responses.

Nucleic Acids/Polynucleotides

[0275] Respiratory virus vaccines, as provided herein, comprise at least one (one or more) ribonucleic acid (RNA) (e.g., mRNA) polynucleotide having an open reading frame encoding at least one antigenic polypeptide selected from hMPV, PIV3, RSV, MeV and BetaCoV (e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1) antigenic polypeptides. The term “nucleic acid” includes any compound and/or substance that comprises a polymer of nucleotides (nucleotide monomer). These polymers are referred to as polynucleotides. Thus, the terms “nucleic acid” and “polynucleotide” are used interchangeably.

[0276] Nucleic acids may be or may include, for example, ribonucleic acids (RNAs), deoxyribonucleic acids (DNAs), threose nucleic acids (TNAs), glycol nucleic acids (GNAs), peptide nucleic acids (PNAs), locked nucleic acids (LNAs), including LNA having a β-D-ribo configuration, α-LNA having an α-L-ribo configuration (a diastereomer of LNA), 2'-amino-LNA having a 2'-amino functionalization, and 2'-amino-α-LNA having a 2'-amino functionalization), ethylene nucleic acids (ENAs), cyclohexenyl nucleic acids (CeNA) or chimeras or combinations thereof.

[0277] In some embodiments, polynucleotides of the present disclosure function as messenger RNA (mRNA). “Mes-

senger RNA” (mRNA) refers to any polynucleotide that encodes a (at least one) polypeptide (a naturally-occurring, non-naturally-occurring, or modified polymer of amino acids) and can be translated to produce the encoded polypeptide in vitro, in vivo, in situ or ex vivo. The skilled artisan will appreciate that, except where otherwise noted, polynucleotide sequences set forth in the instant application will recite “T”s in a representative DNA sequence but where the sequence represents RNA (e.g., mRNA), the “T”s would be substituted for “U”s. Thus, any of the RNA polynucleotides encoded by a DNA identified by a particular sequence identification number may also comprise the corresponding RNA (e.g., mRNA) sequence encoded by the DNA, where each “T” of the DNA sequence is substituted with “U.”

[0278] The basic components of an mRNA molecule typically include at least one coding region, a 5' untranslated region (UTR), a 3' UTR, a 5' cap and a poly-A tail. Polynucleotides of the present disclosure may function as mRNA but can be distinguished from wild-type mRNA in their functional and/or structural design features, which serve to overcome existing problems of effective polypeptide expression using nucleic-acid based therapeutics.

[0279] In some embodiments, a RNA polynucleotide of an RNA (e.g., mRNA) vaccine encodes 2-10, 2-9, 2-8, 2-7, 2-6, 2-5, 2-4, 2-3, 3-10, 3-9, 3-8, 3-7, 3-6, 3-5, 3-4, 4-10, 4-9, 4-8, 4-7, 4-6, 4-5, 5-10, 5-9, 5-8, 5-7, 5-6, 6-10, 6-9, 6-8, 6-7, 7-10, 7-9, 7-8, 8-10, 8-9 or 9-10 antigenic polypeptides. In some embodiments, a RNA (e.g., mRNA) polynucleotide of a respiratory virus vaccine encodes at least 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 antigenic polypeptides. In some embodiments, a RNA (e.g., mRNA) polynucleotide of a respiratory virus vaccine encodes at least 100 or at least 200 antigenic polypeptides. In some embodiments, a RNA polynucleotide of an respiratory virus vaccine encodes 1-10, 5-15, 10-20, 15-25, 20-30, 25-35, 30-40, 35-45, 40-50, 1-50, 1-100, 2-50 or 2-100 antigenic polypeptides.

[0280] Polynucleotides of the present disclosure, in some embodiments, are codon optimized. Codon optimization methods are known in the art and may be used as provided herein. Codon optimization, in some embodiments, may be used to match codon frequencies in target and host organisms to ensure proper folding; bias GC content to increase mRNA stability or reduce secondary structures; minimize tandem repeat codons or base runs that may impair gene construction or expression; customize transcriptional and translational control regions; insert or remove protein trafficking sequences; remove/add post translation modification sites in encoded protein (e.g. glycosylation sites); add, remove or shuffle protein domains; insert or delete restriction sites; modify ribosome binding sites and mRNA degradation sites; adjust translational rates to allow the various domains of the protein to fold properly; or to reduce or eliminate problem secondary structures within the polynucleotide. Codon optimization tools, algorithms and services are known in the art—non-limiting examples include services from GeneArt (Life Technologies), DNA2.0 (Menlo Park Calif.) and/or proprietary methods. In some embodiments, the open reading frame (ORF) sequence is optimized using optimization algorithms.

[0281] In some embodiments, a codon optimized sequence shares less than 95% sequence identity, less than 90% sequence identity, less than 85% sequence identity, less than 80% sequence identity, or less than 75% sequence identity to a naturally-occurring or wild-type sequence (e.g., a natu-

rally-occurring or wild-type mRNA sequence encoding a polypeptide or protein of interest (e.g., an antigenic protein or antigenic polypeptide)).

[0282] In some embodiments, a codon-optimized sequence shares between 65% and 85% (e.g., between about 67% and about 85%, or between about 67% and about 80%) sequence identity to a naturally-occurring sequence or a wild-type sequence (e.g., a naturally-occurring or wild-type mRNA sequence encoding a polypeptide or protein of interest (e.g., an antigenic protein or polypeptide)). In some embodiments, a codon-optimized sequence shares between 65% and 75%, or about 80% sequence identity to a naturally-occurring sequence or wild-type sequence (e.g., a naturally-occurring or wild-type mRNA sequence encoding a polypeptide or protein of interest (e.g., an antigenic protein or polypeptide)).

[0283] In some embodiments a codon-optimized RNA (e.g., mRNA) may, for instance, be one in which the levels of G/C are enhanced. The G/C-content of nucleic acid molecules may influence the stability of the RNA. RNA having an increased amount of guanine (G) and/or cytosine (C) residues may be functionally more stable than nucleic acids containing a large amount of adenine (A) and thymine (T) or uracil (U) nucleotides. WO02/098443 discloses a pharmaceutical composition containing an mRNA stabilized by sequence modifications in the translated region. Due to the degeneracy of the genetic code, the modifications work by substituting existing codons for those that promote greater RNA stability without changing the resulting amino acid. The approach is limited to coding regions of the RNA.

Antigens/Antigenic Polypeptides

[0284] In some embodiments, an antigenic polypeptide (e.g., a hMPV, PIV3, RSV, MeV or BetaCoV antigenic polypeptide) is longer than 25 amino acids and shorter than 50 amino acids. Polypeptides include gene products, naturally occurring polypeptides, synthetic polypeptides, homologs, orthologs, paralogs, fragments and other equivalents, variants, and analogs of the foregoing. A polypeptide may be a single molecule or may be a multi-molecular complex such as a dimer, trimer or tetramer. Polypeptides may also comprise single chain polypeptides or multichain polypeptides, such as antibodies or insulin, and may be associated or linked to each other. Most commonly, disulfide linkages are found in multichain polypeptides. The term “polypeptide” may also apply to amino acid polymers in which at least one amino acid residue is an artificial chemical analogue of a corresponding naturally-occurring amino acid.

[0285] A “polypeptide variant” is a molecule that differs in its amino acid sequence relative to a native sequence or a reference sequence. Amino acid sequence variants may possess substitutions, deletions, insertions, or a combination of any two or three of the foregoing, at certain positions within the amino acid sequence, as compared to a native sequence or a reference sequence. Ordinarily, variants possess at least 50% identity to a native sequence or a reference sequence. In some embodiments, variants share at least 80% identity or at least 90% identity with a native sequence or a reference sequence.

[0286] In some embodiments “variant mimics” are provided. A “variant mimic” contains at least one amino acid that would mimic an activated sequence. For example, glutamate may serve as a mimic for phospho-threonine

and/or phospho-serine. Alternatively, variant mimics may result in deactivation or in an inactivated product containing the mimic. For example, phenylalanine may act as an inactivating substitution for tyrosine, or alanine may act as an inactivating substitution for serine.

[0287] “Orthologs” refers to genes in different species that evolved from a common ancestral gene by speciation. Normally, orthologs retain the same function in the course of evolution. Identification of orthologs is important for reliable prediction of gene function in newly sequenced genomes.

[0288] “Analog” is meant to include polypeptide variants that differ by one or more amino acid alterations, for example, substitutions, additions or deletions of amino acid residues that still maintain one or more of the properties of the parent or starting polypeptide.

[0289] The present disclosure provides several types of compositions that are polynucleotide or polypeptide based, including variants and derivatives. These include, for example, substitutional, insertional, deletion and covalent variants and derivatives. The term “derivative” is synonymous with the term “variant” and generally refers to a molecule that has been modified and/or changed in any way relative to a reference molecule or a starting molecule.

[0290] As such, polynucleotides encoding peptides or polypeptides containing substitutions, insertions and/or additions, deletions and covalent modifications with respect to reference sequences, in particular the polypeptide sequences disclosed herein, are included within the scope of this disclosure. For example, sequence tags or amino acids, such as one or more lysines, can be added to peptide sequences (e.g., at the N-terminal or C-terminal ends). Sequence tags can be used for peptide detection, purification or localization. Lysines can be used to increase peptide solubility or to allow for biotinylation. Alternatively, amino acid residues located at the carboxy and amino terminal regions of the amino acid sequence of a peptide or protein may optionally be deleted providing for truncated sequences. Certain amino acids (e.g., C-terminal residues or N-terminal residues) alternatively may be deleted depending on the use of the sequence, as for example, expression of the sequence as part of a larger sequence that is soluble, or linked to a solid support.

[0291] “Substitutional variants” when referring to polypeptides are those that have at least one amino acid residue in a native or starting sequence removed and a different amino acid inserted in its place at the same position. Substitutions may be single, where only one amino acid in the molecule has been substituted, or they may be multiple, where two or more (e.g., 3, 4 or 5) amino acids have been substituted in the same molecule.

[0292] As used herein the term “conservative amino acid substitution” refers to the substitution of an amino acid that is normally present in the sequence with a different amino acid of similar size, charge, or polarity. Examples of conservative substitutions include the substitution of a non-polar (hydrophobic) residue such as isoleucine, valine and leucine for another non-polar residue. Likewise, examples of conservative substitutions include the substitution of one polar (hydrophilic) residue for another such as between arginine and lysine, between glutamine and asparagine, and between glycine and serine. Additionally, the substitution of a basic residue such as lysine, arginine or histidine for another, or the substitution of one acidic residue such as

aspartic acid or glutamic acid for another acidic residue are additional examples of conservative substitutions. Examples of non-conservative substitutions include the substitution of a non-polar (hydrophobic) amino acid residue such as isoleucine, valine, leucine, alanine, methionine for a polar (hydrophilic) residue such as cysteine, glutamine, glutamic acid or lysine and/or a polar residue for a non-polar residue.

[0293] “Features” when referring to polypeptide or polynucleotide are defined as distinct amino acid sequence-based or nucleotide-based components of a molecule respectively. Features of the polypeptides encoded by the polynucleotides include surface manifestations, local conformational shape, folds, loops, half-loops, domains, half-domains, sites, termini and any combination(s) thereof.

[0294] As used herein when referring to polypeptides the term “domain” refers to a motif of a polypeptide having one or more identifiable structural or functional characteristics or properties (e.g., binding capacity, serving as a site for protein-protein interactions).

[0295] As used herein when referring to polypeptides the terms “site” as it pertains to amino acid based embodiments is used synonymously with “amino acid residue” and “amino acid side chain.” As used herein when referring to polynucleotides the terms “site” as it pertains to nucleotide based embodiments is used synonymously with “nucleotide.” A site represents a position within a peptide or polypeptide or polynucleotide that may be modified, manipulated, altered, derivatized or varied within the polypeptide-based or polynucleotide-based molecules.

[0296] As used herein the terms “termini” or “terminus” when referring to polypeptides or polynucleotides refers to an extremity of a polypeptide or polynucleotide respectively. Such extremity is not limited only to the first or final site of the polypeptide or polynucleotide but may include additional amino acids or nucleotides in the terminal regions. Polypeptide-based molecules may be characterized as having both an N-terminus (terminated by an amino acid with a free amino group (NH₂)) and a C-terminus (terminated by an amino acid with a free carboxyl group (COOH)). Proteins are in some cases made up of multiple polypeptide chains brought together by disulfide bonds or by non-covalent forces (multimers, oligomers). These proteins have multiple N- and C-termini. Alternatively, the termini of the polypeptides may be modified such that they begin or end, as the case may be, with a non-polypeptide based moiety such as an organic conjugate.

[0297] As recognized by those skilled in the art, protein fragments, functional protein domains, and homologous proteins are also considered to be within the scope of polypeptides of interest. For example, provided herein is any protein fragment (meaning a polypeptide sequence at least one amino acid residue shorter than a reference polypeptide sequence but otherwise identical) of a reference protein having a length of 10, 20, 30, 40, 50, 60, 70, 80, 90, 100 or longer than 100 amino acids. In another example, any protein that includes a stretch of 20, 30, 40, 50, or 100 (contiguous) amino acids that are 40%, 50%, 60%, 70%, 80%, 90%, 95%, or 100% identical to any of the sequences described herein can be utilized in accordance with the disclosure. In some embodiments, a polypeptide includes 2, 3, 4, 5, 6, 7, 8, 9, 10, or more mutations as shown in any of the sequences provided herein or referenced herein. In another example, any protein that includes a stretch of 20, 30, 40, 50, or 100 amino acids that are greater than 80%,

90%, 95%, or 100% identical to any of the sequences described herein, wherein the protein has a stretch of 5, 10, 15, 20, 25, or 30 amino acids that are less than 80%, 75%, 70%, 65% to 60% identical to any of the sequences described herein can be utilized in accordance with the disclosure.

[0298] Polypeptide or polynucleotide molecules of the present disclosure may share a certain degree of sequence similarity or identity with the reference molecules (e.g., reference polypeptides or reference polynucleotides), for example, with art-described molecules (e.g., engineered or designed molecules or wild-type molecules). The term “identity,” as known in the art, refers to a relationship between the sequences of two or more polypeptides or polynucleotides, as determined by comparing the sequences. In the art, identity also means the degree of sequence relatedness between two sequences as determined by the number of matches between strings of two or more amino acid residues or nucleic acid residues. Identity measures the percent of identical matches between the smaller of two or more sequences with gap alignments (if any) addressed by a particular mathematical model or computer program (e.g., “algorithms”). Identity of related peptides can be readily calculated by known methods. “% identity” as it applies to polypeptide or polynucleotide sequences is defined as the percentage of residues (amino acid residues or nucleic acid residues) in the candidate amino acid or nucleic acid sequence that are identical with the residues in the amino acid sequence or nucleic acid sequence of a second sequence after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent identity. Methods and computer programs for the alignment are well known in the art. Identity depends on a calculation of percent identity but may differ in value due to gaps and penalties introduced in the calculation. Generally, variants of a particular polynucleotide or polypeptide have at least 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% but less than 100% sequence identity to that particular reference polynucleotide or polypeptide as determined by sequence alignment programs and parameters described herein and known to those skilled in the art. Such tools for alignment include those of the BLAST suite (Stephen F. Altschul, et al. (1997). “Gapped BLAST and PSI-BLAST: a new generation of protein database search programs,” *Nucleic Acids Res.* 25:3389-3402). Another popular local alignment technique is based on the Smith-Waterman algorithm (Smith, T. F. & Waterman, M. S. (1981) “Identification of common molecular subsequences.” *J. Mol. Biol.* 147:195-197). A general global alignment technique based on dynamic programming is the Needleman-Wunsch algorithm (Needleman, S. B. & Wunsch, C. D. (1970) “A general method applicable to the search for similarities in the amino acid sequences of two proteins.” *J. Mol. Biol.* 48:443-453). More recently, a Fast Optimal Global Sequence Alignment Algorithm (FOGSAA) was developed that purportedly produces global alignment of nucleotide and protein sequences faster than other optimal global alignment methods, including the Needleman-Wunsch algorithm. Other tools are described herein, specifically in the definition of “identity” below.

[0299] As used herein, the term “homology” refers to the overall relatedness between polymeric molecules, e.g. between nucleic acid molecules (e.g. DNA molecules and/or RNA molecules) and/or between polypeptide molecules.

Polymeric molecules (e.g. nucleic acid molecules (e.g. DNA molecules and/or RNA molecules) and/or polypeptide molecules) that share a threshold level of similarity or identity determined by alignment of matching residues are termed homologous. Homology is a qualitative term that describes a relationship between molecules and can be based upon the quantitative similarity or identity. Similarity or identity is a quantitative term that defines the degree of sequence match between two compared sequences. In some embodiments, polymeric molecules are considered to be "homologous" to one another if their sequences are at least 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% identical or similar. The term "homologous" necessarily refers to a comparison between at least two sequences (polynucleotide or polypeptide sequences). Two polynucleotide sequences are considered homologous if the polypeptides they encode are at least 50%, 60%, 70%, 80%, 90%, 95%, or even 99% for at least one stretch of at least 20 amino acids. In some embodiments, homologous polynucleotide sequences are characterized by the ability to encode a stretch of at least 4-5 uniquely specified amino acids. For polynucleotide sequences less than 60 nucleotides in length, homology is determined by the ability to encode a stretch of at least 4-5 uniquely specified amino acids. Two protein sequences are considered homologous if the proteins are at least 50%, 60%, 70%, 80%, or 90% identical for at least one stretch of at least 20 amino acids.

[0300] Homology implies that the compared sequences diverged in evolution from a common origin. The term "homolog" refers to a first amino acid sequence or nucleic acid sequence (e.g., gene (DNA or RNA) or protein sequence) that is related to a second amino acid sequence or nucleic acid sequence by descent from a common ancestral sequence. The term "homolog" may apply to the relationship between genes and/or proteins separated by the event of speciation or to the relationship between genes and/or proteins separated by the event of genetic duplication. "Orthologs" are genes (or proteins) in different species that evolved from a common ancestral gene (or protein) by speciation. Typically, orthologs retain the same function in the course of evolution. "Paralogs" are genes (or proteins) related by duplication within a genome. Orthologs retain the same function in the course of evolution, whereas paralogs evolve new functions, even if these are related to the original one.

[0301] The term "identity" refers to the overall relatedness between polymeric molecules, for example, between polynucleotide molecules (e.g. DNA molecules and/or RNA molecules) and/or between polypeptide molecules. Calculation of the percent identity of two polynucleic acid sequences, for example, can be performed by aligning the two sequences for optimal comparison purposes (e.g., gaps can be introduced in one or both of a first and a second nucleic acid sequences for optimal alignment and non-identical sequences can be disregarded for comparison purposes). In certain embodiments, the length of a sequence aligned for comparison purposes is at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or 100% of the length of the reference sequence. The nucleotides at corresponding nucleotide positions are then compared. When a position in the first sequence is occupied by the same nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity

between the two sequences is a function of the number of identical positions shared by the sequences, taking into account the number of gaps, and the length of each gap, which needs to be introduced for optimal alignment of the two sequences. The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. For example, the percent identity between two nucleic acid sequences can be determined using methods such as those described in Computational Molecular Biology, Lesk, A. M., ed., Oxford University Press, New York, 1988; Biocomputing: Informatics and Genome Projects, Smith, D. W., ed., Academic Press, New York, 1993; Sequence Analysis in Molecular Biology, von Heinje, G., Academic Press, 1987; Computer Analysis of Sequence Data, Part I, Griffin, A. M., and Griffin, H. G., eds., Humana Press, New Jersey, 1994; and Sequence Analysis Primer, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; each of which is incorporated herein by reference. For example, the percent identity between two nucleic acid sequences can be determined using the algorithm of Meyers and Miller (CABIOS, 1989, 4:11-17), which has been incorporated into the ALIGN program (version 2.0) using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4. The percent identity between two nucleic acid sequences can, alternatively, be determined using the GAP program in the GCG software package using an NWSgapdna.CMP matrix. Methods commonly employed to determine percent identity between sequences include, but are not limited to those disclosed in Carillo, H., and Lipman, D., *SIAM J Applied Math.*, 48:1073 (1988); incorporated herein by reference. Techniques for determining identity are codified in publicly available computer programs. Exemplary computer software to determine homology between two sequences include, but are not limited to, GCG program package, Devereux, J., et al., *Nucleic Acids Research*, 12(1), 387 (1984), BLASTP, BLASTN, and FASTA Altschul, S. F. et al., *J. Molec. Biol.*, 215, 403 (1990)).

Multiprotein and Multicomponent Vaccines

[0302] The present disclosure encompasses respiratory virus vaccines comprising multiple RNA (e.g., mRNA) polynucleotides, each encoding a single antigenic polypeptide, as well as respiratory virus vaccines comprising a single RNA polynucleotide encoding more than one antigenic polypeptide (e.g., as a fusion polypeptide). Thus, a vaccine composition comprising a RNA (e.g., mRNA) polynucleotide having an open reading frame encoding a first antigenic polypeptide and a RNA (e.g., mRNA) polynucleotide having an open reading frame encoding a second antigenic polypeptide encompasses (a) vaccines that comprise a first RNA polynucleotide encoding a first antigenic polypeptide and a second RNA polynucleotide encoding a second antigenic polypeptide, and (b) vaccines that comprise a single RNA polynucleotide encoding a first and second antigenic polypeptide (e.g., as a fusion polypeptide). RNA (e.g., mRNA) vaccines of the present disclosure, in some embodiments, comprise 2-10 (e.g., 2, 3, 4, 5, 6, 7, 8, 9 or 10), or more, RNA polynucleotides having an open reading frame, each of which encodes a different antigenic polypeptide (or a single RNA polynucleotide encoding 2-10, or more, different antigenic polypeptides). The antigenic polypeptides may be selected from hMPV, PIV3, RSV, MEV and BetaCoV (e.g., selected from MERS-CoV, SARS-CoV,

HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1) antigenic polypeptides.

[0303] In some embodiments, a respiratory virus vaccine comprises a RNA (e.g., mRNA) polynucleotide having an open reading frame encoding a viral capsid protein, a RNA (e.g., mRNA) polynucleotide having an open reading frame encoding a viral premembrane/membrane protein, and a RNA (e.g., mRNA) polynucleotide having an open reading frame encoding a viral envelope protein. In some embodiments, a respiratory virus vaccine comprises a RNA (e.g., mRNA) polynucleotide having an open reading frame encoding a viral fusion (F) protein and a RNA polynucleotide having an open reading frame encoding a viral major surface glycoprotein (G protein). In some embodiments, a vaccine comprises a RNA (e.g., mRNA) polynucleotide having an open reading frame encoding a viral F protein. In some embodiments, a vaccine comprises a RNA (e.g., mRNA) polynucleotide having an open reading frame encoding a viral G protein. In some embodiments, a vaccine comprises a RNA (e.g., mRNA) polynucleotide having an open reading frame encoding a HN protein.

[0304] In some embodiments, a multicomponent vaccine comprises at least one RNA (e.g., mRNA) polynucleotide encoding at least one antigenic polypeptide fused to a signal peptide (e.g., any one of SEQ ID NO: 15-19). The signal peptide may be fused at the N-terminus or the C-terminus of an antigenic polypeptide. An antigenic polypeptide fused to a signal peptide may be selected from hMPV, PIV3, RSV, MEV and BetaCoV (e.g., selected from MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and HCoV-HKU1) antigenic polypeptides.

Signal Peptides

[0305] In some embodiments, antigenic polypeptides encoded by respiratory virus RNA (e.g., mRNA) polynucleotides comprise a signal peptide. Signal peptides, comprising the N-terminal 15-60 amino acids of proteins, are typically needed for the translocation across the membrane on the secretory pathway and, thus, universally control the entry of most proteins both in eukaryotes and prokaryotes to the secretory pathway. Signal peptides generally include three regions: an N-terminal region of differing length, which usually comprises positively charged amino acids; a hydrophobic region; and a short carboxy-terminal peptide region. In eukaryotes, the signal peptide of a nascent precursor protein (pre-protein) directs the ribosome to the rough endoplasmic reticulum (ER) membrane and initiates the transport of the growing peptide chain across it for processing. ER processing produces mature proteins, wherein the signal peptide is cleaved from precursor proteins, typically by a ER-resident signal peptidase of the host cell, or they remain uncleaved and function as a membrane anchor. A signal peptide may also facilitate the targeting of the protein to the cell membrane. The signal peptide, however, is not responsible for the final destination of the mature protein. Secretory proteins devoid of additional address tags in their sequence are by default secreted to the external environment. During recent years, a more advanced view of signal peptides has evolved, showing that the functions and immunodominance of certain signal peptides are much more versatile than previously anticipated.

[0306] Respiratory virus vaccines of the present disclosure may comprise, for example, RNA (e.g., mRNA) polynucleotides encoding an artificial signal peptide, wherein the

signal peptide coding sequence is operably linked to and is in frame with the coding sequence of the antigenic polypeptide. Thus, respiratory virus vaccines of the present disclosure, in some embodiments, produce an antigenic polypeptide comprising an antigenic polypeptide (e.g., hMPV, PIV3, RSV, MeV or BetaCoV) fused to a signal peptide. In some embodiments, a signal peptide is fused to the N-terminus of the antigenic polypeptide. In some embodiments, a signal peptide is fused to the C-terminus of the antigenic polypeptide.

[0307] In some embodiments, the signal peptide fused to the antigenic polypeptide is an artificial signal peptide. In some embodiments, an artificial signal peptide fused to the antigenic polypeptide encoded by the RNA (e.g., mRNA) vaccine is obtained from an immunoglobulin protein, e.g., an IgE signal peptide or an IgG signal peptide. In some embodiments, a signal peptide fused to the antigenic polypeptide encoded by a RNA (e.g., mRNA) vaccine is an Ig heavy chain epsilon-1 signal peptide (IgE HC SP) having the sequence of: MDWTWILFLVAAATRVHS (SEQ ID NO: 16). In some embodiments, a signal peptide fused to the antigenic polypeptide encoded by the (e.g., mRNA) RNA (e.g., mRNA) vaccine is an IgGk chain V-III region HAH signal peptide (IgGk SP) having the sequence of MET-PAQLFLLLLWLPDITG (SEQ ID NO: 15). In some embodiments, the signal peptide is selected from: Japanese encephalitis PRM signal sequence (MLGSNSGQRV-VFTILLLLVAPAYS; SEQ ID NO: 17), VSVg protein signal sequence (MKCLLYLAFLFIGVNCA; SEQ ID NO: 18) and Japanese encephalitis JEV signal sequence (MWLVSLAIVTACAGA; SEQ ID NO: 19).

[0308] In some embodiments, the antigenic polypeptide encoded by a RNA (e.g., mRNA) vaccine comprises an amino acid sequence identified by any one of SEQ ID NO: 5-8, 12-13, 24-34, 47-50 or 54-56 (Tables 3, 6, 11, 14 or 17; see also amino acid sequences of Tables 4, 7, 12 or 15) fused to a signal peptide identified by any one of SEQ ID NO: 15-19 (Table 8). The examples disclosed herein are not meant to be limiting and any signal peptide that is known in the art to facilitate targeting of a protein to ER for processing and/or targeting of a protein to the cell membrane may be used in accordance with the present disclosure.

[0309] A signal peptide may have a length of 15-60 amino acids. For example, a signal peptide may have a length of 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, or 60 amino acids. In some embodiments, a signal peptide has a length of 20-60, 25-60, 30-60, 35-60, 40-60, 45-60, 50-60, 55-60, 15-55, 20-55, 25-55, 30-55, 35-55, 40-55, 45-55, 50-55, 15-50, 20-50, 25-50, 30-50, 35-50, 40-50, 45-50, 15-45, 20-45, 25-45, 30-45, 35-45, 40-45, 15-40, 20-40, 25-40, 30-40, 35-40, 15-35, 20-35, 25-35, 30-35, 15-30, 20-30, 25-30, 15-25, 20-25, or 15-20 amino acids.

[0310] A signal peptide is typically cleaved from the nascent polypeptide at the cleavage junction during ER processing. The mature antigenic polypeptide produced by a respiratory virus RNA (e.g., mRNA) vaccine of the present disclosure typically does not comprise a signal peptide.

Chemical Modifications

[0311] Respiratory virus vaccines of the present disclosure, in some embodiments, comprise at least RNA (e.g., mRNA) polynucleotide having an open reading frame

encoding at least one antigenic polypeptide that comprises at least one chemical modification.

[0312] The terms “chemical modification” and “chemically modified” refer to modification with respect to adenosine (A), guanosine (G), uridine (U), thymidine (T) or cytidine (C) ribonucleosides or deoxyribonucleosides in at least one of their position, pattern, percent or population. Generally, these terms do not refer to the ribonucleotide modifications in naturally occurring 5'-terminal mRNA cap moieties. With respect to a polypeptide, the term “modification” refers to a modification relative to the canonical set 20 amino acids. Polypeptides, as provided herein, are also considered “modified” if they contain amino acid substitutions, insertions or a combination of substitutions and insertions.

[0313] Polynucleotides (e.g., RNA polynucleotides, such as mRNA polynucleotides), in some embodiments, comprise various (more than one) different modifications. In some embodiments, a particular region of a polynucleotide contains one, two or more (optionally different) nucleoside or nucleotide modifications. In some embodiments, a modified RNA polynucleotide (e.g., a modified mRNA polynucleotide), introduced to a cell or organism, exhibits reduced degradation in the cell or organism, respectively, relative to an unmodified polynucleotide. In some embodiments, a modified RNA polynucleotide (e.g., a modified mRNA polynucleotide), introduced into a cell or organism, may exhibit reduced immunogenicity in the cell or organism, respectively (e.g., a reduced innate response).

[0314] Modifications of polynucleotides include, without limitation, those described herein. Polynucleotides (e.g., RNA polynucleotides, such as mRNA polynucleotides) may comprise modifications that are naturally-occurring, non-naturally-occurring or the polynucleotide may comprise a combination of naturally-occurring and non-naturally-occurring modifications. Polynucleotides may include any useful modification, for example, of a sugar, a nucleobase, or an internucleoside linkage (e.g., to a linking phosphate, to a phosphodiester linkage or to the phosphodiester backbone).

[0315] Polynucleotides (e.g., RNA polynucleotides, such as mRNA polynucleotides), in some embodiments, comprise non-natural modified nucleotides that are introduced during synthesis or post-synthesis of the polynucleotides to achieve desired functions or properties. The modifications may be present on an internucleotide linkages, purine or pyrimidine bases, or sugars. The modification may be introduced with chemical synthesis or with a polymerase enzyme at the terminal of a chain or anywhere else in the chain. Any of the regions of a polynucleotide may be chemically modified.

[0316] The present disclosure provides for modified nucleosides and nucleotides of a polynucleotide (e.g., RNA polynucleotides, such as mRNA polynucleotides). A “nucleoside” refers to a compound containing a sugar molecule (e.g., a pentose or ribose) or a derivative thereof in combination with an organic base (e.g., a purine or pyrimidine) or a derivative thereof (also referred to herein as “nucleobase”). A nucleotide” refers to a nucleoside, including a phosphate group. Modified nucleotides may be synthesized by any useful method, such as, for example, chemically, enzymatically, or recombinantly, to include one or more modified or non-natural nucleosides. Polynucleotides may comprise a region or regions of linked nucleosides. Such regions may have variable backbone linkages. The

linkages may be standard phosphodiester linkages, in which case the polynucleotides would comprise regions of nucleotides.

[0317] Modified nucleotide base pairing encompasses not only the standard adenosine-thymine, adenosine-uracil, or guanosine-cytosine base pairs, but also base pairs formed between nucleotides and/or modified nucleotides comprising non-standard or modified bases, wherein the arrangement of hydrogen bond donors and hydrogen bond acceptors permits hydrogen bonding between a non-standard base and a standard base or between two complementary non-standard base structures. One example of such non-standard base pairing is the base pairing between the modified nucleotide inosine and adenine, cytosine or uracil. Any combination of base/sugar or linker may be incorporated into polynucleotides of the present disclosure.

[0318] Modifications of polynucleotides (e.g., RNA polynucleotides, such as mRNA polynucleotides) that are useful in the vaccines of the present disclosure include, but are not limited to the following: 2-methylthio-N6-(cis-hydroxyisopentenyl)adenosine; 2-methylthio-N6-methyladenosine; 2-methylthio-N6-threonyl carbamoyladenosine; N6-glycylcarbamoyladenosine; N6-isopentenyladenosine; N6-methyladenosine; N6-threonylcarbamoyladenosine; 1,2'-O-dimethyladenosine; 1'-methyladenosine; 2'-O-methyladenosine; 2'-O-ribosyladenosine (phosphate); 2-methyladenosine; 2-methylthio-N6 isopentenyladenosine; 2-methylthio-N6-hydroxynorvalyl carbamoyladenosine; 2'-O-methyladenosine; 2'-O-ribosyladenosine (phosphate); Isopentenyladenosine; N6-(cis-hydroxyisopentenyl)adenosine; N6,2'-O-dimethyladenosine; N6,2'-O-dimethyladenosine; N6,N6,2'-O-trimethyladenosine; N6,N6-dimethyladenosine; N6-acetyladenosine; N6-hydroxynorvalylcarbamoyladenosine; N6-methyl-N6-threonylcarbamoyladenosine; 2-methyladenosine; 2-methylthio-N6-isopentenyladenosine; 7-deaza-adenosine; N1-methyl-adenosine; N6, N6 (dimethyl)adenine; N6-cis-hydroxy-isopentenyl-adenosine; α -thio-adenosine; 2 (amino)adenine; 2 (aminopropyl)adenine; 2 (methylthio) N6 (isopentenyl)adenine; 2-(alkyl)adenine; 2-(aminoalkyl)adenine; 2-(aminopropyl)adenine; 2-(halo)adenine; 2-(halo)adenine; 2-(propyl)adenine; 2'-Amino-2'-deoxy-ATP; 2'-Azido-2'-deoxy-ATP; 2'-Deoxy-2'-a-aminoadenosine TP; 2'-Deoxy-2'-a-azidoadenosine TP; 6 (alkyl)adenine; 6 (methyl)adenine; 6-(alkyl)adenine; 6-(methyl)adenine; 7 (deaza)adenine; 8 (alkenyl)adenine; 8 (alkynyl)adenine; 8 (amino)adenine; 8 (thioalkyl)adenine; 8-(alkenyl)adenine; 8-(alkyl)adenine; 8-(alkynyl)adenine; 8-(amino)adenine; 8-(halo)adenine; 8-(hydroxyl)adenine; 8-(thioalkyl)adenine; 8-(thiol)adenine; 8-azido-adenosine; aza adenine; deaza adenine; N6 (methyl)adenine; N6-(isopentyl)adenine; 7-deaza-8-aza-adenosine; 7-methyladenine; 1-Deazaadenosine TP; 2'Fluoro-N6-Bz-deoxyadenosine TP; 2'-O Me-2-Amino-ATP; 2'O-methyl-N6-Bz-deoxyadenosine TP; 2'-a-Ethynyladenosine TP; 2-aminoadenine; 2-Aminoadenosine TP; 2-Amino-ATP; 2'-a-Trifluoromethyladenosine TP; 2-Azidoadenosine TP; 2'-b-Ethynyladenosine TP; 2-Bromoadenosine TP; 2'-b-Trifluoromethyladenosine TP; 2-Chloroadenosine TP; 2'-Deoxy-2',2'-difluoroadenosine TP; 2'-Deoxy-2'-a-mercaptopadenosine TP; 2'-Deoxy-2'-a-thiomethoxyadenosine TP; 2'-Deoxy-2'-b-aminoadenosine TP; 2'-Deoxy-2'-b-azidoadenosine TP; 2'-Deoxy-2'-b-bromoadenosine TP; 2'-Deoxy-2'-b-chloroadenosine TP; 2'-Deoxy-2'-b-fluoroadenosine TP; 2'-Deoxy-2'-b-iodoadenosine

TP; 2'-Deoxy-2'-b-mercaptadenosine TP; 2'-Deoxy-2'-b-thiomethoxyadenosine TP; 2-Fluoroadenosine TP; 2-Iodo-adenosine TP; 2-Mercaptadenosine TP; 2-methoxy-adenine; 2-methylthio-adenine; 2-Trifluoromethyladenosine TP; 3-Deaza-3-bromoadenosine TP; 3-Deaza-3-chloroadenosine TP; 3-Deaza-3-fluoroadenosine TP; 3-Deaza-3-iodoadenosine TP; 3-Deazaadenosine TP; 4'-Azidoadenosine TP; 4'-Carbocyclic adenosine TP; 4'-Ethynyladenosine TP; 5'-Homo-adenosine TP; 8-Aza-ATP; 8-bromo-adenosine TP; 8-Trifluoromethyladenosine TP; 9-Deazaadenosine TP; 2-aminopurine; 7-deaza-2,6-diaminopurine; 7-deaza-8-aza-2,6-diaminopurine; 7-deaza-8-aza-2-aminopurine; 2,6-diaminopurine; 7-deaza-8-aza-adenine, 7-deaza-2-aminopurine; 2-thiocytidine; 3-methylcytidine; 5-formylcytidine; 5-hydroxymethylcytidine; 5-methylcytidine; N4-acetylcytidine; 2'-O-methylcytidine; 2'-O-methylcytidine; 5,2'-O-dimethylcytidine; 5-formyl-2'-O-methylcytidine; Lysidine; N4,2'-O-dimethylcytidine; N4-acetyl-2'-O-methylcytidine; N4-methylcytidine; N4,N4-Dimethyl-2'-OMe-Cytidine TP; 4-methylcytidine; 5-aza-cytidine; Pseudo-iso-cytidine; pyrrolo-cytidine; α -thio-cytidine; 2-(thio)cytosine; 2'-Amino-2'-deoxy-CTP; 2'-Azido-2'-deoxy-CTP; 2'-Deoxy-2'-a-aminocytidine TP; 2'-Deoxy-2'-a-azidocytidine TP; 3 (deaza) 5 (aza)cytosine; 3 (methyl)cytosine; 3-(alkyl)cytosine; 3-(deaza) 5 (aza)cytosine; 3-(methyl)cytidine; 4,2'-O-dimethylcytidine; 5 (halo)cytosine; 5 (methyl)cytosine; 5 (propynyl)cytosine; 5 (trifluoromethyl)cytosine; 5-(alkyl)cytosine; 5-(alkynyl)cytosine; 5-(halo)cytosine; 5-(propynyl)cytosine; 5-(trifluoromethyl)cytosine; 5-bromo-cytidine; 5-iodo-cytidine; 5-propynyl cytosine; 6-(azo)cytosine; 6-aza-cytidine; aza cytosine; deaza cytosine; N4 (acetyl) cytosine; 1-methyl-1-deaza-pseudoisocytidine; 1-methyl-pseudoisocytidine; 2-methoxy-5-methyl-cytidine; 2-methoxy-cytidine; 2-thio-5-methyl-cytidine; 4-methoxy-1-methyl-pseudoisocytidine; 4-methoxy-pseudoisocytidine; 4-thio-1-methyl-1-deaza-pseudoisocytidine; 4-thio-1-methyl-pseudoisocytidine; 4-thio-pseudoisocytidine; 5-azazebularine; 5-methyl-zebularine; pyrrolo-pseudoisocytidine; Zebularine; (E)-5-(2-Bromo-vinyl)cytidine TP; 2,2'-anhydro-cytidine TP hydrochloride; 2'Fluor-N4-Bz-cytidine TP; 2'Fluor-N4-Acetyl-cytidine TP; 2'-O-Methyl-N4-Acetyl-cytidine TP; 2'-O-methyl-N4-Bz-cytidine TP; 2'-a-Ethynylcytidine TP; 2'-a-Trifluoromethylcytidine TP; 2'-b-Ethynylcytidine TP; 2'-b-Trifluoromethylcytidine TP; 2'-Deoxy-2',2'-difluorocytidine TP; 2'-Deoxy-2'-a-mercaptocytidine TP; 2'-Deoxy-2'-a-thiomethoxycytidine TP; 2'-Deoxy-2'-b-aminocytidine TP; 2'-Deoxy-2'-b-azidocytidine TP; 2'-Deoxy-2'-b-bromocytidine TP; 2'-Deoxy-2'-b-chlorocytidine TP; 2'-Deoxy-2'-b-fluorocytidine TP; 2'-Deoxy-2'-b-iodocytidine TP; 2'-Deoxy-2'-b-mercaptocytidine TP; 2'-Deoxy-2'-b-thiomethoxycytidine TP; 2'-O-Methyl-5-(1-propynyl)cytidine TP; 3'-Ethynylcytidine TP; 4'-Azidocytidine TP; 4'-Carbocyclic cytidine TP; 4'-Ethynylcytidine TP; 5-(1-Propynyl)ara-cytidine TP; 5-(2-Chloro-phenyl)-2-thiocytidine TP; 5-(4-Amino-phenyl)-2-thiocytidine TP; 5-Aminoallyl-CTP; 5-Cyanocytidine TP; 5-Ethynylara-cytidine TP; 5-Ethynylcytidine TP; 5'-Homo-cytidine TP; 5-Methoxycytidine TP; 5-Trifluoromethyl-Cytidine TP; N4-Amino-cytidine TP; N4-Benzoyl-cytidine TP; Pseudoisocytidine TP; 7-methylguanosine; N2,2'-O-dimethylguanosine; N2-methylguanosine; Wyosine; 1,2'-O-dimethylguanosine; 1-methylguanosine; 2'-O-methylguanosine; 2'-O-ribosylguanosine (phosphate); 2'-O-methylguanosine; 2'-O-ribosylguanosine (phosphate); 7-aminomethyl-7-

deazaguanosine; 7-cyano-7-deazaguanosine; Archaeosine; Methylwyo sine; N2,7-dimethylguanosine; N2,N2,2'-O-trimethylguanosine; N2,N2,7-trimethylguanosine; N2,N2-dimethylguanosine; N2,7,2'-O-trimethylguanosine; 6-thioguanosine; 7-deaza-guanosine; 8-oxo-guanosine; N1-methyl-guanosine; α -thio-guanosine; 2 (propyl)guanine; 2-(alkyl)guanine; 2'-Amino-2'-deoxy-GTP; 2'-Azido-2'-deoxy-GTP; 2'-Deoxy-2'-a-aminoguanosine TP; 2'-Deoxy-2'-a-azidoguanosine TP; 6 (methyl)guanine; 6-(alkyl)guanine; 6-(methyl)guanine; 6-methyl-guanosine; 7 (alkyl)guanine; 7 (deaza)guanine; 7 (methyl)guanine; 7-(alkyl)guanine; 7-(deaza)guanine; 7-(methyl)guanine; 8 (alkyl)guanine; 8 (alkynyl)guanine; 8 (halo)guanine; 8 (thioalkyl)guanine; 8-(alkenyl)guanine; 8-(alkyl)guanine; 8-(alkynyl)guanine; 8-(amino)guanine; 8-(halo)guanine; 8-(hydroxyl)guanine; 8-(thioalkyl)guanine; 8-(thiol)guanine; aza guanine; deaza guanine; N (methyl)guanine; N-(methyl)guanine; 1-methyl-6-thio-guanosine; 6-methoxy-guanosine; 6-thio-7-deaza-8-aza-guanosine; 6-thio-7-deaza-guanosine; 6-thio-7-methyl-guanosine; 7-deaza-8-aza-guanosine; 7-methyl-8-oxo-guanosine; N2,N2-dimethyl-6-thio-guanosine; N2-methyl-6-thio-guanosine; 1-Me-GTP; 2'Fluoro-N2-isobutylguanosine TP; 2'-O-methyl-N2-isobutyl-guanosine TP; 2'-a-Ethynylguanosine TP; 2'-a-Trifluoromethylguanosine TP; 2'-b-Ethynylguanosine TP; 2'-b-Trifluoromethylguanosine TP; 2'-Deoxy-2',2'-difluoroguanosine TP; 2'-Deoxy-2'-a-mercaptoguanosine TP; 2'-Deoxy-2'-a-thiomethoxyguanosine TP; 2'-Deoxy-2'-b-aminoguanosine TP; 2'-Deoxy-2'-b-azidoguanosine TP; 2'-Deoxy-2'-b-bromoguanosine TP; 2'-Deoxy-2'-b-chloroguanosine TP; 2'-Deoxy-2'-b-fluoroguanosine TP; 2'-Deoxy-2'-b-iodoguanosine TP; 2'-Deoxy-2'-b-mercaptoguanosine TP; 2'-Deoxy-2'-b-thiomethoxyguanosine TP; 4'-Azidoguanosine TP; 4'-Carbocyclic guanosine TP; 4'-Ethynylguanosine TP; 5'-Homo-guanosine TP; 8-bromo-guanosine TP; 9-Deazaguanosine TP; N2-isobutyl-guanosine TP; 1-methylinosine; Inosine; 1,2'-O-dimethylinosine; 2'-O-methylinosine; 7-methylinosine; 2'-O-methylinosine; Epoxyqueuosine; galactosyl-queuosine; Mannosylqueuosine; Queuosine; allyl-amino-thymidine; aza thymidine; deaza thymidine; deoxy-thymidine; 2'-O-methyluridine; 2-thiouridine; 3-methyluridine; 5-carboxymethyluridine; 5-hydroxyuridine; 5-methyluridine; 5-aurinomethyl-2-thiouridine; 5-taurinomethyluridine; Dihydrouridine; Pseudouridine; (3-(3-amino-3-carboxypropyl)uridine; 1-methyl-3-(3-amino-5-carboxypropyl)pseudouridine; 1-methylpseudouridine; 1-methyl-pseudouridine; 2'-O-methyluridine; 2'-O-methylpseudouridine; 2'-O-methyluridine; 2-thio-2'-O-methyluridine; 3-(3-amino-3-carboxypropyl)uridine; 3,2'-O-dimethyluridine; 3-Methyl-pseudo-Uridine TP; 4-thiouridine; 5-(carboxyhydroxymethyl)uridine; 5-(carboxyhydroxymethyl)uridine methyl ester; 5,2'-O-dimethyluridine; 5,6-dihydro-uridine; 5-aminomethyl-2-thiouridine; 5-carbamoylmethyl-2'-O-methyluridine; 5-carbamoylmethyluridine; 5-carboxyhydroxymethyluridine; 5-carboxyhydroxymethyluridine methyl ester; 5-carboxymethylaminomethyl-2'-O-methyluridine; 5-carboxymethylaminomethyl-2-thiouridine; 5-carboxymethylaminomethyl-2-thiouridine; 5-carboxymethylaminomethyluridine; 5-carboxymethylaminomethyluridine; 5-methoxycarbonylmethyl-2'-O-methyluridine; 5-methoxycarbonylmethyl-2-thiouridine; 5-methoxycarbonylmethyluridine; 5-methoxyuridine; 5-methyl-2-thiouridine; 5-methylaminomethyl-2-selenouridine; 5-methylaminomethyl-2-

thiouridine; 5-methylaminomethyluridine; 5-Methyldihydrouridine; 5-Oxyacetic acid-Uridine TP; 5-Oxyacetic acid-methyl ester-Uridine TP; N1-methylpseudo-uridine; uridine 5-oxyacetic acid; uridine 5-oxyacetic acid methyl ester; 3-(3-Amino-3-carboxypropyl)-Uridine TP; 5-(iso-Pentenylaminomethyl)-2-thiouridine TP; 5-(iso-Pentenylaminomethyl)-2'-O-methyluridine TP; 5-(iso-Pentenylaminomethyl)uridine TP; 5-propynyl uracil; α -thio-uridine; 1 (aminoalkylamino-carbonylethyl-2 (thio)-pseudouracil; 1 (aminoalkylaminocarbonylethyl-2,4-(dithio)pseudouracil; 1 (aminoalkylaminocarbonylethyl-4 (thio)pseudouracil; 1 (aminoalkylaminocarbonylethyl-2 (thio)-pseudouracil; 1 (aminocarbonylethyl-2,4-(dithio)pseudouracil; 1 (aminocarbonylethyl-4 (thio)pseudouracil; 1 (aminocarbonylethyl-2 (thio)-pseudouracil; 1 substituted 2 (thio)-pseudouracil; 1 substituted 2,4-(dithio)pseudouracil; 1 substituted 4 (thio)pseudouracil; 1 substituted pseudouracil; 1-(aminoalkylamino-carbonylethyl-2-(thio)-pseudouracil; 1-Methyl-3-(3-amino-3-carboxypropyl) pseudouridine TP; 1-Methyl-3-(3-amino-3-carboxypropyl)pseudo-UTP; 1-Methyl-pseudo-UTP; 2 (thio)pseudouracil; 2' deoxy uridine; 2' fluorouridine; 2-(thio)uracil; 2,4-(dithio)pseudouracil; 2' methyl; 2' amino, 2'azido, 2'fluoro-guanosine; 2'-Amino-2'-deoxy-UTP; 2'-Azido-2'-deoxy-UTP; 2'-Azido-deoxyuridine TP; 2'-O-methylpseudouridine; 2' deoxy uridine; 2' fluorouridine; 2'-Deoxy-2'-aminouridine TP; 2'-Deoxy-2'-a-azidouridine TP; 2-methylpseudouridine; 3 (3 amino-3 carboxypropyl)uracil; 4 (thio)pseudouracil; 4-(thio)pseudouracil; 4-(thio)uracil; 5 (1,3-diazole-1-alkyl)uracil; 5 (2-aminopropyl)uracil; 5 (aminoalkyl)uracil; 5 (dimethylaminoalkyl)uracil; 5 (guanidiniumalkyl)uracil; 5 (methoxycarbonylmethyl)-2-(thio)uracil; 5 (methoxycarbonyl-methyl)uracil; 5 (methyl) 2 (thio)uracil; 5 (methyl) 2,4 (dithio)uracil; 5 (methyl) 4 (thio)uracil; 5 (methylaminomethyl)-2 (thio)uracil; 5 (methylaminomethyl)-2,4 (dithio)uracil; 5 (methylaminomethyl)-4 (thio)uracil; 5 (propynyl)uracil; 5 (trifluoromethyl)uracil; 5-(2-aminopropyl)uracil; 5-(alkyl)-2-(thio)pseudouracil; 5-(alkyl)-2,4 (dithio)pseudouracil; 5-(alkyl)-4 (thio)pseudouracil; 5-(alkyl)pseudouracil; 5-(alkyl)uracil; 5-(alkynyl)uracil; 5-(allylamino)uracil; 5-(cyanoalkyl)uracil; 5-(dialkylaminoalkyl)uracil; 5-(dimethylaminoalkyl)uracil; 5-(guanidiniumalkyl)uracil; 5-(halo)uracil; 5-(1,3-diazole-1-alkyl)uracil; 5-(methoxy)uracil; 5-(methoxycarbonylmethyl)-2-(thio)uracil; 5-(methoxycarbonyl-methyl)uracil; 5-(methyl) 2(thio)uracil; 5-(methyl) 2,4 (dithio)uracil; 5-(methyl) 4 (thio)uracil; 5-(methyl)-2-(thio)pseudouracil; 5-(methyl)-2,4 (dithio)pseudouracil; 5-(methyl)-4 (thio)pseudouracil; 5-(methyl)pseudouracil; 5-(methylaminomethyl)-2 (thio)uracil; 5-(methylaminomethyl)-2,4(dithio)uracil; 5-(methylaminomethyl)-4-(thio)uracil; 5-(propynyl)uracil; 5-(trifluoromethyl)uracil; 5-aminoallyl-uridine; 5-bromo-uridine; 5-iodo-uridine; 5-uracil; 6 (azo)uracil; 6-(azo)uracil; 6-aza-uridine; ally-amino-uracil; aza uracil; deaza uracil; N3 (methyl)uracil; P pseudo-UTP-1-2-ethanoic acid; Pseudouracil; 4-Thio-pseudo-UTP; 1-carboxymethyl-pseudouridine; 1-methyl-1-deaza-pseudouridine; 1-propynyl-uridine; 1-taurinomethyl-1-methyl-uridine; 1-taurinomethyl-4-thio-uridine; 1-taurinomethyl-pseudouridine; 2-methoxy-4-thio-pseudouridine; 2-thio-1-methyl-1-deaza-pseudouridine; 2-thio-1-methyl-pseudouridine; 2-thio-5-aza-uridine; 2-thio-dihy-

dropseudouridine; 2-thio-dihydrouridine; 2-thio-pseudouridine; 4-methoxy-2-thio-pseudouridine; 4-methoxy-pseudouridine; 4-thio-1-methyl-pseudouridine; 4-thio-pseudouridine; 5-aza-uridine; Dihydropseudouridine; (\pm)-1-(2-Hydroxypropyl)pseudouridine TP; (2R)-1-(2-Hydroxypropyl)pseudouridine TP; (2S)-1-(2-Hydroxypropyl)pseudouridine TP; (E)-5-(2-Bromo-vinyl)ara-uridine TP; (E)-5-(2-Bromo-vinyl)uridine TP; (Z)-5-(2-Bromo-vinyl)ara-uridine TP; (Z)-5-(2-Bromo-vinyl)uridine TP; 1-(2,2,2-Trifluoroethyl)-pseudo-UTP; 1-(2,2,3,3,3-Pentafluoropropyl)pseudouridine TP; 1-(2,2-Diethoxyethyl)pseudouridine TP; 1-(2,4,6-Trimethylbenzyl)pseudouridine TP; 1-(2,4,6-Trimethyl-benzyl)pseudo-UTP; 1-(2,4,6-Trimethyl-phenyl)pseudo-UTP; 1-(2-Amino-2-carboxyethyl)pseudo-UTP; 1-(2-Amino-ethyl)pseudo-UTP; 1-(2-Hydroxyethyl)pseudouridine TP; 1-(2-Methoxyethyl)pseudouridine TP; 1-(3,4-Bis-trifluoromethoxybenzyl)pseudouridine TP; 1-(3,4-Dimethoxybenzyl)pseudouridine TP; 1-(3-Amino-3-carboxypropyl)pseudo-UTP; 1-(3-Amino-propyl)pseudo-UTP; 1-(3-Cyclopropyl-prop-2-ynyl)pseudouridine TP; 1-(4-Amino-4-carboxybutyl)pseudo-UTP; 1-(4-Amino-benzyl)pseudo-UTP; 1-(4-Amino-butyl)pseudo-UTP; 1-(4-Aminophenyl)pseudo-UTP; 1-(4-Azidobenzyl)pseudouridine TP; 1-(4-Bromobenzyl)pseudouridine TP; 1-(4-Chlorobenzyl)pseudouridine TP; 1-(4-Fluorobenzyl)pseudouridine TP; 1-(4-Iodobenzyl)pseudouridine TP; 1-(4-Methanesulfonylbenzyl)pseudouridine TP; 1-(4-Methoxybenzyl)pseudouridine TP; 1-(4-Methoxy-benzyl)pseudo-UTP; 1-(4-Methoxyphenyl)pseudo-UTP; 1-(4-Methylbenzyl)pseudouridine TP; 1-(4-Methyl-benzyl)pseudo-UTP; 1-(4-Nitrobenzyl)pseudouridine TP; 1-(4-Nitro-benzyl)pseudo-UTP; 1-(4-Nitro-phenyl)pseudo-UTP; 1-(4-Thiomethoxybenzyl)pseudouridine TP; 1-(4-Trifluoromethoxybenzyl)pseudouridine TP; 1-(4-Trifluoromethylbenzyl)pseudouridine TP; 1-(5-Amino-pentyl)pseudo-UTP; 1-(6-Amino-hexyl)pseudo-UTP; 1,6-Dimethyl-pseudo-UTP; 1-[3-(2-[2-(2-Aminoethoxy)-ethoxy]-ethoxy)-propionyl]pseudouridine TP; 1-{3-[2-(2-Aminoethoxy)-ethoxy]-propionyl} pseudouridine TP; 1-Acetylpsudouridine TP; 1-Alkyl-6-(1-propynyl)-pseudo-UTP; 1-Alkyl-6-(2-propynyl)-pseudo-UTP; 1-Alkyl-6-allyl-pseudo-UTP; 1-Alkyl-6-ethynyl-pseudo-UTP; 1-Alkyl-6-homoallylpseudo-UTP; 1-Alkyl-6-vinyl-pseudo-UTP; 1-Allylpseudouridine TP; 1-Aminomethyl-pseudo-UTP; 1-Benzoylpseudouridine TP; 1-Benzyloxymethylpseudouridine TP; 1-Benzyl-pseudo-UTP; 1-Biotinyl-PEG2-pseudouridine TP; 1-Biotinylpseudouridine TP; 1-Butyl-pseudo-UTP; 1-Cyanomethylpseudouridine TP; 1-Cyclobutylmethylpseudo-UTP; 1-Cyclobutyl-pseudo-UTP; 1-Cycloheptylmethyl-pseudo-UTP; 1-Cycloheptyl-pseudo-UTP; 1-Cyclohexylmethyl-pseudo-UTP; 1-Cyclohexyl-pseudo-UTP; 1-Cyclooctylmethyl-pseudo-UTP; 1-Cyclooctyl-pseudo-UTP; 1-Cyclopentylmethyl-pseudo-UTP; 1-Cyclopentylpseudo-UTP; 1-Cyclopropylmethyl-pseudo-UTP; 1-Cyclopropyl-pseudo-UTP; 1-Ethyl-pseudo-UTP; 1-Hexylpseudo-UTP; 1-Homoallylpseudouridine TP; 1-Hydroxymethylpseudouridine TP; 1-iso-propyl-pseudo-UTP; 1-Me-2-thio-pseudo-UTP; 1-Me-4-thio-pseudo-UTP; 1-Me-alpha-thio-pseudo-UTP; 1-Methanesulfonylmethylpseudouridine TP; 1-Methoxymethylpseudouridine TP; 1-Methyl-6-(2,2,2-Trifluoroethyl)pseudo-UTP; 1-Methyl-6-(4-morpholino)-pseudo-UTP; 1-Methyl-6-(4-thiomorpholino)-pseudo-UTP; 1-Methyl-6-(substituted phenyl)pseudo-UTP; 1-Methyl-6-amino-pseudo-UTP; 1-Methyl-6-

azido-pseudo-UTP; 1-Methyl-6-bromo-pseudo-UTP; 1-Methyl-6-butyl-pseudo-UTP; 1-Methyl-6-chloro-pseudo-UTP; 1-Methyl-6-cyano-pseudo-UTP; 1-Methyl-6-dimethylamino-pseudo-UTP; 1-Methyl-6-ethoxy-pseudo-UTP; 1-Methyl-6-ethylcarboxylate-pseudo-UTP; 1-Methyl-6-ethyl-pseudo-UTP; 1-Methyl-6-fluoro-pseudo-UTP; 1-Methyl-6-formyl-pseudo-UTP; 1-Methyl-6-hydroxyamino-pseudo-UTP; 1-Methyl-6-hydroxy-pseudo-UTP; 1-Methyl-6-iodo-pseudo-UTP; 1-Methyl-6-iso-propyl-pseudo-UTP; 1-Methyl-6-methoxy-pseudo-UTP; 1-Methyl-6-methylamino-pseudo-UTP; 1-Methyl-6-phenyl-pseudo-UTP; 1-Methyl-6-propyl-pseudo-UTP; 1-Methyl-6-tert-butyl-pseudo-UTP; 1-Methyl-6-trifluoromethoxy-pseudo-UTP; 1-Methyl-6-trifluoromethyl-pseudo-UTP; 1-Morpholinomethylpseudouridine TP; 1-Pentyl-pseudo-UTP; 1-Phenyl-pseudo-UTP; 1-Pivaloylpseudouridine TP; 1-Propargylpseudouridine TP; 1-Propyl-pseudo-UTP; 1-propynyl-pseudouridine; 1-p-tolyl-pseudo-UTP; 1-tert-Butyl-pseudo-UTP; 1-Thiomethoxymethylpseudouridine TP; 1-Thiomorpholinomethylpseudouridine TP; 1-Trifluoroacetyl-pseudouridine TP; 1-Trifluoromethyl-pseudo-UTP; 1-Vinylpseudouridine TP; 2,2'-anhydro-uridine TP; 2'-bromo-deoxyuridine TP; 2'-F-5-Methyl-2'-deoxy-UTP; 2'-OMe-5-Me-UTP; 2'-OMe-pseudo-UTP; 2'-a-Ethynyluridine TP; 2'-a-Trifluoromethyluridine TP; 2'-b-Ethynyluridine TP; 2'-b-Trifluoromethyluridine TP; 2'-Deoxy-2',2'-difluorouridine TP; 2'-Deoxy-2'-a-mercaptopuridine TP; 2'-Deoxy-2'-a-thiomethoxyuridine TP; 2'-Deoxy-2'-b-aminouridine TP; 2'-Deoxy-2'-b-azidouridine TP; 2'-Deoxy-2'-b-bromouridine TP; 2'-Deoxy-2'-b-chlorouridine TP; 2'-Deoxy-2'-b-fluorouridine TP; 2'-Deoxy-2'-b-iodouridine TP; 2'-Deoxy-2'-b-mercaptopuridine TP; 2'-Deoxy-2'-b-thiomethoxyuridine TP; 2-methoxy-4-thio-uridine; 2-methoxyuridine; 2'-O-Methyl-5-(1-propynyl)uridine TP; 3-Alkyl-pseudo-UTP; 4'-Azidouridine TP; 4'-Carbocyclic uridine TP; 4'-Ethynyluridine TP; 5-(1-Propynyl)ara-uridine TP; 5-(2-Furanyl)uridine TP; 5-Cyanouridine TP; 5-Dimethylaminouridine TP; 5'-Homo-uridine TP; 5-iodo-2'-fluoro-deoxyuridine TP; 5-Phenylethynyluridine TP; 5-Tri-deuteromethyl-6-deuterouridine TP; 5-Trifluoromethyl-Uridine TP; 5-Vinylarauridine TP; 6-(2,2,2-Trifluoroethyl)-pseudo-UTP; 6-(4-Morpholino)-pseudo-UTP; 6-(4-Thiomorpholino)-pseudo-UTP; 6-(Substituted-Phenyl)-pseudo-UTP; 6-Amino-pseudo-UTP; 6-Azido-pseudo-UTP; 6-Bromo-pseudo-UTP; 6-Butyl-pseudo-UTP; 6-Chloro-pseudo-UTP; 6-Cyano-pseudo-UTP; 6-Dimethylamino-pseudo-UTP; 6-Ethoxy-pseudo-UTP; 6-Ethylcarboxylate-pseudo-UTP; 6-Ethyl-pseudo-UTP; 6-Fluoro-pseudo-UTP; 6-Formyl-pseudo-UTP; 6-Hydroxyamino-pseudo-UTP; 6-Hydroxy-pseudo-UTP; 6-Iodo-pseudo-UTP; 6-iso-Propyl-pseudo-UTP; 6-Methoxy-pseudo-UTP; 6-Methylamino-pseudo-UTP; 6-Methyl-pseudo-UTP; 6-Phenyl-pseudo-UTP; 6-Phenyl-pseudo-UTP; 6-Propyl-pseudo-UTP; 6-tert-Butyl-pseudo-UTP; 6-Trifluoromethoxy-pseudo-UTP; 6-Trifluoromethyl-pseudo-UTP; Alpha-thio-pseudo-UTP; Pseudouridine 1-(4-methylbenzenesulfonic acid) TP; Pseudouridine 1-(4-methylbenzoic acid) TP; Pseudouridine TP 1-[3-{2-(2-[2-(2-ethoxy)-ethoxy]-ethoxy)-ethoxy}] propionic acid; Pseudouridine TP 1-[3-{2-(2-[2-(2-ethoxy)-ethoxy]-ethoxy)-ethoxy}] propionic acid; Pseudouridine TP 1-[3-{2-(2-[2-(2-ethoxy)-ethoxy]-ethoxy)-ethoxy}] propionic acid; Pseudouridine TP 1-methylphos-

phonic acid; Pseudouridine TP 1-methylphosphonic acid diethyl ester; Pseudo-UTP-N1-3-propionic acid; Pseudo-UTP-N1-4-butanoic acid; Pseudo-UTP-N1-5-pentanoic acid; Pseudo-UTP-N1-6-hexanoic acid; Pseudo-UTP-N1-7-heptanoic acid; Pseudo-UTP-N1-methyl-p-benzoic acid; Pseudo-UTP-N1-p-benzoic acid; Wybutosine; Hydroxywybutosine; Isowyosine; Peroxywybutosine; undermodified hydroxywybutosine; 4-demethylwyosine; 2,6-(diamino)purine; 1-(aza)-2-(thio)-3-(aza)-phenoxazin-1-yl; 1,3-(diaz)-2-(oxo)-phenthiazin-1-yl; 1,3-(diaz)-2-(oxo)-phenoxazin-1-yl; 1,3,5-(triaz)-2,6-(diox)-naphthalene; 2 (amino) purine; 2,4,5-(trimethyl)phenyl; 2' methyl, 2'amino, 2'azido, 2'fluoro-cytidine; 2' methyl, 2'amino, 2'azido, 2'fluoro-adenine; 2'methyl, 2'amino, 2'azido, 2'fluoro-uridine; 2'-amino-2'-deoxyribose; 2-amino-6-Chloro-purine; 2-aza-inosinyl; 2'-azido-2'-deoxyribose; 2'fluoro-2'-deoxyribose; 2'-fluoromodified bases; 2'-O-methyl-ribose; 2-oxo-7-aminopyridopyrimidin-3-yl; 2-oxo-pyridopyrimidine-3-yl; 2-pyridinone; 3 nitropyrrole; 3-(methyl)-7-(propynyl) isocarbostyryl; 3-(methyl)isocarbostyryl; 4-(fluoro)-6-(methyl)benzimidazole; 4-(methyl)benzimidazole; 4-(methyl)indolyl; 4,6-(dimethyl)indolyl; 5 nitroindole; 5 substituted pyrimidines; 5-(methyl)isocarbostyryl; 5-nitroindole; 6-(aza)pyrimidine; 6-(azo)thymine; 6-(methyl)-7-(aza)indolyl; 6-chloro-purine; 6-phenyl-pyrrolo-pyrimidin-2-on-3-yl; 7-(aminoalkylhydroxy)-1-(aza)-2-(thio)-3-(aza)-phenthiazin-1-yl; 7-(aminoalkylhydroxy)-1-(aza)-2-(thio)-3-(aza)-phenoxazin-1-yl; 7-(aminoalkylhydroxy)-1,3-(diaz)-2-(oxo)-phenoxazin-1-yl; 7-(aminoalkylhydroxy)-1,3-(diaz)-2-(oxo)-phenthiazin-1-yl; 7-(aminoalkylhydroxy)-1,3-(diaz)-2-(oxo)-phenoxazin-1-yl; 7-(aza)indolyl; 7-(guanidiniumalkylhydroxy)-1-(aza)-2-(thio)-3-(aza)-phenoxazin-1-yl; 7-(guanidiniumalkylhydroxy)-1-(aza)-2-(thio)-3-(aza)-phenthiazin-1-yl; 7-(guanidiniumalkylhydroxy)-1-(aza)-2-(thio)-3-(aza)-phenoxazin-1-yl; 7-(guanidiniumalkylhydroxy)-1,3-(diaz)-2-(oxo)-phenoxazin-1-yl; 7-(guanidiniumalkylhydroxy)-1,3-(diaz)-2-(oxo)-phenthiazin-1-yl; 7-(guanidiniumalkylhydroxy)-1,3-(diaz)-2-(oxo)-phenoxazin-1-yl; 7-(propynyl)isocarbostyryl; 7-(propynyl)isocarbostyryl, propynyl-7-(aza)indolyl; 7-deaza-inosinyl; 7-substituted 1-(aza)-2-(thio)-3-(aza)-phenoxazin-1-yl; 7-substituted 1,3-(diaz)-2-(oxo)-phenoxazin-1-yl; 9-(methyl)-imidizopyridinyl; Aminoindolyl; Anthracenyl; bis-ortho-(aminoalkylhydroxy)-6-phenyl-pyrrolo-pyrimidin-2-on-3-yl; bis-ortho-substituted-6-phenyl-pyrrolo-pyrimidin-2-on-3-yl; Difluorotolyl; Hypoxanthine; Imidizopyridinyl; Inosinyl; Isocarbostyryl; Isoguanisine; N2-substituted purines; N6-methyl-2-amino-purine; N6-substituted purines; N-alkylated derivative; Naphthalenyl; Nitrobenzimidazolyl; Nitroimidazolyl; Nitroindazolyl; Nitropyrazolyl; Nubularine; O6-substituted purines; O-alkylated derivative; ortho-(aminoalkylhydroxy)-6-phenyl-pyrrolo-pyrimidin-2-on-3-yl; ortho-substituted-6-phenyl-pyrrolo-pyrimidin-2-on-3-yl; Oxoformycin TP; para-(aminoalkylhydroxy)-6-phenyl-pyrrolo-pyrimidin-2-on-3-yl; para-substituted-6-phenyl-pyrrolo-pyrimidin-2-on-3-yl; Pentacenyl; Phenanthracenyl; Phenyl; propynyl-7-(aza)indolyl; Pyrenyl; pyridopyrimidin-3-yl; pyridopyrimidin-3-yl, 2-oxo-7-amino-pyridopyrimidin-3-yl; pyrrolo-pyrimidin-2-on-3-yl; Pyrrolopyrimidinyl; Pyrrolopyrazinyl; Stilbenzyl; substituted 1,2,4-triazoles; Tetracenyl; Tubercidine; Xanthine; Xanthosine-5'-TP; 2-thio-zebularine; 5-aza-2-thio-zebularine; 7-deaza-2-amino-purine; pyridin-4-one ribo-

nucleoside; 2-Amino-riboside-TP; Formycin A TP; Formycin B TP; Pyrrolosine TP; 2'-OH-ara-adenosine TP; 2'-OH-ara-cytidine TP; 2'-OH-ara-uridine TP; 2'-OH-ara-guanosine TP; 5-(2-carbomethoxyvinyl)uridine TP; and N6-(19-Amino-pentaoxanonadecyl)adenosine TP.

[0319] In some embodiments, polynucleotides (e.g., RNA polynucleotides, such as mRNA polynucleotides) include a combination of at least two (e.g., 2, 3, 4 or more) of the aforementioned modified nucleobases.

[0320] In some embodiments, modified nucleobases in polynucleotides (e.g., RNA polynucleotides, such as mRNA polynucleotides) are selected from the group consisting of pseudouridine (ψ), N1-methylpseudouridine ($m^1\psi$), N1-ethylpseudouridine, 2-thiouridine, 4'-thiouridine, 5-methylcytosine, 2-thio-1-methyl-1-deaza-pseudouridine, 2-thio-1-methyl-pseudouridine, 2-thio-5-aza-uridine, 2-thio-dihydropseudouridine, 2-thio-dihydrouridine, 2-thio-pseudouridine, 4-methoxy-2-thio-pseudouridine, 4-methoxy-pseudouridine, 4-thio-1-methyl-pseudouridine, 4-thio-pseudouridine, 5-aza-uridine, dihydropseudouridine, 5-methoxyuridine and 2'-O-methyl uridine. In some embodiments, polynucleotides (e.g., RNA polynucleotides, such as mRNA polynucleotides) include a combination of at least two (e.g., 2, 3, 4 or more) of the aforementioned modified nucleobases.

[0321] In some embodiments, modified nucleobases in polynucleotides (e.g., RNA polynucleotides, such as mRNA polynucleotides) are selected from the group consisting of 1-methyl-pseudouridine ($m^1\psi$), 5-methoxy-uridine (mo^5U), 5-methyl-cytidine (m^5C), pseudouridine (ψ), α -thio-guanosine and α -thio-adenosine. In some embodiments, polynucleotides includes a combination of at least two (e.g., 2, 3, 4 or more) of the aforementioned modified nucleobases.

[0322] In some embodiments, polynucleotides (e.g., RNA polynucleotides, such as mRNA polynucleotides) comprise pseudouridine (ψ) and 5-methyl-cytidine (m^5C). In some embodiments, polynucleotides (e.g., RNA polynucleotides, such as mRNA polynucleotides) comprise 1-methyl-pseudouridine ($m^1\psi$). In some embodiments, polynucleotides (e.g., RNA polynucleotides, such as mRNA polynucleotides) comprise 1-methyl-pseudouridine ($m^1\psi$) and 5-methyl-cytidine (m^5C). In some embodiments, polynucleotides (e.g., RNA polynucleotides, such as mRNA polynucleotides) comprise 2-thiouridine (s^2U). In some embodiments, polynucleotides (e.g., RNA polynucleotides, such as mRNA polynucleotides) comprise 2-thiouridine and 5-methyl-cytidine (m^5C). In some embodiments, polynucleotides (e.g., RNA polynucleotides, such as mRNA polynucleotides) comprise methoxy-uridine (mo^5U). In some embodiments, polynucleotides (e.g., RNA polynucleotides, such as mRNA polynucleotides) comprise 5-methoxy-uridine (mo^5U) and 5-methyl-cytidine (m^5C). In some embodiments, polynucleotides (e.g., RNA polynucleotides, such as mRNA polynucleotides) comprise 2'-O-methyl uridine and 5-methyl-cytidine (m^5C). In some embodiments, polynucleotides (e.g., RNA polynucleotides, such as mRNA polynucleotides) comprise N6-methyl-adenosine (m^6A). In some embodiments, polynucleotides (e.g., RNA polynucleotides, such as mRNA polynucleotides) comprise N6-methyl-adenosine (m^6A) and 5-methyl-cytidine (m^5C).

[0323] In some embodiments, polynucleotides (e.g., RNA polynucleotides, such as mRNA polynucleotides) are uniformly modified (e.g., fully modified, modified throughout the entire sequence) for a particular modification. For example, a polynucleotide can be uniformly modified with 5-methyl-cytidine (m^5C), meaning that all cytosine residues in the mRNA sequence are replaced with 5-methyl-cytidine (m^5C). Similarly, a polynucleotide can be uniformly modified for any type of nucleoside residue present in the sequence by replacement with a modified residue such as those set forth above.

[0324] Exemplary nucleobases and nucleosides having a modified cytosine include N4-acetyl-cytidine ($ac4C$), 5-methyl-cytidine (m^5C), 5-halo-cytidine (e.g., 5-iodo-cytidine), 5-hydroxymethyl-cytidine (hm^5C), 1-methyl-pseudoisocytidine, 2-thio-cytidine (s^2C), and 2-thio-5-methyl-cytidine.

[0325] In some embodiments, a modified nucleobase is a modified uridine. Exemplary nucleobases and In some embodiments, a modified nucleobase is a modified cytosine. nucleosides having a modified uridine include 5-cyano uridine, and 4'-thio uridine.

[0326] In some embodiments, a modified nucleobase is a modified adenine. Exemplary nucleobases and nucleosides having a modified adenine include 7-deaza-adenine, 1-methyl-adenosine (m^1A), 2-methyl-adenine (m^2A), and N6-methyl-adenosine (m^6A).

[0327] In some embodiments, a modified nucleobase is a modified guanine. Exemplary nucleobases and nucleosides having a modified guanine include inosine (I), 1-methyl-inosine (m^1I), wyosine (imG), methylwyosine ($mimG$), 7-deaza-guanosine, 7-cyano-7-deaza-guanosine ($preQ0$), 7-aminomethyl-7-deaza-guanosine ($preQ1$), 7-methyl-guanosine (m^7G), 1-methyl-guanosine (m^1G), 8-oxo-guanosine, 7-methyl-8-oxo-guanosine.

[0328] The polynucleotides of the present disclosure may be partially or fully modified along the entire length of the molecule. For example, one or more or all or a given type of nucleotide (e.g., purine or pyrimidine, or any one or more or all of A, G, U, C) may be uniformly modified in a polynucleotide of the disclosure, or in a given predetermined sequence region thereof (e.g., in the mRNA including or excluding the polyA tail). In some embodiments, all nucleotides X in a polynucleotide of the present disclosure (or in a given sequence region thereof) are modified nucleotides, wherein X may any one of nucleotides A, G, U, C, or any one of the combinations A+G, A+U, A+C, G+U, G+C, U+C, A+G+U, A+G+C, G+U+C or A+G+C.

[0329] The polynucleotide may contain from about 1% to about 100% modified nucleotides (either in relation to overall nucleotide content, or in relation to one or more types of nucleotide, i.e., any one or more of A, G, U or C) or any intervening percentage (e.g., from 1% to 20%, from 1% to 25%, from 1% to 50%, from 1% to 60%, from 1% to 70%, from 1% to 80%, from 1% to 90%, from 1% to 95%, from 10% to 20%, from 10% to 25%, from 10% to 50%, from 10% to 60%, from 10% to 70%, from 10% to 80%, from 10% to 90%, from 10% to 95%, from 10% to 100%, from 20% to 25%, from 20% to 50%, from 20% to 60%, from 20% to 70%, from 20% to 80%, from 20% to 90%, from 20% to 95%, from 20% to 100%, from 50% to 60%, from 50% to 70%, from 50% to 80%, from 50% to 90%, from 50% to 95%, from 50% to 100%, from 70% to 80%, from 70% to 90%, from 70% to 95%, from 70% to 100%,

from 80% to 90%, from 80% to 95%, from 80% to 100%, from 90% to 95%, from 90% to 100%, and from 95% to 100%). Any remaining percentage is accounted for by the presence of unmodified A, G, U, or C.

[0330] The polynucleotides may contain at a minimum 1% and at maximum 100% modified nucleotides, or any intervening percentage, such as at least 5% modified nucleotides, at least 10% modified nucleotides, at least 25% modified nucleotides, at least 50% modified nucleotides, at least 80% modified nucleotides, or at least 90% modified nucleotides. For example, the polynucleotides may contain a modified pyrimidine such as a modified uracil or cytosine. In some embodiments, at least 5%, at least 10%, at least 25%, at least 50%, at least 80%, at least 90% or 100% of the uracil in the polynucleotide is replaced with a modified uracil (e.g., a 5-substituted uracil). The modified uracil can be replaced by a compound having a single unique structure, or can be replaced by a plurality of compounds having different structures (e.g., 2, 3, 4 or more unique structures). In some embodiments, at least 5%, at least 10%, at least 25%, at least 50%, at least 80%, at least 90% or 100% of the cytosine in the polynucleotide is replaced with a modified cytosine (e.g., a 5-substituted cytosine). The modified cytosine can be replaced by a compound having a single unique structure, or can be replaced by a plurality of compounds having different structures (e.g., 2, 3, 4 or more unique structures).

[0331] Thus, in some embodiments, the RNA (e.g., mRNA) vaccines comprise a 5'UTR element, an optionally codon optimized open reading frame, and a 3'UTR element, a poly(A) sequence and/or a polyadenylation signal wherein the RNA is not chemically modified.

[0332] In some embodiments, the modified nucleobase is a modified uracil. Exemplary nucleobases and nucleosides having a modified uracil include pseudouridine (ψ), pyridin-4-one ribonucleoside, 5-aza-uridine, 6-aza-uridine, 2-thio-5-aza-uridine, 2-thio-uridine (s^2U), 4-thio-uridine (s^4U), 4-thio-pseudouridine, 2-thio-pseudouridine, 5-hydroxy-uridine (ho^5U), 5-aminoallyl-uridine, 5-halo-uridine (e.g., 5-iodo-uridine or 5-bromo-uridine), 3-methyl-uridine (m^3U), 5-methoxy-uridine (mo^5U), uridine 5-oxyacetic acid (cmo^5U), uridine 5-oxyacetic acid methyl ester ($mcmo^5U$), 5-carboxymethyl-uridine (cm^5U), 1-carboxymethyl-pseudouridine, 5-carboxyhydroxymethyl-uridine (chm^5U), 5-carboxyhydroxymethyl-uridine methyl ester ($mchm^5U$), 5-methoxycarbonylmethyl-uridine (mcm^5U), 5-methoxycarbonylmethyl-2-thio-uridine (mcm^5s^2U), 5-aminomethyl-2-thio-uridine (nm^5s^2U), 5-methylaminomethyl-uridine (mm^5U), 5-methylaminomethyl-2-thio-uridine (mm^5s^2U), 5-methylaminomethyl-2-seleno-uridine (mm^5se^2U), 5-carbamoylmethyl-uridine (ncm^5U), 5-carboxymethylaminomethyl-uridine ($cmnm^5U$), 5-carboxymethylaminomethyl-2-thio-uridine ($cmnm^5s^2U$), 5-propynyl-uridine, 1-propynyl-pseudouridine, 5-taurinomethyl-uridine (tm^5U), 1-taurinomethyl-pseudouridine, 5-taurinomethyl-2-thio-uridine (tm^5s^2U), 1-taurinomethyl-4-thio-pseudouridine, 5-methyl-uridine (m^5U , i.e., having the nucleobase deoxythymine), 1-methyl-pseudouridine ($m^1\psi$), 5-methyl-2-thio-uridine (m^5s^2U), 1-methyl-4-thio-pseudouridine ($m^1s^4\psi$), 4-thio-1-methyl-pseudouridine, 3-methyl-pseudouridine ($m^3\psi$), 2-thio-1-methyl-pseudouridine, 1-methyl-1-deaza-pseudouridine, 2-thio-1-methyl-1-deaza-pseudouridine, dihydrouridine (D), dihydropseudouridine, 5,6-dihydrouridine, 5-methyl-dihydrouridine (m^5D), 2-thio-dihydrouridine, 2-thio-dihydropseudouridine, 2-methoxy-

uridine, 2-methoxy-4-thio-uridine, 4-methoxy-pseudouridine, 4-methoxy-2-thio-pseudouridine, N1-methyl-pseudouridine, 3-(3-amino-3-carboxypropyl)uridine (acp^3U), 1-methyl-3-(3-amino-3-carboxypropyl)pseudouridine ($acp^3\psi$), 5-(isopentenylaminomethyl)uridine (inm^5U), 5-(isopentenylaminomethyl)-2-thio-uridine (inm^5s^2U), α -thio-uridine, 2'-O-methyl-uridine (Um), 5,2'-O-dimethyl-uridine (m^5Um), 2'-O-methyl-pseudouridine (ψm), 2-thio-2'-O-methyl-uridine (s^2Um), 5-methoxycarbonylmethyl-2'-O-methyl-uridine (mcm^5Um), 5-carbamoylmethyl-2'-O-methyl-uridine (ncm^5Um), 5-carboxymethylaminomethyl-2'-O-methyl-uridine ($cmnm^5Um$), 3,2'-O-dimethyl-uridine (m^3Um), and 5-(isopentenylaminomethyl)-2'-O-methyl-uridine (inm^5Um), 1-thio-uridine, deoxythymidine, 2'-F-ara-uridine, 2'-F-uridine, 2'-OH-ara-uridine, 5-(2-carbomethoxyvinyl) uridine, and 5-[3-(1-E-propenylamino)] uridine.

[0333] In some embodiments, the modified nucleobase is a modified cytosine. Exemplary nucleobases and nucleosides having a modified cytosine include 5-aza-cytidine, 6-aza-cytidine, pseudoisocytidine, 3-methyl-cytidine (m^3C), N4-acetyl-cytidine (ac^4C), 5-formyl-cytidine (f^5C), N4-methyl-cytidine (m^4C), 5-methyl-cytidine (m^5C), 5-halo-cytidine (e.g., 5-iodo-cytidine), 5-hydroxymethyl-cytidine (hm^5C), 1-methyl-pseudoisocytidine, pyrrolo-cytidine, pyrrolo-pseudoisocytidine, 2-thio-cytidine (s^2C), 2-thio-5-methyl-cytidine, 4-thio-pseudoisocytidine, 4-thio-1-methyl-pseudoisocytidine, 4-thio-1-methyl-1-deazapseudoisocytidine, 1-methyl-1-deazapseudoisocytidine, zebularine, 5-aza-zebularine, 5-methyl-zebularine, 5-aza-2-thio-zebularine, 2-thio-zebularine, 2-methoxy-cytidine, 2-methoxy-5-methyl-cytidine, 4-methoxy-pseudoisocytidine, 4-methoxy-1-methyl-pseudoisocytidine, lysidine (k_2C), α -thio-cytidine, 2'-O-methyl-cytidine (Cm), 5,2'-O-dimethyl-cytidine (m^5Cm), N4-acetyl-2'-O-methyl-cytidine (ac^4Cm), N4,2'-O-dimethyl-cytidine (m^4Cm), 5-formyl-2'-O-methyl-cytidine (f^5Cm), N4,N4,2'-O-trimethyl-cytidine (m^42Cm), 1-thio-cytidine, 2'-F-ara-cytidine, 2'-F-cytidine, and 2'-OH-ara-cytidine.

[0334] In some embodiments, the modified nucleobase is a modified adenine. Exemplary nucleobases and nucleosides having a modified adenine include 2-amino-purine, 2, 6-diaminopurine, 2-amino-6-halo-purine (e.g., 2-amino-6-chloro-purine), 6-halo-purine (e.g., 6-chloro-purine), 2-amino-6-methyl-purine, 8-azido-adenosine, 7-deaza-adenine, 7-deaza-8-aza-adenine, 7-deaza-2-amino-purine, 7-deaza-8-aza-2-amino-purine, 7-deaza-2,6-diaminopurine, 7-deaza-8-aza-2,6-diaminopurine, 1-methyl-adenosine (m^1A), 2-methyl-adenine (m^2A), N6-methyl-adenosine (m^6A), 2-methylthio-N6-methyl-adenosine (ms^2m^6A), N6-isopentenyl-adenosine (i^6A), 2-methylthio-N6-isopentenyl-adenosine (ms^2i^6A), N6-(cis-hydroxyisopentenyl)adenosine (io^6A), 2-methylthio-N6-(cis-hydroxyisopentenyl)adenosine (ms^2io^6A), N6-glycylcarbamoyl-adenosine (g^6A), N6-threonylcarbamoyl-adenosine (t^6A), N6-methyl-N6-threonylcarbamoyl-adenosine (m^6t^6A), 2-methylthio-N6-threonylcarbamoyl-adenosine (ms^2g^6A), N6,N6-dimethyl-adenosine (m^62A), N6-hydroxynorvalylcarbamoyl-adenosine (hn^6A), 2-methylthio-N6-hydroxynorvalylcarbamoyl-adenosine (ms^2hn^6A), N6-acetyl-adenosine (ac^6A), 7-methyl-adenine, 2-methylthio-adenine, 2-methoxy-adenine, α -thio-adenosine, 2'-O-methyl-adenosine (Am), N6,2'-O-dimethyl-adenosine (m^6Am), N6,N6,2'-O-trimethyl-adenosine (m^62Am), 1,2'-

O-dimethyl-adenosine (m^1Am), 2'-O-ribosyladenosine (phosphate) ($Ar(p)$), 2-amino-N6-methyl-purine, 1-thio-adenosine, 8-azido-adenosine, 2'-F-ara-adenosine, 2'-F-adenosine, 2'-OH-ara-adenosine, and N6-(19-amino-penta-oxanonadecyl)-adenosine.

[0335] In some embodiments, the modified nucleobase is a modified guanine. Exemplary nucleobases and nucleosides having a modified guanine include inosine (I), 1-methyl-inosine (m^1I), wyosine (imG), methylwyosine (mimG), 4-demethyl-wyosine (imG-14), isowyosine (imG2), wybutosine (yW), peroxywybutosine (o2yW), hydroxywybutosine (OhyW), undermodified hydroxywybutosine (OhyW*), 7-deaza-guanosine, queuosine (Q), epoxyqueuosine (oQ), galactosyl-queuosine (galQ), mannosyl-queuosine (manQ), 7-cyano-7-deaza-guanosine ($preQ_6$), 7-aminomethyl-7-deaza-guanosine ($preQ_1$), archaeosine (G^+), 7-deaza-8-aza-guanosine, 6-thio-guanosine, 6-thio-7-deaza-guanosine, 6-thio-7-deaza-8-aza-guanosine, 7-methyl-guanosine (m^7G), 6-thio-7-methyl-guanosine, 7-methyl-inosine, 6-methoxy-guanosine, 1-methyl-guanosine (m^1G), N2-methyl-guanosine (m^2G), N2,N2-dimethyl-guanosine (m^2_2G), N2,7-dimethyl-guanosine ($m^{2,7}G$), N2, N2,7-dimethyl-guanosine ($m^{2,2,7}G$), 8-oxo-guanosine, 7-methyl-8-oxo-guanosine, 1-methyl-6-thio-guanosine, N2-methyl-6-thio-guanosine, N2,N2-dimethyl-6-thio-guanosine, α -thio-guanosine, 2'-O-methyl-guanosine (Gm), N2-methyl-2'-O-methyl-guanosine (m^2Gm), N2,N2-dimethyl-2'-O-methyl-guanosine (m^2_2Gm), 1-methyl-2'-O-methyl-guanosine (m^1Gm), N2,7-dimethyl-2'-O-methyl-guanosine ($m^{2,7}Gm$), 2'-O-methyl-inosine (Im), 1,2'-O-dimethyl-inosine (m^1Im), 2'-O-ribosylguanosine (phosphate) ($Gr(p)$), 1-thio-guanosine, O6-methyl-guanosine, 2'-F-ara-guanosine, and 2'-F-guanosine.

N-Linked Glycosylation Site Mutants

[0336] N-linked glycans of viral proteins play important roles in modulating the immune response. Glycans can be important for maintaining the appropriate antigenic conformations, shielding potential neutralization epitopes, and may alter the proteolytic susceptibility of proteins. Some viruses have putative N-linked glycosylation sites. Deletion or modification of an N-linked glycosylation site may enhance the immune response. Thus, the present disclosure provides, in some embodiments, RNA (e.g., mRNA) vaccines comprising nucleic acids (e.g., mRNA) encoding antigenic polypeptides that comprise a deletion or modification at one or more N-linked glycosylation sites.

In Vitro Transcription of RNA (e.g., mRNA)

[0337] Respiratory virus vaccines of the present disclosure comprise at least one RNA polynucleotide, such as a mRNA (e.g., modified mRNA). mRNA, for example, is transcribed in vitro from template DNA, referred to as an "in vitro transcription template." In some embodiments, an in vitro transcription template encodes a 5' untranslated (UTR) region, contains an open reading frame, and encodes a 3' UTR and a polyA tail. The particular nucleic acid sequence composition and length of an in vitro transcription template will depend on the mRNA encoded by the template.

[0338] A "5' untranslated region" (5'UTR) refers to a region of an mRNA that is directly upstream (i.e., 5') from the start codon (i.e., the first codon of an mRNA transcript translated by a ribosome) that does not encode a polypeptide.

[0339] A "3' untranslated region" (3'UTR) refers to a region of an mRNA that is directly downstream (i.e., 3') from the stop codon (i.e., the codon of an mRNA transcript that signals a termination of translation) that does not encode a polypeptide.

[0340] An "open reading frame" is a continuous stretch of DNA beginning with a start codon (e.g., methionine (ATG)), and ending with a stop codon (e.g., TAA, TAG or TGA) and encodes a polypeptide. A "polyA tail" is a region of mRNA that is downstream, e.g., directly downstream (i.e., 3'), from the 3' UTR that contains multiple, consecutive adenosine monophosphates. A polyA tail may contain 10 to 300 adenosine monophosphates. For example, a polyA tail may contain 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290 or 300 adenosine monophosphates. In some embodiments, a polyA tail contains 50 to 250 adenosine monophosphates. In a relevant biological setting (e.g., in cells, in vivo) the poly(A) tail functions to protect mRNA from enzymatic degradation, e.g., in the cytoplasm, and aids in transcription termination, export of the mRNA from the nucleus and translation.

[0341] In some embodiments, a polynucleotide includes 200 to 3,000 nucleotides. For example, a polynucleotide may include 200 to 500, 200 to 1000, 200 to 1500, 200 to 3000, 500 to 1000, 500 to 1500, 500 to 2000, 500 to 3000, 1000 to 1500, 1000 to 2000, 1000 to 3000, 1500 to 3000, or 2000 to 3000 nucleotides.

Flagellin Adjuvants Flagellin is an approximately 500 amino acid monomeric protein that polymerizes to form the flagella associated with bacterial motion. Flagellin is expressed by a variety of flagellated bacteria (*Salmonella typhimurium* for example) as well as non-flagellated bacteria (such as *Escherichia coli*). Sensing of flagellin by cells of the innate immune system (dendritic cells, macrophages, etc.) is mediated by the Toll-like receptor 5 (TLRS) as well as by Nod-like receptors (NLRs) Ipaf and Naip5. TLRs and NLRs have been identified as playing a role in the activation of innate immune response and adaptive immune response. As such, flagellin provides an adjuvant effect in a vaccine.

[0342] The nucleotide and amino acid sequences encoding known flagellin polypeptides are publicly available in the NCBI GenBank database. The flagellin sequences from *S. Typhimurium*, *H. Pylori*, *V. Cholera*, *S. marcesens*, *S. flexneri*, *T. Pallidum*, *L. pneumophila*, *B. burgdorferi*, *C. difficile*, *R. meliloti*, *A. tumefaciens*, *R. lupini*, *B. clarridgeiae*, *P. Mirabilis*, *B. subtilis*, *L. monocytogenes*, *P. aeruginosa*, and *E. coli*, among others are known.

[0343] A flagellin polypeptide, as used herein, refers to a full length flagellin protein, immunogenic fragments thereof, and peptides having at least 50% sequence identity to a flagellin protein or immunogenic fragments thereof. Exemplary flagellin proteins include flagellin from *Salmonella typhi* (UniPro Entry number: Q56086), *Salmonella typhimurium* (A0A0C9DG09), *Salmonella enteritidis* (A0A0C9BAB7), and *Salmonella choleraesuis* (Q6V2X8), and SEQ ID NO: 54-56 (Table 17). In some embodiments, the flagellin polypeptide has at least 60%, 70%, 75%, 80%, 90%, 95%, 97%, 98%, or 99% sequence identity to a flagellin protein or immunogenic fragments thereof.

[0344] In some embodiments, the flagellin polypeptide is an immunogenic fragment. An immunogenic fragment is a portion of a flagellin protein that provokes an immune response. In some embodiments, the immune response is a

TLRS immune response. An example of an immunogenic fragment is a flagellin protein in which all or a portion of a hinge region has been deleted or replaced with other amino acids. For example, an antigenic polypeptide may be inserted in the hinge region. Hinge regions are the hyper-variable regions of a flagellin. Hinge regions of a flagellin are also referred to as “D3 domain or region,” “propeller domain or region,” “hypervariable domain or region” and “variable domain or region.” “At least a portion of a hinge region,” as used herein, refers to any part of the hinge region of the flagellin, or the entirety of the hinge region. In other embodiments an immunogenic fragment of flagellin is a 20, 25, 30, 35, or 40 amino acid C-terminal fragment of flagellin.

[0345] The flagellin monomer is formed by domains D0 through D3. D0 and D1, which form the stem, are composed of tandem long alpha helices and are highly conserved among different bacteria. The D1 domain includes several stretches of amino acids that are useful for TLRS activation. The entire D1 domain or one or more of the active regions within the domain are immunogenic fragments of flagellin. Examples of immunogenic regions within the D1 domain include residues 88-114 and residues 411-431 (in *Salmonella typhimurium* FliC flagellin. Within the 13 amino acids in the 88-100 region, at least 6 substitutions are permitted between *Salmonella* flagellin and other flagellins that still preserve TLRS activation. Thus, immunogenic fragments of flagellin include flagellin like sequences that activate TLRS and contain a 13 amino acid motif that is 53% or more identical to the *Salmonella* sequence in 88-100 of FliC (LQVRRELAVQSAN; SEQ ID NO: 84).

[0346] In some embodiments, the RNA (e.g., mRNA) vaccine includes an RNA that encodes a fusion protein of flagellin and one or more antigenic polypeptides. A “fusion protein” as used herein, refers to a linking of two components of the construct. In some embodiments, a carboxy-terminus of the antigenic polypeptide is fused or linked to an amino terminus of the flagellin polypeptide. In other embodiments, an amino-terminus of the antigenic polypeptide is fused or linked to a carboxy-terminus of the flagellin polypeptide. The fusion protein may include, for example, one, two, three, four, five, six or more flagellin polypeptides linked to one, two, three, four, five, six or more antigenic polypeptides. When two or more flagellin polypeptides and/or two or more antigenic polypeptides are linked such a construct may be referred to as a “multimer.”

[0347] Each of the components of a fusion protein may be directly linked to one another or they may be connected through a linker. For instance, the linker may be an amino acid linker. The amino acid linker encoded for by the RNA (e.g., mRNA) vaccine to link the components of the fusion protein may include, for instance, at least one member selected from the group consisting of a lysine residue, a glutamic acid residue, a serine residue and an arginine residue. In some embodiments the linker is 1-30, 1-25, 1-20, 5-10, 5, 15, or 5-20 amino acids in length.

[0348] In other embodiments the RNA (e.g., mRNA) vaccine includes at least two separate RNA polynucleotides, one encoding one or more antigenic polypeptides and the other encoding the flagellin polypeptide. The at least two RNA polynucleotides may be co-formulated in a carrier such as a lipid nanoparticle.

Broad Spectrum RNA (e.g., mRNA) Vaccines

[0349] There may be situations where persons are at risk for infection with more than one strain of hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1). RNA (e.g., mRNA) therapeutic vaccines are particularly amenable to combination vaccination approaches due to a number of factors including, but not limited to, speed of manufacture, ability to rapidly tailor vaccines to accommodate perceived geographical threat, and the like. Moreover, because the vaccines utilize the human body to produce the antigenic protein, the vaccines are amenable to the production of larger, more complex antigenic proteins, allowing for proper folding, surface expression, antigen presentation, etc. in the human subject. To protect against more than one strain of hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1), a combination vaccine can be administered that includes RNA (e.g., mRNA) encoding at least one antigenic polypeptide protein (or antigenic portion thereof) of a first respiratory virus and further includes RNA encoding at least one antigenic polypeptide protein (or antigenic portion thereof) of a second respiratory virus. RNA (e.g., mRNA) can be co-formulated, for example, in a single lipid nanoparticle (LNP) or can be formulated in separate LNPs for co-administration.

Methods of Treatment

[0350] Provided herein are compositions (e.g., pharmaceutical compositions), methods, kits and reagents for prevention and/or treatment of respiratory diseases/infections in humans and other mammals. Respiratory virus RNA (e.g., mRNA) vaccines can be used as therapeutic or prophylactic agents, alone or in combination with other vaccine(s). They may be used in medicine to prevent and/or treat respiratory disease/infection. In exemplary aspects, the RNA (e.g., mRNA) vaccines of the present disclosure are used to provide prophylactic protection from hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1). Prophylactic protection from hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1) can be achieved following administration of a RNA (e.g., mRNA) vaccine of the present disclosure. Respiratory virus RNA (e.g., mRNA) vaccines of the present disclosure may be used to treat or prevent viral “co-infections” containing two or more respiratory infections. Vaccines can be administered once, twice, three times, four times or more, but it is likely sufficient to administer the vaccine once (optionally followed by a single booster). It is possible, although less desirable, to administer the vaccine to an infected individual to achieve a therapeutic response. Dosing may need to be adjusted accordingly.

[0351] A method of eliciting an immune response in a subject against hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1) is provided in aspects of the present disclosure. The method involves administering to the subject a respiratory virus RNA (e.g., mRNA) vaccine comprising at least one RNA (e.g., mRNA) polynucleotide having an open reading

frame encoding at least one hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1) antigenic polypeptide thereof, thereby inducing in the subject an immune response specific to hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1) antigenic polypeptide or an immunogenic fragment thereof, wherein anti-antigenic polypeptide antibody titer in the subject is increased following vaccination relative to anti-antigenic polypeptide antibody titer in a subject vaccinated with a prophylactically effective dose of a traditional vaccine against hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1). An “anti-antigenic polypeptide antibody” is a serum antibody that binds specifically to the antigenic polypeptide.

[0352] In some embodiments, a RNA (e.g., mRNA) vaccine (e.g., a hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1 RNA vaccine) capable of eliciting an immune response is administered intramuscularly via a composition including a compound according to Formula (I), (IA), (II), (IIa), (IIb), (IIc), (IId) or (IIE) (e.g., Compound 3, 18, 20, 25, 26, 29, 30, 60, 108-112, or 122).

[0353] A prophylactically effective dose is a therapeutically effective dose that prevents infection with the virus at a clinically acceptable level. In some embodiments the therapeutically effective dose is a dose listed in a package insert for the vaccine. A traditional vaccine, as used herein, refers to a vaccine other than the RNA (e.g., mRNA) vaccines of the present disclosure. For instance, a traditional vaccine includes but is not limited to live/attenuated microorganism vaccines, killed/inactivated microorganism vaccines, subunit vaccines, protein antigen vaccines, DNA vaccines, VLP vaccines, etc. In exemplary embodiments, a traditional vaccine is a vaccine that has achieved regulatory approval and/or is registered by a national drug regulatory body, for example the Food and Drug Administration (FDA) in the United States or the European Medicines Agency (EMA).

[0354] In some embodiments the anti-antigenic polypeptide antibody titer in the subject is increased 1 log to 10 log following vaccination relative to anti-antigenic polypeptide antibody titer in a subject vaccinated with a prophylactically effective dose of a traditional vaccine against hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1).

[0355] In some embodiments the anti-antigenic polypeptide antibody titer in the subject is increased 1 log, 2 log, 3 log, 5 log or 10 log following vaccination relative to anti-antigenic polypeptide antibody titer in a subject vaccinated with a prophylactically effective dose of a traditional vaccine against hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1).

[0356] A method of eliciting an immune response in a subject against hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-

HKU1) is provided in other aspects of the disclosure. The method involves administering to the subject a respiratory virus RNA (e.g., mRNA) vaccine comprising at least one RNA (e.g., mRNA) polynucleotide having an open reading frame encoding at least one hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1) antigenic polypeptide or an immunogenic fragment thereof, thereby inducing in the subject an immune response specific to hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1) antigenic polypeptide or an immunogenic fragment thereof, wherein the immune response in the subject is equivalent to an immune response in a subject vaccinated with a traditional vaccine against the hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1) at 2 times to 100 times the dosage level relative to the RNA (e.g., mRNA) vaccine.

[0357] In some embodiments, the immune response in the subject is equivalent to an immune response in a subject vaccinated with a traditional vaccine at 2, 3, 4, 5, 10, 50, 100 times the dosage level relative to the hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1) RNA (e.g., mRNA) vaccine.

[0358] In some embodiments the immune response in the subject is equivalent to an immune response in a subject vaccinated with a traditional vaccine at 10-100 times, or 100-1000 times, the dosage level relative to the hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1) RNA (e.g., mRNA) vaccine.

[0359] In some embodiments the immune response is assessed by determining [protein] antibody titer in the subject.

[0360] Some aspects of the present disclosure provide a method of eliciting an immune response in a subject against a In some embodiments the immune response in the subject is equivalent to an immune response in a subject vaccinated with a traditional vaccine at 2, 3, 4, 5, 10, 50, 100 times the dosage level relative to the hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1) RNA (e.g., mRNA) vaccine by administering to the subject a respiratory virus RNA (e.g., mRNA) vaccine comprising at least one RNA (e.g., mRNA) polynucleotide having an open reading frame encoding at least one hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1) antigenic polypeptide, thereby inducing in the subject an immune response specific to the antigenic polypeptide or an immunogenic fragment thereof, wherein the immune response in the subject is induced 2 days to 10 weeks earlier relative to an immune response induced in a subject vaccinated with a prophylactically effective dose of a traditional vaccine against the hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or

HCoV-HKU1). In some embodiments, the immune response in the subject is induced in a subject vaccinated with a prophylactically effective dose of a traditional vaccine at 2 times to 100 times the dosage level relative to the RNA (e.g., mRNA) vaccine.

[0361] In some embodiments, the immune response in the subject is induced 2 days earlier, or 3 days earlier, relative to an immune response induced in a subject vaccinated with a prophylactically effective dose of a traditional vaccine.

[0362] In some embodiments the immune response in the subject is induced 1 week, 2 weeks, 3 weeks, 5 weeks, or 10 weeks earlier relative to an immune response induced in a subject vaccinated with a prophylactically effective dose of a traditional vaccine.

[0363] Also provided herein is a method of eliciting an immune response in a subject against hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1) by administering to the subject a respiratory virus RNA (e.g., mRNA) vaccine having an open reading frame encoding a first antigenic polypeptide, wherein the RNA polynucleotide does not include a stabilization element, and wherein an adjuvant is not co-formulated or co-administered with the vaccine.

Therapeutic and Prophylactic Compositions

[0364] Provided herein are compositions (e.g., pharmaceutical compositions), methods, kits and reagents for prevention, treatment or diagnosis of hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1) in humans and other mammals, for example. Respiratory virus RNA (e.g. mRNA) vaccines can be used as therapeutic or prophylactic agents. They may be used in medicine to prevent and/or treat infectious disease. In some embodiments, the respiratory RNA (e.g., mRNA) vaccines of the present disclosure are used for the priming of immune effector cells, for example, to activate peripheral blood mononuclear cells (PBMCs) ex vivo, which are then infused (re-infused) into a subject.

[0365] In some embodiments, respiratory virus vaccine containing RNA (e.g., mRNA) polynucleotides as described herein can be administered to a subject (e.g., a mammalian subject, such as a human subject), and the RNA (e.g., mRNA) polynucleotides are translated in vivo to produce an antigenic polypeptide.

[0366] The respiratory virus RNA (e.g., mRNA) vaccines may be induced for translation of a polypeptide (e.g., antigen or immunogen) in a cell, tissue or organism. In some embodiments, such translation occurs in vivo, although such translation may occur ex vivo, in culture or in vitro. In some embodiments, the cell, tissue or organism is contacted with an effective amount of a composition containing a respiratory virus RNA (e.g., mRNA) vaccine that contains a polynucleotide that has at least one a translatable region encoding an antigenic polypeptide.

[0367] An “effective amount” of an respiratory virus RNA (e.g. mRNA) vaccine is provided based, at least in part, on the target tissue, target cell type, means of administration, physical characteristics of the polynucleotide (e.g., size, and extent of modified nucleosides) and other components of the vaccine, and other determinants. In general, an effective amount of the respiratory virus RNA (e.g., mRNA) vaccine composition provides an induced or boosted immune

response as a function of antigen production in the cell, preferably more efficient than a composition containing a corresponding unmodified polynucleotide encoding the same antigen or a peptide antigen. Increased antigen production may be demonstrated by increased cell transfection (the percentage of cells transfected with the RNA, e.g., mRNA, vaccine), increased protein translation from the polynucleotide, decreased nucleic acid degradation (as demonstrated, for example, by increased duration of protein translation from a modified polynucleotide), or altered antigen specific immune response of the host cell.

[0368] In some embodiments, RNA (e.g. mRNA) vaccines (including polynucleotides their encoded polypeptides) in accordance with the present disclosure may be used for treatment of hMPV, PIV3, RSV, MeV and/or BetaCoV (including MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH and/or HCoV-HKU1).

[0369] Respiratory RNA (e.g. mRNA) vaccines may be administered prophylactically or therapeutically as part of an active immunization scheme to healthy individuals or early in infection during the incubation phase or during active infection after onset of symptoms. In some embodiments, the amount of RNA (e.g., mRNA) vaccine of the present disclosure provided to a cell, a tissue or a subject may be an amount effective for immune prophylaxis.

[0370] Respiratory virus RNA (e.g. mRNA) vaccines may be administered with other prophylactic or therapeutic compounds. As a non-limiting example, a prophylactic or therapeutic compound may be an adjuvant or a booster. As used herein, when referring to a prophylactic composition, such as a vaccine, the term “booster” refers to an extra administration of the prophylactic (vaccine) composition. A booster (or booster vaccine) may be given after an earlier administration of the prophylactic composition. The time of administration between the initial administration of the prophylactic composition and the booster may be, but is not limited to, 1 minute, 2 minutes, 3 minutes, 4 minutes, 5 minutes, 6 minutes, 7 minutes, 8 minutes, 9 minutes, 10 minutes, 15 minutes, 20 minutes, 35 minutes, 40 minutes, 45 minutes, 50 minutes, 55 minutes, 1 hour, 2 hours, 3 hours, 4 hours, 5 hours, 6 hours, 7 hours, 8 hours, 9 hours, 10 hours, 11 hours, 12 hours, 13 hours, 14 hours, 15 hours, 16 hours, 17 hours, 18 hours, 19 hours, 20 hours, 21 hours, 22 hours, 23 hours, 1 day, 36 hours, 2 days, 3 days, 4 days, 5 days, 6 days, 1 week, 10 days, 2 weeks, 3 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 1 year, 18 months, 2 years, 3 years, 4 years, 5 years, 6 years, 7 years, 8 years, 9 years, 10 years, 11 years, 12 years, 13 years, 14 years, 15 years, 16 years, 17 years, 18 years, 19 years, 20 years, 25 years, 30 years, 35 years, 40 years, 45 years, 50 years, 55 years, 60 years, 65 years, 70 years, 75 years, 80 years, 85 years, 90 years, 95 years or more than 99 years. In some embodiments, the time of administration between the initial administration of the prophylactic composition and the booster may be, but is not limited to, 1 week, 2 weeks, 3 weeks, 1 month, 2 months, 3 months, 6 months or 1 year.

[0371] In some embodiments, respiratory virus RNA (e.g. mRNA) vaccines may be administered intramuscularly or intradermally, similarly to the administration of inactivated vaccines known in the art.

[0372] Respiratory virus RNA (e.g. mRNA) vaccines may be utilized in various settings depending on the prevalence

of the infection or the degree or level of unmet medical need. As a non-limiting example, the RNA (e.g., mRNA) vaccines may be utilized to treat and/or prevent a variety of respiratory infections. RNA (e.g., mRNA) vaccines have superior properties in that they produce much larger antibody titers and produce responses early than commercially available anti-viral agents/compositions.

[0373] Provided herein are pharmaceutical compositions including respiratory virus RNA (e.g. mRNA) vaccines and RNA (e.g. mRNA) vaccine compositions and/or complexes optionally in combination with one or more pharmaceutically acceptable excipients.

[0374] Respiratory virus RNA (e.g. mRNA) vaccines may be formulated or administered alone or in conjunction with one or more other components. For instance, hMPV/PIV3/RSV RNA (e.g., mRNA) vaccines (vaccine compositions) may comprise other components including, but not limited to, adjuvants.

[0375] In some embodiments, respiratory virus (e.g. mRNA) vaccines do not include an adjuvant (they are adjuvant free).

[0376] Respiratory virus RNA (e.g. mRNA) vaccines may be formulated or administered in combination with one or more pharmaceutically-acceptable excipients. In some embodiments, vaccine compositions comprise at least one additional active substances, such as, for example, a therapeutically-active substance, a prophylactically-active substance, or a combination of both. Vaccine compositions may be sterile, pyrogen-free or both sterile and pyrogen-free. General considerations in the formulation and/or manufacture of pharmaceutical agents, such as vaccine compositions, may be found, for example, in Remington: The Science and Practice of Pharmacy 21st ed., Lippincott Williams & Wilkins, 2005 (incorporated herein by reference in its entirety). In some embodiments, respiratory virus RNA (e.g. mRNA) vaccines are administered to humans, human patients or subjects. For the purposes of the present disclosure, the phrase "active ingredient" generally refers to the RNA (e.g., mRNA) vaccines or the polynucleotides contained therein, for example, RNA polynucleotides (e.g., mRNA polynucleotides) encoding antigenic polypeptides.

[0377] Formulations of the respiratory virus vaccine compositions described herein may be prepared by any method known or hereafter developed in the art of pharmacology. In general, such preparatory methods include the step of bringing the active ingredient (e.g., mRNA polynucleotide) into association with an excipient and/or one or more other accessory ingredients, and then, if necessary and/or desirable, dividing, shaping and/or packaging the product into a desired single- or multi-dose unit.

[0378] Relative amounts of the active ingredient, the pharmaceutically acceptable excipient, and/or any additional ingredients in a pharmaceutical composition in accordance with the disclosure will vary, depending upon the identity, size, and/or condition of the subject treated and further depending upon the route by which the composition is to be administered. By way of example, the composition may comprise between 0.1% and 100%, e.g., between 0.5 and 50%, between 1-30%, between 5-80%, at least 80% (w/w) active ingredient.

[0379] Respiratory virus RNA (e.g. mRNA) vaccines can be formulated using one or more excipients to: (1) increase stability; (2) increase cell transfection; (3) permit the sustained or delayed release (e.g., from a depot formulation);

(4) alter the biodistribution (e.g., target to specific tissues or cell types); (5) increase the translation of encoded protein in vivo; and/or (6) alter the release profile of encoded protein (antigen) in vivo. In addition to traditional excipients such as any and all solvents, dispersion media, diluents, or other liquid vehicles, dispersion or suspension aids, surface active agents, isotonic agents, thickening or emulsifying agents, preservatives, excipients can include, without limitation, lipidoids, liposomes, lipid nanoparticles, polymers, lipoplexes, core-shell nanoparticles, peptides, proteins, cells transfected with respiratory virus RNA (e.g. mRNA) vaccines (e.g., for transplantation into a subject), hyaluronidase, nanoparticle mimics and combinations thereof.

Stabilizing Elements

[0380] Naturally-occurring eukaryotic mRNA molecules have been found to contain stabilizing elements, including, but not limited to untranslated regions (UTR) at their 5'-end (5'UTR) and/or at their 3'-end (3'UTR), in addition to other structural features, such as a 5'-cap structure or a 3'-poly(A) tail. Both the 5'UTR and the 3'UTR are typically transcribed from the genomic DNA and are elements of the premature mRNA. Characteristic structural features of mature mRNA, such as the 5'-cap and the 3'-poly(A) tail are usually added to the transcribed (premature) mRNA during mRNA processing. The 3'-poly(A) tail is typically a stretch of adenine nucleotides added to the 3'-end of the transcribed mRNA. It can comprise up to about 400 adenine nucleotides. In some embodiments the length of the 3'-poly(A) tail may be an essential element with respect to the stability of the individual mRNA.

[0381] In some embodiments the RNA (e.g., mRNA) vaccine may include one or more stabilizing elements. Stabilizing elements may include for instance a histone stem-loop. A stem-loop binding protein (SLBP), a 32 kDa protein has been identified. It is associated with the histone stem-loop at the 3'-end of the histone messages in both the nucleus and the cytoplasm. Its expression level is regulated by the cell cycle; it peaks during the S-phase, when histone mRNA levels are also elevated. The protein has been shown to be essential for efficient 3'-end processing of histone pre-mRNA by the U7 snRNP. SLBP continues to be associated with the stem-loop after processing, and then stimulates the translation of mature histone mRNAs into histone proteins in the cytoplasm. The RNA binding domain of SLBP is conserved through metazoa and protozoa; its binding to the histone stem-loop depends on the structure of the loop. The minimum binding site includes at least three nucleotides 5' and two nucleotides 3' relative to the stem-loop.

[0382] In some embodiments, the RNA (e.g., mRNA) vaccines include a coding region, at least one histone stem-loop, and optionally, a poly(A) sequence or polyadenylation signal. The poly(A) sequence or polyadenylation signal generally should enhance the expression level of the encoded protein. The encoded protein, in some embodiments, is not a histone protein, a reporter protein (e.g. Luciferase, GFP, EGFP, β -Galactosidase, EGFP), or a marker or selection protein (e.g. alpha-Globin, Galactokinase and Xanthine:guanine phosphoribosyl transferase (GPT)).

[0383] In some embodiments, the combination of a poly (A) sequence or polyadenylation signal and at least one histone stem-loop, even though both represent alternative

mechanisms in nature, acts synergistically to increase the protein expression beyond the level observed with either of the individual elements. It has been found that the synergistic effect of the combination of poly(A) and at least one histone stem-loop does not depend on the order of the elements or the length of the poly(A) sequence.

[0384] In some embodiments, the RNA (e.g., mRNA) vaccine does not comprise a histone downstream element (HDE). "Histone downstream element" (HDE) includes a purine-rich polynucleotide stretch of approximately 15 to 20 nucleotides 3' of naturally occurring stem-loops, representing the binding site for the U7 snRNA, which is involved in processing of histone pre-mRNA into mature histone mRNA. Ideally, the inventive nucleic acid does not include an intron.

[0385] In some embodiments, the RNA (e.g., mRNA) vaccine may or may not contain an enhancer and/or promoter sequence, which may be modified or unmodified or which may be activated or inactivated. In some embodiments, the histone stem-loop is generally derived from histone genes, and includes an intramolecular base pairing of two neighboring partially or entirely reverse complementary sequences separated by a spacer, including (e.g., consisting of) a short sequence, which forms the loop of the structure. The unpaired loop region is typically unable to base pair with either of the stem loop elements. It occurs more often in RNA, as is a key component of many RNA secondary structures, but may be present in single-stranded DNA as well. Stability of the stem-loop structure generally depends on the length, number of mismatches or bulges, and base composition of the paired region. In some embodiments, wobble base pairing (non-Watson-Crick base pairing) may result. In some embodiments, the at least one histone stem-loop sequence comprises a length of 15 to 45 nucleotides.

[0386] In other embodiments the RNA (e.g., mRNA) vaccine may have one or more AU-rich sequences removed. These sequences, sometimes referred to as AURES are destabilizing sequences found in the 3'UTR. The AURES may be removed from the RNA (e.g., mRNA) vaccines. Alternatively the AURES may remain in the RNA (e.g., mRNA) vaccine.

Nanoparticle Formulations In some embodiments, respiratory virus RNA (e.g. mRNA) vaccines are formulated in a nanoparticle. In some embodiments, respiratory virus RNA (e.g. mRNA) vaccines are formulated in a lipid nanoparticle. In some embodiments, respiratory virus RNA (e.g. mRNA) vaccines are formulated in a lipid-polycation complex, referred to as a cationic lipid nanoparticle. As a non-limiting example, the polycation may include a cationic peptide or a polypeptide such as, but not limited to, polylysine, polyornithine and/or polyarginine. In some embodiments, respiratory virus RNA (e.g., mRNA) vaccines are formulated in a lipid nanoparticle that includes a non-cationic lipid such as, but not limited to, cholesterol or dioleoyl phosphatidylethanolamine (DOPE).

[0387] A lipid nanoparticle formulation may be influenced by, but not limited to, the selection of the cationic lipid component, the degree of cationic lipid saturation, the nature of the PEGylation, ratio of all components and biophysical parameters such as size. In one example by Semple et al. (*Nature Biotech.* 2010 28:172-176), the lipid nanoparticle formulation is composed of 57.1% cationic lipid, 7.1% dipalmitoylphosphatidylcholine, 34.3% cholesterol, and 1.4% PEG-c-DMA. As another example, changing the com-

position of the cationic lipid can more effectively deliver siRNA to various antigen presenting cells (Basha et al. *Mol Ther.* 2011 19:2186-2200).

[0388] In some embodiments, lipid nanoparticle formulations may comprise 35 to 45% cationic lipid, 40% to 50% cationic lipid, 50% to 60% cationic lipid and/or 55% to 65% cationic lipid. In some embodiments, the ratio of lipid to RNA (e.g., mRNA) in lipid nanoparticles may be 5:1 to 20:1, 10:1 to 25:1, 15:1 to 30:1 and/or at least 30:1.

[0389] In some embodiments, the ratio of PEG in the lipid nanoparticle formulations may be increased or decreased and/or the carbon chain length of the PEG lipid may be modified from C14 to C18 to alter the pharmacokinetics and/or biodistribution of the lipid nanoparticle formulations. As a non-limiting example, lipid nanoparticle formulations may contain 0.5% to 3.0%, 1.0% to 3.5%, 1.5% to 4.0%, 2.0% to 4.5%, 2.5% to 5.0% and/or 3.0% to 6.0% of the lipid molar ratio of PEG-c-DOMG (R-3-Rw-methoxy-poly(ethyleneglycol)2000)carbamoyl]-1,2-dimyristyloxypropyl-3-amine) (also referred to herein as PEG-DOMG) as compared to the cationic lipid, DSPC and cholesterol. In some embodiments, the PEG-c-DOMG may be replaced with a PEG lipid such as, but not limited to, PEG-DSG (1,2-Distearoyl-sn-glycerol, methoxypolyethylene glycol), PEG-DMG (1,2-Dimyristoyl-sn-glycerol) and/or PEG-DPG (1,2-Dipalmitoyl-sn-glycerol, methoxypolyethylene glycol). The cationic lipid may be selected from any lipid known in the art such as, but not limited to, DLin-MC3-DMA, DLin-DMA, C12-200 and DLin-KC2-DMA.

[0390] In some embodiments, an respiratory virus RNA (e.g. mRNA) vaccine formulation is a nanoparticle that comprises at least one lipid. The lipid may be selected from, but is not limited to, DLin-DMA, DLin-K-DMA, 98N12-5, C12-200, DLin-MC3-DMA, DLin-KC2-DMA, DODMA, PLGA, PEG, PEG-DMG, PEGylated lipids and amino alcohol lipids. In some embodiments, the lipid may be a cationic lipid such as, but not limited to, DLin-DMA, DLin-D-DMA, DLin-MC3-DMA, DLin-KC2-DMA, DODMA and amino alcohol lipids. The amino alcohol cationic lipid may be the lipids described in and/or made by the methods described in U.S. Patent Publication No. US20130150625, herein incorporated by reference in its entirety. As a non-limiting example, the cationic lipid may be 2-amino-3-[(9Z,12Z)-octadeca-9,12-dien-1-yloxy]-2-[[[(9Z,2Z)-octadeca-9,12-dien-1-yloxy]methyl]propan-1-ol (Compound 1 in US20130150625); 2-amino-3-[(9Z)-octadec-9-en-1-yloxy]-2-[[[(9Z)-octadec-9-en-1-yloxy]methyl]propan-1-ol (Compound 2 in US20130150625); 2-amino-3-[(9Z,12Z)-octadeca-9,12-dien-1-yloxy]-2-[(octyloxy)methyl]propan-1-ol (Compound 3 in US20130150625); and 2-(dimethylamino)-3-[(9Z,12Z)-octadeca-9,12-dien-1-yloxy]-2-[[[(9Z,12Z)-octadeca-9,12-dien-1-yloxy]methyl]propan-1-ol (Compound 4 in US20130150625); or any pharmaceutically acceptable salt or stereoisomer thereof.

[0391] Lipid nanoparticle formulations typically comprise a lipid, in particular, an ionizable cationic lipid, for example, 2,2-dilinoylel-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoylel-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), or di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319), and further comprise a neutral lipid, a sterol and a molecule capable of reducing particle aggregation, for example a PEG or PEG-modified lipid.

[0392] In some embodiments, a lipid nanoparticle formulation consists essentially of (i) at least one lipid selected from the group consisting of 2,2-dilinoylel-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoylel-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319); (ii) a neutral lipid selected from DSPC, DPPC, POPC, DOPE and SM; (iii) a sterol, e.g., cholesterol; and (iv) a PEG-lipid, e.g., PEG-DMG or PEG-cDMA, in a molar ratio of 20-60% cationic lipid: 5-25% neutral lipid: 25-55% sterol; 0.5-15% PEG-lipid.

[0393] In some embodiments, a lipid nanoparticle formulation includes 25% to 75% on a molar basis of a cationic lipid selected from 2,2-dilinoylel-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoylel-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319), e.g., 35 to 65%, 45 to 65%, 60%, 57.5%, 50% or 40% on a molar basis.

[0394] In some embodiments, a lipid nanoparticle formulation includes 0.5% to 15% on a molar basis of the neutral lipid, e.g., 3 to 12%, 5 to 10% or 15%, 10%, or 7.5% on a molar basis. Examples of neutral lipids include, without limitation, DSPC, POPC, DPPC, DOPE and SM. In some embodiments, the formulation includes 5% to 50% on a molar basis of the sterol (e.g., 15 to 45%, 20 to 40%, 40%, 38.5%, 35%, or 31% on a molar basis. A non-limiting example of a sterol is cholesterol. In some embodiments, a lipid nanoparticle formulation includes 0.5% to 20% on a molar basis of the PEG or PEG-modified lipid (e.g., 0.5 to 10%, 0.5 to 5%, 1.5%, 0.5%, 1.5%, 3.5%, or 5% on a molar basis. In some embodiments, a PEG or PEG modified lipid comprises a PEG molecule of an average molecular weight of 2,000 Da. In some embodiments, a PEG or PEG modified lipid comprises a PEG molecule of an average molecular weight of less than 2,000, for example around 1,500 Da, around 1,000 Da, or around 500 Da. Non-limiting examples of PEG-modified lipids include PEG-distearoyl glycerol (PEG-DMG) (also referred herein as PEG-C14 or C14-PEG), PEG-cDMA (further discussed in Reyes et al. J. Controlled Release, 107, 276-287 (2005) the contents of which are herein incorporated by reference in their entirety).

[0395] In some embodiments, lipid nanoparticle formulations include 25-75% of a cationic lipid selected from 2,2-dilinoylel-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoylel-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319), 0.5-15% of the neutral lipid, 5-50% of the sterol, and 0.5-20% of the PEG or PEG-modified lipid on a molar basis.

[0396] In some embodiments, lipid nanoparticle formulations include 35-65% of a cationic lipid selected from 2,2-dilinoylel-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoylel-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319), 3-12% of the neutral lipid, 15-45% of the sterol, and 0.5-10% of the PEG or PEG-modified lipid on a molar basis.

[0397] In some embodiments, lipid nanoparticle formulations include 45-65% of a cationic lipid selected from 2,2-dilinoylel-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoylel-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319),

5-10% of the neutral lipid, 25-40% of the sterol, and 0.5-10% of the PEG or PEG-modified lipid on a molar basis.

[0398] In some embodiments, lipid nanoparticle formulations include 60% of a cationic lipid selected from 2,2-dilinoylel-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoylel-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319), 7.5% of the neutral lipid, 31% of the sterol, and 1.5% of the PEG or PEG-modified lipid on a molar basis.

[0399] In some embodiments, lipid nanoparticle formulations include 50% of a cationic lipid selected from 2,2-dilinoylel-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoylel-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319), 10% of the neutral lipid, 38.5% of the sterol, and 1.5% of the PEG or PEG-modified lipid on a molar basis.

[0400] In some embodiments, lipid nanoparticle formulations include 50% of a cationic lipid selected from 2,2-dilinoylel-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoylel-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319), 10% of the neutral lipid, 35% of the sterol, 4.5% or 5% of the PEG or PEG-modified lipid, and 0.5% of the targeting lipid on a molar basis.

[0401] In some embodiments, lipid nanoparticle formulations include 40% of a cationic lipid selected from 2,2-dilinoylel-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoylel-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319), 15% of the neutral lipid, 40% of the sterol, and 5% of the PEG or PEG-modified lipid on a molar basis.

[0402] In some embodiments, lipid nanoparticle formulations include 57.2% of a cationic lipid selected from 2,2-dilinoylel-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoylel-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319), 7.1% of the neutral lipid, 34.3% of the sterol, and 1.4% of the PEG or PEG-modified lipid on a molar basis.

[0403] In some embodiments, lipid nanoparticle formulations include 57.5% of a cationic lipid selected from the PEG lipid is PEG-cDMA (PEG-cDMA is further discussed in Reyes et al. J. Controlled Release, 107, 276-287 (2005), the contents of which are herein incorporated by reference in their entirety), 7.5% of the neutral lipid, 31.5% of the sterol, and 3.5% of the PEG or PEG-modified lipid on a molar basis.

[0404] In some embodiments, lipid nanoparticle formulations consists essentially of a lipid mixture in molar ratios of 20-70% cationic lipid: 5-45% neutral lipid: 20-55% cholesterol: 0.5-15% PEG-modified lipid. In some embodiments, lipid nanoparticle formulations consists essentially of a lipid mixture in a molar ratio of 20-60% cationic lipid: 5-25% neutral lipid: 25-55% cholesterol: 0.5-15% PEG-modified lipid.

[0405] In some embodiments, the molar lipid ratio is 50/10/38.5/1.5 (mol % cationic lipid/neutral lipid, e.g., DSPC/Chol/PEG-modified lipid, e.g., PEG-DMG, PEG-DSG or PEG-DPG), 57.2/7.1/34.3/1.4 (mol % cationic lipid/neutral lipid, e.g., DPPC/Chol/PEG-modified lipid,

e.g., PEG-cDMA), 40/15/40/5 (mol % cationic lipid/neutral lipid, e.g., DSPC/Chol/PEG-modified lipid, e.g., PEG-DMG), 50/10/35/4.5/0.5 (mol % cationic lipid/neutral lipid, e.g., DSPC/Chol/PEG-modified lipid, e.g., PEG-DSG), 50/10/35/5 (cationic lipid/neutral lipid, e.g., DSPC/Chol/PEG-modified lipid, e.g., PEG-DMG), 40/10/40/10 (mol % cationic lipid/neutral lipid, e.g., DSPC/Chol/PEG-modified lipid, e.g., PEG-DMG or PEG-cDMA), 35/15/40/10 (mol % cationic lipid/neutral lipid, e.g., DSPC/Chol/PEG-modified lipid, e.g., PEG-DMG or PEG-cDMA) or 52/13/30/5 (mol % cationic lipid/neutral lipid, e.g., DSPC/Chol/PEG-modified lipid, e.g., PEG-DMG or PEG-cDMA).

[0406] Non-limiting examples of lipid nanoparticle compositions and methods of making them are described, for example, in Semple et al. (2010) *Nat. Biotechnol.* 28:172-176; Jayarama et al. (2012), *Angew. Chem. Int. Ed.*, S1: 8529-8533; and Maier et al. (2013) *Molecular Therapy* 21, 1570-1578 (the contents of each of which are incorporated herein by reference in their entirety).

[0407] In some embodiments, lipid nanoparticle formulations may comprise a cationic lipid, a PEG lipid and a structural lipid and optionally comprise a non-cationic lipid. As a non-limiting example, a lipid nanoparticle may comprise 40-60% of cationic lipid, 5-15% of a non-cationic lipid, 1-2% of a PEG lipid and 30-50% of a structural lipid. As another non-limiting example, the lipid nanoparticle may comprise 50% cationic lipid, 10% non-cationic lipid, 1.5% PEG lipid and 38.5% structural lipid. As yet another non-limiting example, a lipid nanoparticle may comprise 55% cationic lipid, 10% non-cationic lipid, 2.5% PEG lipid and 32.5% structural lipid. In some embodiments, the cationic lipid may be any cationic lipid described herein such as, but not limited to, DLin-KC2-DMA, DLin-MC3-DMA and L319.

[0408] In some embodiments, the lipid nanoparticle formulations described herein may be 4 component lipid nanoparticles. The lipid nanoparticle may comprise a cationic lipid, a non-cationic lipid, a PEG lipid and a structural lipid. As a non-limiting example, the lipid nanoparticle may comprise 40-60% of cationic lipid, 5-15% of a non-cationic lipid, 1-2% of a PEG lipid and 30-50% of a structural lipid. As another non-limiting example, the lipid nanoparticle may comprise 50% cationic lipid, 10% non-cationic lipid, 1.5% PEG lipid and 38.5% structural lipid. As yet another non-limiting example, the lipid nanoparticle may comprise 55% cationic lipid, 10% non-cationic lipid, 2.5% PEG lipid and 32.5% structural lipid. In some embodiments, the cationic lipid may be any cationic lipid described herein such as, but not limited to, DLin-KC2-DMA, DLin-MC3-DMA and L319.

[0409] In some embodiments, the lipid nanoparticle formulations described herein may comprise a cationic lipid, a non-cationic lipid, a PEG lipid and a structural lipid. As a non-limiting example, the lipid nanoparticle comprise 50% of the cationic lipid DLin-KC2-DMA, 10% of the non-cationic lipid DSPC, 1.5% of the PEG lipid PEG-DOMG and 38.5% of the structural lipid cholesterol. As a non-limiting example, the lipid nanoparticle comprise 50% of the cationic lipid DLin-MC3-DMA, 10% of the non-cationic lipid DSPC, 1.5% of the PEG lipid PEG-DOMG and 38.5% of the structural lipid cholesterol. As a non-limiting example, the lipid nanoparticle comprise 50% of the cationic lipid DLin-MC3-DMA, 10% of the non-cationic lipid DSPC, 1.5% of the PEG lipid PEG-DMG and 38.5% of the

structural lipid cholesterol. As yet another non-limiting example, the lipid nanoparticle comprise 55% of the cationic lipid L319, 10% of the non-cationic lipid DSPC, 2.5% of the PEG lipid PEG-DMG and 32.5% of the structural lipid cholesterol.

[0410] Relative amounts of the active ingredient, the pharmaceutically acceptable excipient, and/or any additional ingredients in a vaccine composition may vary, depending upon the identity, size, and/or condition of the subject being treated and further depending upon the route by which the composition is to be administered. For example, the composition may comprise between 0.1% and 99% (w/w) of the active ingredient. By way of example, the composition may comprise between 0.1% and 100%, e.g., between 0.5 and 50%, between 1-30%, between 5-80%, at least 80% (w/w) active ingredient.

[0411] In some embodiments, the respiratory virus RNA (e.g. mRNA) vaccine composition may comprise the polynucleotide described herein, formulated in a lipid nanoparticle comprising MC3, Cholesterol, DSPC and PEG2000-DMG, the buffer trisodium citrate, sucrose and water for injection. As a non-limiting example, the composition comprises: 2.0 mg/mL of drug substance (e.g., polynucleotides encoding H10N8 hMPV), 21.8 mg/mL of MC3, 10.1 mg/mL of cholesterol, 5.4 mg/mL of DSPC, 2.7 mg/mL of PEG2000-DMG, 5.16 mg/mL of trisodium citrate, 71 mg/mL of sucrose and 1.0 mL of water for injection.

[0412] In some embodiments, a nanoparticle (e.g., a lipid nanoparticle) has a mean diameter of 10-500 nm, 20-400 nm, 30-300 nm, 40-200 nm. In some embodiments, a nanoparticle (e.g., a lipid nanoparticle) has a mean diameter of 50-150 nm, 50-200 nm, 80-100 nm or 80-200 nm.

Liposomes, Lipoplexes, and Lipid Nanoparticles

[0413] The RNA (e.g., mRNA) vaccines of the disclosure can be formulated using one or more liposomes, lipoplexes, or lipid nanoparticles. In some embodiments, pharmaceutical compositions of RNA (e.g., mRNA) vaccines include liposomes. Liposomes are artificially-prepared vesicles which may primarily be composed of a lipid bilayer and may be used as a delivery vehicle for the administration of nutrients and pharmaceutical formulations. Liposomes can be of different sizes such as, but not limited to, a multilamellar vesicle (MLV) which may be hundreds of nanometers in diameter and may contain a series of concentric bilayers separated by narrow aqueous compartments, a small unilamellar vesicle (SUV) which may be smaller than 50 nm in diameter, and a large unilamellar vesicle (LUV) which may be between 50 and 500 nm in diameter. Liposome design may include, but is not limited to, opsonins or ligands in order to improve the attachment of liposomes to unhealthy tissue or to activate events such as, but not limited to, endocytosis. Liposomes may contain a low or a high pH in order to improve the delivery of the pharmaceutical formulations.

[0414] The formation of liposomes may depend on the physicochemical characteristics such as, but not limited to, the pharmaceutical formulation entrapped and the liposomal ingredients, the nature of the medium in which the lipid vesicles are dispersed, the effective concentration of the entrapped substance and its potential toxicity, any additional processes involved during the application and/or delivery of the vesicles, the optimization size, polydispersity and the shelf-life of the vesicles for the intended application, and the

batch-to-batch reproducibility and possibility of large-scale production of safe and efficient liposomal products.

[0415] In some embodiments, pharmaceutical compositions described herein may include, without limitation, liposomes such as those formed from 1,2-dioleoyloxy-N,N-dimethylaminopropane (DODMA) liposomes, DiLa2 liposomes from Marina Biotech (Bothell, Wash.), 1,2-dilinoleoyloxy-3-dimethylaminopropane (DLin-DMA), 2,2-dilinoleyl-4-(2-dimethylaminoethyl)-[1,3]-dioxolane (DLin-KC2-DMA), and MC3 (US20100324120; herein incorporated by reference in its entirety) and liposomes which may deliver small molecule drugs such as, but not limited to, DOXIL® from Janssen Biotech, Inc. (Horsham, Pa.).

[0416] In some embodiments, pharmaceutical compositions described herein may include, without limitation, liposomes such as those formed from the synthesis of stabilized plasmid-lipid particles (SPLP) or stabilized nucleic acid lipid particle (SNALP) that have been previously described and shown to be suitable for oligonucleotide delivery in vitro and in vivo (see Wheeler et al. *Gene Therapy*. 1999 6:271-281; Zhang et al. *Gene Therapy*. 1999 6:1438-1447; Jeffs et al. *Pharm Res*. 2005 22:362-372; Morrissey et al., *Nat Biotechnol*. 2005 2:1002-1007; Zimmermann et al., *Nature*. 2006 441:111-114; Heyes et al. *J Contr Rel*. 2005 107:276-287; Semple et al. *Nature Biotech*. 2010 28:172-176; Judge et al. *J Clin Invest*. 2009 119:661-673; deFougerolles *Hum Gene Ther*. 2008 19:125-132; U.S. Patent Publication No US20130122104; all of which are incorporated herein in their entireties). The original manufacture method by Wheeler et al. was a detergent dialysis method, which was later improved by Jeffs et al. and is referred to as the spontaneous vesicle formation method. The liposome formulations are composed of 3 to 4 lipid components in addition to the polynucleotide. As an example a liposome can contain, but is not limited to, 55% cholesterol, 20% distearylphosphatidyl choline (DSPC), 10% PEG-S-DSG, and 15% 1,2-dioleoyloxy-N,N-dimethylaminopropane (DODMA), as described by Jeffs et al. As another example, certain liposome formulations may contain, but are not limited to, 48% cholesterol, 20% DSPC, 2% PEG-c-DMA, and 30% cationic lipid, where the cationic lipid can be 1,2-distearloxy-N,N-dimethylaminopropane (DSDMA), DODMA, DLin-DMA, or 1,2-dilinolenyloxy-3-dimethylaminopropane (DLenDMA), as described by Heyes et al.

[0417] In some embodiments, liposome formulations may comprise from about 25.0% cholesterol to about 40.0% cholesterol, from about 30.0% cholesterol to about 45.0% cholesterol, from about 35.0% cholesterol to about 50.0% cholesterol and/or from about 48.5% cholesterol to about 60% cholesterol. In some embodiments, formulations may comprise a percentage of cholesterol selected from the group consisting of 28.5%, 31.5%, 33.5%, 36.5%, 37.0%, 38.5%, 39.0% and 43.5%. In some embodiments, formulations may comprise from about 5.0% to about 10.0% DSPC and/or from about 7.0% to about 15.0% DSPC.

[0418] In some embodiments, the RNA (e.g., mRNA) vaccine pharmaceutical compositions may be formulated in liposomes such as, but not limited to, DiLa2 liposomes (Marina Biotech, Bothell, Wash.), SMARTICLES® (Marina Biotech, Bothell, Wash.), neutral DOPC (1,2-dioleoyl-sn-glycero-3-phosphocholine) based liposomes (e.g., siRNA delivery for ovarian cancer (Landen et al. *Cancer Biology &*

Therapy 2006 5(12):1708-1713); herein incorporated by reference in its entirety) and hyaluronan-coated liposomes (Quiet Therapeutics, Israel).

[0419] In some embodiments, the cationic lipid may be a low molecular weight cationic lipid such as those described in U.S. Patent Application No. 20130090372, the contents of which are herein incorporated by reference in their entirety.

[0420] In some embodiments, the RNA (e.g., mRNA) vaccines may be formulated in a lipid vesicle, which may have crosslinks between functionalized lipid bilayers.

[0421] In some embodiments, the RNA (e.g., mRNA) vaccines may be formulated in a lipid-polycation complex. The formation of the lipid-polycation complex may be accomplished by methods known in the art and/or as described in U.S. Pub. No. 20120178702, herein incorporated by reference in its entirety. As a non-limiting example, the polycation may include a cationic peptide or a polypeptide such as, but not limited to, polylysine, polyornithine and/or polyarginine. In some embodiments, the RNA (e.g., mRNA) vaccines may be formulated in a lipid-polycation complex, which may further include a non-cationic lipid such as, but not limited to, cholesterol or dioleoyl phosphatidylethanolamine (DOPE).

[0422] In some embodiments, the ratio of PEG in the lipid nanoparticle (LNP) formulations may be increased or decreased and/or the carbon chain length of the PEG lipid may be modified from C14 to C18 to alter the pharmacokinetics and/or biodistribution of the LNP formulations. As a non-limiting example, LNP formulations may contain from about 0.5% to about 3.0%, from about 1.0% to about 3.5%, from about 1.5% to about 4.0%, from about 2.0% to about 4.5%, from about 2.5% to about 5.0% and/or from about 3.0% to about 6.0% of the lipid molar ratio of PEG-c-DOMG (R-3-[(w-methoxy-poly(ethyleneglycol)2000)carbamoyl]1,2-dimyrityloxypropyl-3-amine) (also referred to herein as PEG-DOMG) as compared to the cationic lipid, DSPC and cholesterol. In some embodiments, the PEG-c-DOMG may be replaced with a PEG lipid such as, but not limited to, PEG-DSG (1,2-Distearoyl-sn-glycerol, methoxypolyethylene glycol), PEG-DMG (1,2-Dimyrityl-sn-glycerol) and/or PEG-DPG (1,2-Dipalmitoyl-sn-glycerol, methoxypolyethylene glycol). The cationic lipid may be selected from any lipid known in the art such as, but not limited to, DLin-MC3-DMA, DLin-DMA, C12-200 and DLin-KC2-DMA.

[0423] In some embodiments, the RNA (e.g., mRNA) vaccines may be formulated in a lipid nanoparticle.

[0424] In some embodiments, the RNA (e.g., mRNA) vaccine formulation comprising the polynucleotide is a nanoparticle which may comprise at least one lipid. The lipid may be selected from, but is not limited to, DLin-DMA, DLin-K-DMA, 98N12-5, C12-200, DLin-MC3-DMA, DLin-KC2-DMA, DODMA, PLGA, PEG, PEG-DMG, PEGylated lipids and amino alcohol lipids. In another aspect, the lipid may be a cationic lipid such as, but not limited to, DLin-DMA, DLin-D-DMA, DLin-MC3-DMA, DLin-KC2-DMA, DODMA and amino alcohol lipids. The amino alcohol cationic lipid may be the lipids described in and/or made by the methods described in U.S. Patent Publication No. US20130150625, herein incorporated by reference in its entirety. As a non-limiting example, the cationic lipid may be 2-amino-3-[(9Z,12Z)-octadeca-9,12-dien-1-yloxy]-2-[[[(9Z,2Z)-octadeca-9,12-dien-1-yloxy]methyl]propan-1-ol (Compound 1 in US20130150625);

2-amino-3-[(9Z)-octadec-9-en-1-yloxy]-2-[[[(9Z)-octadec-9-en-1-yloxy]methyl]propan-1-ol (Compound 2 in US20130150625); 2-amino-3-[(9Z,12Z)-octadeca-9,12-dien-1-yloxy]-2-[(octyloxy)methyl]propan-1-ol (Compound 3 in US20130150625); and 2-(dimethylamino)-3-[(9Z,12Z)-octadeca-9,12-dien-1-yloxy]-2-[[[(9Z,12Z)-octadeca-9,12-dien-1-yloxy]methyl]propan-1-ol (Compound 4 in US20130150625); or any pharmaceutically acceptable salt or stereoisomer thereof.

[0425] Lipid nanoparticle formulations typically comprise a lipid, in particular, an ionizable cationic lipid, for example, 2,2-dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoleyl-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), or di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319), and further comprise a neutral lipid, a sterol and a molecule capable of reducing particle aggregation, for example a PEG or PEG-modified lipid.

[0426] In some embodiments, the lipid nanoparticle formulation consists essentially of (i) at least one lipid selected from the group consisting of 2,2-dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoleyl-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319); (ii) a neutral lipid selected from DSPC, DPPC, POPC, DOPE and SM; (iii) a sterol, e.g., cholesterol; and (iv) a PEG-lipid, e.g., PEG-DMG or PEG-cDMA, in a molar ratio of about 20-60% cationic lipid: 5-25% neutral lipid: 25-55% sterol; 0.5-15% PEG-lipid.

[0427] In some embodiments, the formulation includes from about 25% to about 75% on a molar basis of a cationic lipid selected from 2,2-dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoleyl-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319), e.g., from about 35 to about 65%, from about 45 to about 65%, about 60%, about 57.5%, about 50% or about 40% on a molar basis.

[0428] In some embodiments, the formulation includes from about 0.5% to about 15% on a molar basis of the neutral lipid e.g., from about 3 to about 12%, from about 5 to about 10% or about 15%, about 10%, or about 7.5% on a molar basis. Examples of neutral lipids include, but are not limited to, DSPC, POPC, DPPC, DOPE and SM. In some embodiments, the formulation includes from about 5% to about 50% on a molar basis of the sterol (e.g., about 15 to about 45%, about 20 to about 40%, about 40%, about 38.5%, about 35%, or about 31% on a molar basis. An exemplary sterol is cholesterol. In some embodiments, the formulation includes from about 0.5% to about 20% on a molar basis of the PEG or PEG-modified lipid (e.g., about 0.5 to about 10%, about 0.5 to about 5%, about 1.5%, about 0.5%, about 1.5%, about 3.5%, or about 5% on a molar basis. In some embodiments, the PEG or PEG modified lipid comprises a PEG molecule of an average molecular weight of 2,000 Da. In other embodiments, the PEG or PEG modified lipid comprises a PEG molecule of an average molecular weight of less than 2,000, for example around 1,500 Da, around 1,000 Da, or around 500 Da. Examples of PEG-modified lipids include, but are not limited to, PEG-distearoyl glycerol (PEG-DMG) (also referred herein as PEG-C14 or C14-PEG), PEG-cDMA (further discussed in Reyes et al. *J. Controlled Release*, 107, 276-287 (2005) the contents of which are herein incorporated by reference in their entirety)

[0429] In some embodiments, the formulations of the present disclosure include 25-75% of a cationic lipid selected from 2,2-dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoleyl-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319), 0.5-15% of the neutral lipid, 5-50% of the sterol, and 0.5-20% of the PEG or PEG-modified lipid on a molar basis.

[0430] In some embodiments, the formulations of the present disclosure include 35-65% of a cationic lipid selected from 2,2-dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoleyl-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319), 3-12% of the neutral lipid, 15-45% of the sterol, and 0.5-10% of the PEG or PEG-modified lipid on a molar basis.

[0431] In some embodiments, the formulations of the present disclosure include 45-65% of a cationic lipid selected from 2,2-dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoleyl-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319), 5-10% of the neutral lipid, 25-40% of the sterol, and 0.5-10% of the PEG or PEG-modified lipid on a molar basis.

[0432] In some embodiments, the formulations of the present disclosure include about 60% of a cationic lipid selected from 2,2-dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoleyl-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319), about 7.5% of the neutral lipid, about 31% of the sterol, and about 1.5% of the PEG or PEG-modified lipid on a molar basis. In some embodiments, the formulations of the present disclosure include about 50% of a cationic lipid selected from 2,2-dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoleyl-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319), about 10% of the neutral lipid, about 38.5% of the sterol, and about 1.5% of the PEG or PEG-modified lipid on a molar basis.

[0433] In some embodiments, the formulations of the present disclosure include about 50% of a cationic lipid selected from 2,2-dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoleyl-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319), about 10% of the neutral lipid, about 35% of the sterol, about 4.5% or about 5% of the PEG or PEG-modified lipid, and about 0.5% of the targeting lipid on a molar basis.

[0434] In some embodiments, the formulations of the present disclosure include about 40% of a cationic lipid selected from 2,2-dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoleyl-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319), about 15% of the neutral lipid, about 40% of the sterol, and about 5% of the PEG or PEG-modified lipid on a molar basis.

[0435] In some embodiments, the formulations of the present disclosure include about 57.2% of a cationic lipid selected from 2,2-dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoleyl-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-

yl) 9-((4-(dimethylamino)butanoyloxy)heptadecanedioate (L319), about 7.1% of the neutral lipid, about 34.3% of the sterol, and about 1.4% of the PEG or PEG-modified lipid on a molar basis.

[0436] In some embodiments, the formulations of the present disclosure include about 57.5% of a cationic lipid selected from the PEG lipid is PEG-cDMA (PEG-cDMA is further discussed in Reyes et al. (J. Controlled Release, 107, 276-287 (2005), the contents of which are herein incorporated by reference in their entirety), about 7.5% of the neutral lipid, about 31.5% of the sterol, and about 3.5% of the PEG or PEG-modified lipid on a molar basis.

[0437] In some embodiments, lipid nanoparticle formulation consists essentially of a lipid mixture in molar ratios of about 20-70% cationic lipid: 5-45% neutral lipid: 20-55% cholesterol: 0.5-15% PEG-modified lipid; more preferably in a molar ratio of about 20-60% cationic lipid: 5-25% neutral lipid: 25-55% cholesterol: 0.5-15% PEG-modified lipid.

[0438] In some embodiments, the molar lipid ratio is approximately 50/10/38.5/1.5 (mol % cationic lipid/neutral lipid, e.g., DSPC/Chol/PEG-modified lipid, e.g., PEG-DMG, PEG-DSG or PEG-DPG), 57.2/7.1134.3/1.4 (mol % cationic lipid/neutral lipid, e.g., DPPC/Chol/PEG-modified lipid, e.g., PEG-cDMA), 40/15/40/5 (mol % cationic lipid/neutral lipid, e.g., DSPC/Chol/PEG-modified lipid, e.g., PEG-DMG), 50/10/35/4.5/0.5 (mol % cationic lipid/neutral lipid, e.g., DSPC/Chol/PEG-modified lipid, e.g., PEG-DSG), 50/10/35/5 (cationic lipid/neutral lipid, e.g., DSPC/Chol/PEG-modified lipid, e.g., PEG-DMG), 40/10/40/10 (mol % cationic lipid/neutral lipid, e.g., DSPC/Chol/PEG-modified lipid, e.g., PEG-DMG or PEG-cDMA), 35/15/40/10 (mol % cationic lipid/neutral lipid, e.g., DSPC/Chol/PEG-modified lipid, e.g., PEG-DMG or PEG-cDMA) or 52/13/30/5 (mol % cationic lipid/neutral lipid, e.g., DSPC/Chol/PEG-modified lipid, e.g., PEG-DMG or PEG-cDMA).

[0439] Examples of lipid nanoparticle compositions and methods of making same are described, for example, in Semple et al. (2010) *Nat. Biotechnol.* 28:172-176; Jayarama et al. (2012), *Angew. Chem. Int. Ed.*, S1: 8529-8533; and Maier et al. (2013) *Molecular Therapy* 21, 1570-1578 (the contents of each of which are incorporated herein by reference in their entirety).

[0440] In some embodiments, the lipid nanoparticle formulations described herein may comprise a cationic lipid, a PEG lipid and a structural lipid and optionally comprise a non-cationic lipid. As a non-limiting example, the lipid nanoparticle may comprise about 40-60% of cationic lipid, about 5-15% of a non-cationic lipid, about 1-2% of a PEG lipid and about 30-50% of a structural lipid. As another non-limiting example, the lipid nanoparticle may comprise about 50% cationic lipid, about 10% non-cationic lipid, about 1.5% PEG lipid and about 38.5% structural lipid. As yet another non-limiting example, the lipid nanoparticle may comprise about 55% cationic lipid, about 10% non-cationic lipid, about 2.5% PEG lipid and about 32.5% structural lipid. In some embodiments, the cationic lipid may be any cationic lipid described herein such as, but not limited to, Dlin-KC2-DMA, Dlin-MC3-DMA and L319.

[0441] In some embodiments, the lipid nanoparticle formulations described herein may be 4 component lipid nanoparticles. The lipid nanoparticle may comprise a cationic lipid, a non-cationic lipid, a PEG lipid and a structural lipid. As a non-limiting example, the lipid nanoparticle may

comprise about 40-60% of cationic lipid, about 5-15% of a non-cationic lipid, about 1-2% of a PEG lipid and about 30-50% of a structural lipid. As another non-limiting example, the lipid nanoparticle may comprise about 50% cationic lipid, about 10% non-cationic lipid, about 1.5% PEG lipid and about 38.5% structural lipid. As yet another non-limiting example, the lipid nanoparticle may comprise about 55% cationic lipid, about 10% non-cationic lipid, about 2.5% PEG lipid and about 32.5% structural lipid. In some embodiments, the cationic lipid may be any cationic lipid described herein such as, but not limited to, Dlin-KC2-DMA, Dlin-MC3-DMA and L319.

[0442] In some embodiments, the lipid nanoparticle formulations described herein may comprise a cationic lipid, a non-cationic lipid, a PEG lipid and a structural lipid. As a non-limiting example, the lipid nanoparticle comprise about 50% of the cationic lipid Dlin-KC2-DMA, about 10% of the non-cationic lipid DSPC, about 1.5% of the PEG lipid PEG-DOMG and about 38.5% of the structural lipid cholesterol. As a non-limiting example, the lipid nanoparticle comprise about 50% of the cationic lipid Dlin-MC3-DMA, about 10% of the non-cationic lipid DSPC, about 1.5% of the PEG lipid PEG-DOMG and about 38.5% of the structural lipid cholesterol. As a non-limiting example, the lipid nanoparticle comprise about 50% of the cationic lipid Dlin-MC3-DMA, about 10% of the non-cationic lipid DSPC, about 1.5% of the PEG lipid PEG-DMG and about 38.5% of the structural lipid cholesterol. As yet another non-limiting example, the lipid nanoparticle comprise about 55% of the cationic lipid L319, about 10% of the non-cationic lipid DSPC, about 2.5% of the PEG lipid PEG-DMG and about 32.5% of the structural lipid cholesterol.

[0443] As a non-limiting example, the cationic lipid may be selected from (20Z,23Z)-N,N-dimethylnonacos-20,23-dien-10-amine, (17Z,20Z)-N,N-dimethylhexacos-17,20-dien-9-amine, (1Z,19Z)-N,N-dimethylpentacos-1 6, 19-dien-8-amine, (13Z,16Z)-N,N-dimethyldocos-13,16-dien-5-amine, (12Z,15Z)-N,N-dimethylhenicos-12,15-dien-4-amine, (14Z,17Z)-N,N-dimethyltricos-14,17-dien-6-amine, (15Z,18Z)-N,N-dimethyltetracos-15,18-dien-7-amine, (18Z,21Z)-N,N-dimethylheptacos-18,21-dien-10-amine, (15Z,18Z)-N,N-dimethyltetracos-15,18-dien-5-amine, (14Z,17Z)-N,N-dimethyltricos-14,17-dien-4-amine, (19Z,22Z)-N,N-dimethyloctacos-19,22-dien-9-amine, (18Z,21 Z)-N,N-dimethylheptacos-18,21 -dien-8-amine, (17Z,20Z)-N,N-dimethylhexacos-17,20-dien-7-amine, (16Z,19Z)-N,N-dimethylpentacos-16,19-dien-6-amine, (22Z,25Z)-N,N-dimethylhentriaconta-22,25-dien-10-amine, (21 Z,24Z)-N,N-dimethyltriaconta-21,24-dien-9-amine, (18Z)-N,N-dimethylheptacos-18-en-10-amine, (17Z)-N,N-dimethylhexacos-17-en-9-amine, (19Z,22Z)-N,N-dimethyloctacos-19,22-dien-7-amine, N,N-dimethylheptacosan-10-amine, (20Z,23Z)-N-ethyl-N-methylnonacos-20,23-dien-10-amine, 1-[(11Z,14Z)-1-nonylicos-11,14-dien-1-yl] pyrrolidine, (20Z)-N,N-dimethylheptacos-20-en-1 0-amine, (15Z)-N,N-dimethylheptacos-15-en-1 0-amine, (14Z)-N,N-dimethylnonacos-14-en-10-amine, (17Z)-N,N-dimethylnonacos-17-en-10-amine, (24Z)-N,N-dimethyltritriacont-24-en-10-amine, (20Z)-N,N-dimethylnonacos-20-en-1 0-amine, (22Z)-N,N-dimethylhentriacont-22-en-10-amine, (16Z)-N,N-dimethylpentacos-16-en-8-amine, (12Z,15Z)-N,N-dimethyl-2-nonylhenicos-12,15-dien-1-amine, (13Z,16Z)-N,N-dimethyl-3-nonyldocos-13,16-dien-1-amine, N,N-dimethyl-1-[(1S,

2R)-2-octylcyclopropyl]heptadecan-8-amine, 1-[(1S,2R)-2-hexylcyclopropyl]-N,N-dimethylnonadecan-10-amine, N,N-dimethyl-1-[(1S,2R)-2-octylcyclopropyl]nonadecan-10-amine, N,N-dimethyl-21-[(1S,2R)-2-octylcyclopropyl]henicosan-10-amine, N,N-dimethyl-1-[(1S,2S)-2-[(1R,2R)-2-pentylcyclopropyl]methyl]cyclopropyl]nonadecan-10-amine, N,N-dimethyl-1-[(1S,2R)-2-octylcyclopropyl]hexadecan-8-amine, N,N-dimethyl-1-[(1R,2S)-2-undecylcyclopropyl]tetradecan-5-amine, N,N-dimethyl-3-[(1S,2R)-2-octylcyclopropyl]heptyl]dodecan-1-amine, 1-[(1R,2S)-2-heptylcyclopropyl]-N,N-dimethyloctadecan-9-amine, 1-[(1S,2R)-2-decylcyclopropyl]-N,N-dimethylpentadecan-6-amine, N,N-dimethyl-1-[(1S,2R)-2-octylcyclopropyl]pentadecan-8-amine, R,N,N-dimethyl-1-[(9Z,12Z)-octadeca-9,12-dien-1-yloxy]-3-(octyloxy)propan-2-amine, S-N,N-dimethyl-1-[(9Z,12Z)-octadeca-9,12-dien-1-yloxy]-3-(octyloxy)propan-2-amine, 1-[2-[(9Z,12Z)-octadeca-9,12-dien-1-yloxy]-1-[(octyloxy)methyl]ethyl]pyrrolidine, (2S)-N,N-dimethyl-1-[(9Z,12Z)-octadeca-9,12-dien-1-yloxy]-3-[(5Z)-oct-5-en-1-yloxy]propan-2-amine, 1-[2-[(9Z,12Z)-octadeca-9,12-dien-1-yloxy]-1-[(octyloxy)methyl]ethyl]azetidine, (2S)-1-(hexyloxy)-N,N-dimethyl-3-[(9Z,12Z)-octadeca-9,12-dien-1-yloxy]propan-2-amine, (2S)-1-(heptyloxy)-N,N-dimethyl-3-[(9Z,12Z)-octadeca-9,12-dien-1-yloxy]propan-2-amine, N,N-dimethyl-1-(nonyloxy)-3-[(9Z,12Z)-octadeca-9,12-dien-1-yloxy]propan-2-amine, N,N-dimethyl-1-[(9Z)-octadec-9-en-1-yloxy]-3-(octyloxy)propan-2-amine; (2S)-N,N-dimethyl-1-[(6Z,9Z,12Z)-octadeca-6,9,12-trien-1-yloxy]-3-(octyloxy)propan-2-amine, (2S)-1-[(11Z,14Z)-icosa-11,14-dien-1-yloxy]-N,N-dimethyl-3-(pentyloxy)propan-2-amine, (2S)-1-(hexyloxy)-3-[(11Z,14Z)-icosa-11,14-dien-1-yloxy]-N,N-dimethylpropan-2-amine, 1-[(11Z,14Z)-icosa-11,14-dien-1-yloxy]-N,N-dimethyl-3-(octyloxy)propan-2-amine, 1-[(13Z,16Z)-docosa-13,16-dien-1-yloxy]-N,N-dimethyl-3-(octyloxy)propan-2-amine, (2S)-1-[(13Z,16Z)-docosa-13,16-dien-1-yloxy]-3-(hexyloxy)-N,N-dimethylpropan-2-amine, (2S)-1-[(13Z)-docos-13-en-1-yloxy]-3-(hexyloxy)-N,N-dimethylpropan-2-amine, 1-[(13Z)-docos-13-en-1-yloxy]-N,N-dimethyl-3-(octyloxy)propan-2-amine, 1-[(9Z)-hexadec-9-en-1-yloxy]-N,N-dimethyl-3-(octyloxy)propan-2-amine, (2R)-N,N-dimethyl-H(1-metoyloctyl)oxy]-3-[(9Z,12Z)-octadeca-9,12-dien-1-yloxy]propan-2-amine, (2R)-1-[(3,7-dimethyloctyl)oxy]-N,N-dimethyl-3-[(9Z,12Z)-octadeca-9,12-dien-1-yloxy]propan-2-amine, N,N-dimethyl-1-(octyloxy)-3-[(8-[(1S,2S)-2-[(1R,2R)-2-pentylcyclopropyl]methyl]cyclopropyl]octyl]oxy]propan-2-amine, N,N-dimethyl-1-[[8-(2-octylcyclopropyl)octyl]oxy]-3-(octyloxy)propan-2-amine and (11E,20Z,23Z)-N,N-dimethylnonacosan-11,20,23-trien-10-amine or a pharmaceutically acceptable salt or stereoisomer thereof.

[0444] In some embodiments, the LNP formulations of the RNA (e.g., mRNA) vaccines may contain PEG-c-DOMG at 3% lipid molar ratio. In some embodiments, the LNP formulations of the RNA (e.g., mRNA) vaccines may contain PEG-c-DOMG at 1.5% lipid molar ratio.

[0445] In some embodiments, the pharmaceutical compositions of the RNA (e.g., mRNA) vaccines may include at least one of the PEGylated lipids described in International Publication No. WO2012099755, the contents of which are herein incorporated by reference in their entirety.

[0446] In some embodiments, the LNP formulation may contain PEG-DMG 2000 (1,2-dimyristoyl-sn-glycero-3-

phosphoethanolamine-N-[methoxy(polyethylene glycol)-2000]). In some embodiments, the LNP formulation may contain PEG-DMG 2000, a cationic lipid known in the art and at least one other component. In some embodiments, the LNP formulation may contain PEG-DMG 2000, a cationic lipid known in the art, DSPC and cholesterol. As a non-limiting example, the LNP formulation may contain PEG-DMG 2000, DLin-DMA, DSPC and cholesterol. As another non-limiting example the LNP formulation may contain PEG-DMG 2000, DLin-DMA, DSPC and cholesterol in a molar ratio of 2:40:10:48 (see e.g., Geall et al., Nonviral delivery of self-amplifying RNA (e.g., mRNA) vaccines, PNAS 2012; PMID: 22908294, the contents of each of which are herein incorporated by reference in their entirety).

[0447] The lipid nanoparticles described herein may be made in a sterile environment.

[0448] In some embodiments, the LNP formulation may be formulated in a nanoparticle such as a nucleic acid-lipid particle. As a non-limiting example, the lipid particle may comprise one or more active agents or therapeutic agents; one or more cationic lipids comprising from about 50 mol % to about 85 mol % of the total lipid present in the particle; one or more non-cationic lipids comprising from about 13 mol % to about 49.5 mol % of the total lipid present in the particle; and one or more conjugated lipids that inhibit aggregation of particles comprising from about 0.5 mol % to about 2 mol % of the total lipid present in the particle.

[0449] The nanoparticle formulations may comprise a phosphate conjugate. The phosphate conjugate may increase in vivo circulation times and/or increase the targeted delivery of the nanoparticle. As a non-limiting example, the phosphate conjugates may include a compound of any one of the formulas described in International Application No. WO2013033438, the contents of which are herein incorporated by reference in its entirety.

[0450] The nanoparticle formulation may comprise a polymer conjugate. The polymer conjugate may be a water soluble conjugate. The polymer conjugate may have a structure as described in U.S. Patent Application No. 20130059360, the contents of which are herein incorporated by reference in its entirety. In some embodiments, polymer conjugates with the polynucleotides of the present disclosure may be made using the methods and/or segmented polymeric reagents described in U.S. Patent Application No. 20130072709, the contents of which are herein incorporated by reference in its entirety. In some embodiments, the polymer conjugate may have pendant side groups comprising ring moieties such as, but not limited to, the polymer conjugates described in U.S. Patent Publication No. US20130196948, the contents of which are herein incorporated by reference in its entirety.

[0451] The nanoparticle formulations may comprise a conjugate to enhance the delivery of nanoparticles of the present disclosure in a subject. Further, the conjugate may inhibit phagocytic clearance of the nanoparticles in a subject. In one aspect, the conjugate may be a "self" peptide designed from the human membrane protein CD47 (e.g., the "self" particles described by Rodriguez et al. (*Science* 2013 339, 971-975), herein incorporated by reference in its entirety). As shown by Rodriguez et al., the self peptides delayed macrophage-mediated clearance of nanoparticles which enhanced delivery of the nanoparticles. In another aspect, the conjugate may be the membrane protein CD47 (e.g., see Rodriguez et al. *Science* 2013 339, 971-975, herein

incorporated by reference in its entirety). Rodriguez et al. showed that, similarly to “self” peptides, CD47 can increase the circulating particle ratio in a subject as compared to scrambled peptides and PEG coated nanoparticles.

[0452] In some embodiments, the RNA (e.g., mRNA) vaccines of the present disclosure are formulated in nanoparticles which comprise a conjugate to enhance the delivery of the nanoparticles of the present disclosure in a subject. The conjugate may be the CD47 membrane or the conjugate may be derived from the CD47 membrane protein, such as the “self” peptide described previously. In some embodiments, the nanoparticle may comprise PEG and a conjugate of CD47 or a derivative thereof. In some embodiments, the nanoparticle may comprise both the “self” peptide described above and the membrane protein CD47.

[0453] In some embodiments, a “self” peptide and/or CD47 protein may be conjugated to a virus-like particle or pseudovirion, as described herein for delivery of the RNA (e.g., mRNA) vaccines of the present disclosure.

[0454] In some embodiments, RNA (e.g., mRNA) vaccine pharmaceutical compositions comprising the polynucleotides of the present disclosure and a conjugate that may have a degradable linkage. Non-limiting examples of conjugates include an aromatic moiety comprising an ionizable hydrogen atom, a spacer moiety, and a water-soluble polymer. As a non-limiting example, pharmaceutical compositions comprising a conjugate with a degradable linkage and methods for delivering such pharmaceutical compositions are described in U.S. Patent Publication No. US20130184443, the contents of which are herein incorporated by reference in their entirety.

[0455] The nanoparticle formulations may be a carbohydrate nanoparticle comprising a carbohydrate carrier and a RNA (e.g., mRNA) vaccine. As a non-limiting example, the carbohydrate carrier may include, but is not limited to, an anhydride-modified phytoglycogen or glycogen-type material, phytoglycogen octenyl succinate, phytoglycogen beta-dextrin, anhydride-modified phytoglycogen beta-dextrin. (See e.g., International Publication No. WO2012109121; the contents of which are herein incorporated by reference in their entirety).

[0456] Nanoparticle formulations of the present disclosure may be coated with a surfactant or polymer in order to improve the delivery of the particle. In some embodiments, the nanoparticle may be coated with a hydrophilic coating such as, but not limited to, PEG coatings and/or coatings that have a neutral surface charge. The hydrophilic coatings may help to deliver nanoparticles with larger payloads such as, but not limited to, RNA (e.g., mRNA) vaccines within the central nervous system. As a non-limiting example nanoparticles comprising a hydrophilic coating and methods of making such nanoparticles are described in U.S. Patent Publication No. US20130183244, the contents of which are herein incorporated by reference in their entirety.

[0457] In some embodiments, the lipid nanoparticles of the present disclosure may be hydrophilic polymer particles. Non-limiting examples of hydrophilic polymer particles and methods of making hydrophilic polymer particles are described in U.S. Patent Publication No. US20130210991, the contents of which are herein incorporated by reference in their entirety.

[0458] In some embodiments, the lipid nanoparticles of the present disclosure may be hydrophobic polymer particles.

[0459] Lipid nanoparticle formulations may be improved by replacing the cationic lipid with a biodegradable cationic lipid which is known as a rapidly eliminated lipid nanoparticle (reLNP). Ionizable cationic lipids, such as, but not limited to, DLinDMA, DLin-KC2-DMA, and DLin-MC3-DMA, have been shown to accumulate in plasma and tissues over time and may be a potential source of toxicity. The rapid metabolism of the rapidly eliminated lipids can improve the tolerability and therapeutic index of the lipid nanoparticles by an order of magnitude from a 1 mg/kg dose to a 10 mg/kg dose in rat. Inclusion of an enzymatically degraded ester linkage can improve the degradation and metabolism profile of the cationic component, while still maintaining the activity of the reLNP formulation. The ester linkage can be internally located within the lipid chain or it may be terminally located at the terminal end of the lipid chain. The internal ester linkage may replace any carbon in the lipid chain.

[0460] In some embodiments, the internal ester linkage may be located on either side of the saturated carbon.

[0461] In some embodiments, an immune response may be elicited by delivering a lipid nanoparticle which may include a nanospecies, a polymer and an immunogen. (U.S. Publication No. 20120189700 and International Publication No. WO2012099805; each of which is herein incorporated by reference in their entirety). The polymer may encapsulate the nanospecies or partially encapsulate the nanospecies. The immunogen may be a recombinant protein, a modified RNA and/or a polynucleotide described herein. In some embodiments, the lipid nanoparticle may be formulated for use in a vaccine such as, but not limited to, against a pathogen.

[0462] Lipid nanoparticles may be engineered to alter the surface properties of particles so the lipid nanoparticles may penetrate the mucosal barrier. Mucus is located on mucosal tissue such as, but not limited to, oral (e.g., the buccal and esophageal membranes and tonsil tissue), ophthalmic, gastrointestinal (e.g., stomach, small intestine, large intestine, colon, rectum), nasal, respiratory (e.g., nasal, pharyngeal, tracheal and bronchial membranes), genital (e.g., vaginal, cervical and urethral membranes). Nanoparticles larger than 10-200 nm which are preferred for higher drug encapsulation efficiency and the ability to provide the sustained delivery of a wide array of drugs have been thought to be too large to rapidly diffuse through mucosal barriers. Mucus is continuously secreted, shed, discarded or digested and recycled so most of the trapped particles may be removed from the mucosa tissue within seconds or within a few hours. Large polymeric nanoparticles (200nm -500nm in diameter) which have been coated densely with a low molecular weight polyethylene glycol (PEG) diffused through mucus only 4 to 6-fold lower than the same particles diffusing in water (Lai et al. PNAS 2007 104(5):1482-487; Lai et al. *Adv Drug Deliv Rev.* 2009 61(2): 158-171; each of which is herein incorporated by reference in their entirety). The transport of nanoparticles may be determined using rates of permeation and/or fluorescent microscopy techniques including, but not limited to, fluorescence recovery after photobleaching (FRAP) and high resolution multiple particle tracking (MPT). As a non-limiting example, compositions which can penetrate a mucosal barrier may be made as described in U.S. Pat. No. 8,241,670 or Interna-

tional Patent Publication No. WO2013110028, the contents of each of which are herein incorporated by reference in its entirety.

[0463] The lipid nanoparticle engineered to penetrate mucus may comprise a polymeric material (i.e. a polymeric core) and/or a polymer-vitamin conjugate and/or a tri-block co-polymer. The polymeric material may include, but is not limited to, polyamines, polyethers, polyamides, polyesters, polycarbonates, polyureas, polycarbonates, poly(styrenes), polyimides, polysulfones, polyurethanes, polyacetylenes, polyethylenes, polyethyleneimines, polyisocyanates, polyacrylates, polymethacrylates, polyacrylonitriles, and polyarylates. The polymeric material may be biodegradable and/or biocompatible. Non-limiting examples of biocompatible polymers are described in International Patent Publication No. WO2013116804, the contents of which are herein incorporated by reference in their entirety. The polymeric material may additionally be irradiated. As a non-limiting example, the polymeric material may be gamma irradiated (see e.g., International App. No. WO201282165, herein incorporated by reference in its entirety). Non-limiting examples of specific polymers include poly(caprolactone) (PCL), ethylene vinyl acetate polymer (EVA), poly(lactic acid) (PLA), poly(L-lactic acid) (PLLA), poly(glycolic acid) (PGA), poly(lactic acid-co-glycolic acid) (PLGA), poly(L-lactic acid-co-glycolic acid) (PLLGA), poly(D,L-lactide) (PDLA), poly(L-lactide) (PLLA), poly(D,L-lactide-co-caprolactone), poly(D,L-lactide-co-caprolactone-co-glycolide), poly(D,L-lactide-co-PEO-co-D,L-lactide), poly(D,L-lactide-co-PPO-co-D,L-lactide), polyalkyl cyanoacrylate, polyurethane, poly-L-lysine (PLL), hydroxypropyl methacrylate (HPMA), polyethyleneglycol, poly-L-glutamic acid, poly(hydroxy acids), polyanhydrides, polyorthoesters, poly(ester amides), polyamides, poly(ester ethers), polycarbonates, polyalkylenes such as polyethylene and polypropylene, polyalkylene glycols such as poly(ethylene glycol) (PEG), polyalkylene oxides (PEO), polyalkylene terephthalates such as poly(ethylene terephthalate), polyvinyl alcohols (PVA), polyvinyl ethers, polyvinyl esters such as poly(vinyl acetate), polyvinyl halides such as poly(vinyl chloride) (PVC), polyvinylpyrrolidone, polysiloxanes, polystyrene (PS), polyurethanes, derivatized celluloses such as alkyl celluloses, hydroxyalkyl celluloses, cellulose ethers, cellulose esters, nitro celluloses, hydroxypropylcellulose, carboxymethylcellulose, polymers of acrylic acids, such as poly(methyl(meth)acrylate) (PMMA), poly(ethyl(meth)acrylate), poly(butyl(meth)acrylate), poly(isobutyl(meth)acrylate), poly(hexyl(meth)acrylate), poly(isodecyl(meth)acrylate), poly(lauryl(meth)acrylate), poly(phenyl(meth)acrylate), poly(methyl acrylate), poly(isopropyl acrylate), poly(isobutyl acrylate), poly(octadecyl acrylate) and copolymers and mixtures thereof, polydioxanone and its copolymers, polyhydroxyalkanoates, polypropylene fumarate, polyoxymethylene, poloxamers, poly(ortho)esters, poly(butyric acid), poly(valeric acid), poly(lactide-co-caprolactone), PEG-PLGA-PEG and trimethylene carbonate, polyvinylpyrrolidone. The lipid nanoparticle may be coated or associated with a co-polymer such as, but not limited to, a block co-polymer (such as a branched polyether-polyamide block copolymer described in International Patent Publication No. WO2013012476, herein incorporated by reference in its entirety), and (poly(ethylene glycol))-(poly(propylene oxide))-(poly(ethylene glycol)) triblock copolymer (see e.g., U.S. Publication 20120121718 and U.S. Publication

20100003337 and U.S. Pat. No. 8,263,665, the contents of each of which are herein incorporated by reference in their entirety). The co-polymer may be a polymer that is generally regarded as safe (GRAS) and the formation of the lipid nanoparticle may be in such a way that no new chemical entities are created. For example, the lipid nanoparticle may comprise poloxamers coating PLGA nanoparticles without forming new chemical entities which are still able to rapidly penetrate human mucus (Yang et al. *Angew. Chem. Int. Ed.* 2011 50:2597-2600; the contents of which are herein incorporated by reference in their entirety). A non-limiting scalable method to produce nanoparticles which can penetrate human mucus is described by Xu et al. (see, e.g., *J Control Release* 2013, 170(2):279-86; the contents of which are herein incorporated by reference in their entirety).

[0464] The vitamin of the polymer-vitamin conjugate may be vitamin E. The vitamin portion of the conjugate may be substituted with other suitable components such as, but not limited to, vitamin A, vitamin E, other vitamins, cholesterol, a hydrophobic moiety, or a hydrophobic component of other surfactants (e.g., sterol chains, fatty acids, hydrocarbon chains and alkylene oxide chains).

[0465] The lipid nanoparticle engineered to penetrate mucus may include surface altering agents such as, but not limited to, polynucleotides, anionic proteins (e.g., bovine serum albumin), surfactants (e.g., cationic surfactants such as for example dimethyldioctadecyl-ammonium bromide), sugars or sugar derivatives (e.g., cyclodextrin), nucleic acids, polymers (e.g., heparin, polyethylene glycol and poloxamer), mucolytic agents (e.g., N-acetylcysteine, mugwort, bromelain, papain, clerodendrum, acetylcysteine, bromhexine, carbocisteine, eprazinone, mesna, ambroxol, sobrerol, domiodol, letosteine, stepronin, tiopronin, gelsolin, thymosin β 4 dornase alfa, neltexine, erdocteine) and various DNases including rhDNase. The surface altering agent may be embedded or enmeshed in the particle's surface or disposed (e.g., by coating, adsorption, covalent linkage, or other process) on the surface of the lipid nanoparticle. (see e.g., U.S. Publication 20100215580 and U.S. Publication 20080166414 and US20130164343; the contents of each of which are herein incorporated by reference in their entirety).

[0466] In some embodiments, the mucus penetrating lipid nanoparticles may comprise at least one polynucleotide described herein. The polynucleotide may be encapsulated in the lipid nanoparticle and/or disposed on the surface of the particle. The polynucleotide may be covalently coupled to the lipid nanoparticle. Formulations of mucus penetrating lipid nanoparticles may comprise a plurality of nanoparticles. Further, the formulations may contain particles which may interact with the mucus and alter the structural and/or adhesive properties of the surrounding mucus to decrease mucoadhesion, which may increase the delivery of the mucus penetrating lipid nanoparticles to the mucosal tissue.

[0467] In some embodiments, the mucus penetrating lipid nanoparticles may be a hypotonic formulation comprising a mucosal penetration enhancing coating. The formulation may be hypotonic for the epithelium to which it is being delivered. Non-limiting examples of hypotonic formulations may be found in International Patent Publication No. WO2013110028, the contents of which are herein incorporated by reference in their entirety.

[0468] In some embodiments, in order to enhance the delivery through the mucosal barrier the RNA (e.g., mRNA) vaccine formulation may comprise or be a hypotonic solu-

tion. Hypotonic solutions were found to increase the rate at which mucin particles such as, but not limited to, mucus-penetrating particles, were able to reach the vaginal epithelial surface (see e.g., Ensign et al. *Biomaterials* 2013 34(28):6922-9, the contents of which are herein incorporated by reference in their entirety).

[0469] In some embodiments, the RNA (e.g., mRNA) vaccine is formulated as a lipoplex, such as, without limitation, the ATUPLEX™ system, the DACC system, the DBTC system and other siRNA-lipoplex technology from Silence Therapeutics (London, United Kingdom), STEM-FECT™ from STEMAGENT® (Cambridge, Mass.), and polyethylenimine (PEI) or protamine-based targeted and non-targeted delivery of nucleic acids (Aleku et al. *Cancer Res.* 2008 68:9788-9798; Strumberg et al. *Int J Clin Pharmacol Ther* 2012 50:76-78; Santel et al., *Gene Ther* 2006 13:1222-1234; Santel et al., *Gene Ther* 2006 13:1360-1370; Gutbier et al., *Pulm Pharmacol. Ther.* 2010 23:334-344; Kaufmann et al. *Microvasc Res* 2010 80:286-293; Weide et al. *J Immunother.* 2009 32:498-507; Weide et al. *J Immunother.* 2008 31:180-188; Pascolo *Expert Opin. Biol. Ther.* 4:1285-1294; Fotin-Mleczek et al., 2011 *J. Immunother.* 34:1-15; Song et al., *Nature Biotechnol.* 2005, 23:709-717; Peer et al., *Proc Natl Acad Sci U S A.* 2007 6:104:4095-4100; deFougerolles *Hum Gene Ther.* 2008 19:125-132, the contents of each of which are incorporated herein by reference in their entirety).

[0470] In some embodiments, such formulations may also be constructed or compositions altered such that they passively or actively are directed to different cell types *in vivo*, including but not limited to hepatocytes, immune cells, tumor cells, endothelial cells, antigen presenting cells, and leukocytes (Akinc et al. *Mol Ther.* 2010 18:1357-1364; Song et al., *Nat Biotechnol.* 2005 23:709-717; Judge et al., *J Clin Invest.* 2009 119:661-673; Kaufmann et al., *Microvasc Res* 2010 80:286-293; Santel et al., *Gene Ther* 2006 13:1222-1234; Santel et al., *Gene Ther* 2006 13:1360-1370; Gutbier et al., *Pulm Pharmacol. Ther.* 2010 23:334-344; Basha et al., *Mol. Ther.* 2011 19:2186-2200; Fenske and Cullis, *Expert Opin Drug Deliv.* 2008 5:25-44; Peer et al., *Science.* 2008 319:627-630; Peer and Lieberman, *Gene Ther.* 2011 18:1127-1133, the contents of each of which are incorporated herein by reference in their entirety). One example of passive targeting of formulations to liver cells includes the DLin-DMA, DLin-KC2-DMA and DLin-MC3-DMA-based lipid nanoparticle formulations, which have been shown to bind to apolipoprotein E and promote binding and uptake of these formulations into hepatocytes *in vivo* (Akinc et al. *Mol Ther.* 2010 18:1357-1364, the contents of which are incorporated herein by reference in their entirety). Formulations can also be selectively targeted through expression of different ligands on their surface as exemplified by, but not limited by, folate, transferrin, N-acetylgalactosamine (GalNAc), and antibody targeted approaches (Kolhatkar et al., *Curr Drug Discov Technol.* 2011 8:197-206; Musacchio and Torchilin, *Front Biosci.* 2011 16:1388-1412; Yu et al., *Mol Membr Biol.* 2010 27:286-298; Patil et al., *Crit Rev Ther Drug Carrier Syst.* 2008 25:1-61; Benoit et al., *Biomacromolecules.* 2011 12:2708-2714; Zhao et al., *Expert Opin Drug Deliv.* 2008 5:309-319; Akinc et al., *Mol Ther.* 2010 18:1357-1364; Srinivasan et al., *Methods Mol Biol.* 2012 820:105-116; Ben-Arie et al., *Methods Mol Biol.* 2012 757:497-507; Peer 2010 *J Control Release.* 20:63-68; Peer et al., *Proc Natl Acad Sci U S A.* 2007 104:4095-4100;

Kim et al., *Methods Mol Biol.* 2011 721:339-353; Subramanya et al., *Mol Ther.* 2010 18:2028-2037; Song et al., *Nat Biotechnol.* 2005 23:709-717; Peer et al., *Science.* 2008 319:627-630; Peer and Lieberman, *Gene Ther.* 2011 18:1127-1133, the contents of each of which are incorporated herein by reference in their entirety).

[0471] In some embodiments, the RNA (e.g., mRNA) vaccine is formulated as a solid lipid nanoparticle. A solid lipid nanoparticle (SLN) may be spherical with an average diameter between 10 to 1000 nm. SLN possess a solid lipid core matrix that can solubilize lipophilic molecules and may be stabilized with surfactants and/or emulsifiers. In some embodiments, the lipid nanoparticle may be a self-assembly lipid-polymer nanoparticle (see Zhang et al., *ACS Nano*, 2008, 2 (8), pp 1696-1702; the contents of which are herein incorporated by reference in their entirety). As a non-limiting example, the SLN may be the SLN described in International Patent Publication No. WO2013105101, the contents of which are herein incorporated by reference in their entirety. As another non-limiting example, the SLN may be made by the methods or processes described in International Patent Publication No. WO2013105101, the contents of which are herein incorporated by reference in their entirety.

[0472] Liposomes, lipoplexes, or lipid nanoparticles may be used to improve the efficacy of polynucleotides directed protein production as these formulations may be able to increase cell transfection by the RNA (e.g., mRNA) vaccine; and/or increase the translation of encoded protein. One such example involves the use of lipid encapsulation to enable the effective systemic delivery of polyplex plasmid DNA (Heyes et al., *Mol Ther.* 2007 15:713-720; the contents of which are incorporated herein by reference in their entirety). The liposomes, lipoplexes, or lipid nanoparticles may also be used to increase the stability of the polynucleotide.

[0473] In some embodiments, the RNA (e.g., mRNA) vaccines of the present disclosure can be formulated for controlled release and/or targeted delivery. As used herein, “controlled release” refers to a pharmaceutical composition or compound release profile that conforms to a particular pattern of release to effect a therapeutic outcome. In some embodiments, the RNA (e.g., mRNA) vaccines may be encapsulated into a delivery agent described herein and/or known in the art for controlled release and/or targeted delivery. As used herein, the term “encapsulate” means to enclose, surround or encase. As it relates to the formulation of the compounds of the disclosure, encapsulation may be substantial, complete or partial. The term “substantially encapsulated” means that at least greater than 50, 60, 70, 80, 85, 90, 95, 96, 97, 98, 99, 99.9, 99.9 or greater than 99.999% of the pharmaceutical composition or compound of the disclosure may be enclosed, surrounded or encased within the delivery agent. “Partially encapsulation” means that less than 10, 10, 20, 30, 40 50 or less of the pharmaceutical composition or compound of the disclosure may be enclosed, surrounded or encased within the delivery agent. Advantageously, encapsulation may be determined by measuring the escape or the activity of the pharmaceutical composition or compound of the disclosure using fluorescence and/or electron micrograph. For example, at least 1, 5, 10, 20, 30, 40, 50, 60, 70, 80, 85, 90, 95, 96, 97, 98, 99, 99.9, 99.99 or greater than 99.99% of the pharmaceutical composition or compound of the disclosure are encapsulated in the delivery agent.

[0474] In some embodiments, the controlled release formulation may include, but is not limited to, tri-block co-polymers. As a non-limiting example, the formulation may include two different types of tri-block co-polymers (International Pub. No. WO2012131104 and WO2012131106, the contents of each of which are incorporated herein by reference in their entirety).

[0475] In some embodiments, the RNA (e.g., mRNA) vaccines may be encapsulated into a lipid nanoparticle or a rapidly eliminated lipid nanoparticle and the lipid nanoparticles or a rapidly eliminated lipid nanoparticle may then be encapsulated into a polymer, hydrogel and/or surgical sealant described herein and/or known in the art. As a non-limiting example, the polymer, hydrogel or surgical sealant may be PLGA, ethylene vinyl acetate (EVAc), poloxamer, GELSITE® (Nanotherapeutics, Inc. Alachua, Fla.), HYL-ENEX® (Halozyme Therapeutics, San Diego Calif.), surgical sealants such as fibrinogen polymers (Ethicon Inc. Cornelia, Ga.), TISSELL® (Baxter International, Inc Deerfield, Ill.), PEG-based sealants, and COSEAL® (Baxter International, Inc Deerfield, Ill.).

[0476] In some embodiments, the lipid nanoparticle may be encapsulated into any polymer known in the art which may form a gel when injected into a subject. As another non-limiting example, the lipid nanoparticle may be encapsulated into a polymer matrix which may be biodegradable.

[0477] In some embodiments, the RNA (e.g., mRNA) vaccine formulation for controlled release and/or targeted delivery may also include at least one controlled release coating. Controlled release coatings include, but are not limited to, OPADRY®, polyvinylpyrrolidone/vinyl acetate copolymer, polyvinylpyrrolidone, hydroxypropyl methylcellulose, hydroxypropyl cellulose, hydroxyethyl cellulose, EUDRAGIT RL®, EUDRAGIT RS® and cellulose derivatives such as ethylcellulose aqueous dispersions (AQUACOAT® and SURELEASE®).

[0478] In some embodiments, the RNA (e.g., mRNA) vaccine controlled release and/or targeted delivery formulation may comprise at least one degradable polyester which may contain polycationic side chains. Degradable polyesters include, but are not limited to, poly(serine ester), poly(L-lactide-co-L-lysine), poly(4-hydroxy-L-proline ester), and combinations thereof. In some embodiments, the degradable polyesters may include a PEG conjugation to form a PEGylated polymer.

[0479] In some embodiments, the RNA (e.g., mRNA) vaccine controlled release and/or targeted delivery formulation comprising at least one polynucleotide may comprise at least one PEG and/or PEG related polymer derivatives as described in U.S. Pat. No. 8,404,222, the contents of which are incorporated herein by reference in their entirety.

[0480] In some embodiments, the RNA (e.g., mRNA) vaccine controlled release delivery formulation comprising at least one polynucleotide may be the controlled release polymer system described in US20130130348, the contents of which are incorporated herein by reference in their entirety.

[0481] In some embodiments, the RNA (e.g., mRNA) vaccines of the present disclosure may be encapsulated in a therapeutic nanoparticle, referred to herein as “therapeutic nanoparticle RNA (e.g., mRNA) vaccines.” Therapeutic nanoparticles may be formulated by methods described herein and known in the art such as, but not limited to, International Pub Nos. WO2010005740, WO2010030763,

WO2010005721, WO2010005723, WO2012054923, U.S. Publication Nos. US20110262491, US20100104645, US20100087337, US20100068285, US20110274759, US20100068286, US20120288541, US20130123351 and US20130230567 and U.S. Pat. Nos. 8,206,747, 8,293,276, 8,318,208 and 8,318,211; the contents of each of which are herein incorporated by reference in their entirety. In some embodiments, therapeutic polymer nanoparticles may be identified by the methods described in US Pub No. US20120140790, the contents of which are herein incorporated by reference in their entirety.

[0482] In some embodiments, the therapeutic nanoparticle RNA (e.g., mRNA) vaccine may be formulated for sustained release. As used herein, “sustained release” refers to a pharmaceutical composition or compound that conforms to a release rate over a specific period of time. The period of time may include, but is not limited to, hours, days, weeks, months and years. As a non-limiting example, the sustained release nanoparticle may comprise a polymer and a therapeutic agent such as, but not limited to, the polynucleotides of the present disclosure (see International Pub No. 2010075072 and US Pub No. US20100216804, US20110217377 and US20120201859, the contents of each of which are incorporated herein by reference in their entirety). In another non-limiting example, the sustained release formulation may comprise agents which permit persistent bioavailability such as, but not limited to, crystals, macromolecular gels and/or particulate suspensions (see U.S. Patent Publication No US20130150295, the contents of each of which are incorporated herein by reference in their entirety).

[0483] In some embodiments, the therapeutic nanoparticle RNA (e.g., mRNA) vaccines may be formulated to be target specific. As a non-limiting example, the therapeutic nanoparticles may include a corticosteroid (see International Pub. No. WO2011084518, the contents of which are incorporated herein by reference in their entirety). As a non-limiting example, the therapeutic nanoparticles may be formulated in nanoparticles described in International Pub No. WO2008121949, WO2010005726, WO2010005725, WO2011084521 and US Pub No. US20100069426, US20120004293 and US20100104655, the contents of each of which are incorporated herein by reference in their entirety.

[0484] In some embodiments, the nanoparticles of the present disclosure may comprise a polymeric matrix. As a non-limiting example, the nanoparticle may comprise two or more polymers such as, but not limited to, polyethylenes, polycarbonates, polyanhydrides, polyhydroxyacids, polypropylfumerates, polycaprolactones, polyamides, polyacetals, polyethers, polyesters, poly(orthoesters), polycyanoacrylates, polyvinyl alcohols, polyurethanes, polyphosphazenes, polyacrylates, polymethacrylates, polycyanoacrylates, polyureas, polystyrenes, polyamines, polylysine, poly(ethylene imine), poly(serine ester), poly(L-lactide-co-L-lysine), poly(4-hydroxy-L-proline ester) or combinations thereof.

[0485] In some embodiments, the therapeutic nanoparticle comprises a diblock copolymer. In some embodiments, the diblock copolymer may include PEG in combination with a polymer such as, but not limited to, polyethylenes, polycarbonates, polyanhydrides, polyhydroxyacids, polypropylfumerates, polycaprolactones, polyamides, polyacetals, polyethers, polyesters, poly(orthoesters), polycyanoacry-

lates, polyvinyl alcohols, polyurethanes, polyphosphazenes, polyacrylates, polymethacrylates, polycyanoacrylates, polyureas, polystyrenes, polyamines, polylysine, poly(ethylene imine), poly(serine ester), poly(L-lactide-co-L-lysine), poly(4-hydroxy-L-proline ester) or combinations thereof. In yet another embodiment, the diblock copolymer may be a high-X diblock copolymer such as those described in International Patent Publication No. WO2013120052, the contents of which are incorporated herein by reference in their entirety.

[0486] As a non-limiting example the therapeutic nanoparticle comprises a PLGA-PEG block copolymer (see U.S. Publication No. US20120004293 and U.S. Pat. No. 8,236,330, each of which is herein incorporated by reference in their entirety). In another non-limiting example, the therapeutic nanoparticle is a stealth nanoparticle comprising a diblock copolymer of PEG and PLA or PEG and PLGA (see U.S. Pat. No. 8,246,968 and International Publication No. WO2012166923, the contents of each of which are herein incorporated by reference in their entirety). In yet another non-limiting example, the therapeutic nanoparticle is a stealth nanoparticle or a target-specific stealth nanoparticle as described in U.S. Patent Publication No. US20130172406, the contents of which are herein incorporated by reference in their entirety.

[0487] In some embodiments, the therapeutic nanoparticle may comprise a multiblock copolymer (see e.g., U.S. Pat. Nos. 8,263,665 and 8,287,910 and U.S. Patent Pub. No. US20130195987, the contents of each of which are herein incorporated by reference in their entirety).

[0488] In yet another non-limiting example, the lipid nanoparticle comprises the block copolymer PEG-PLGA-PEG (see e.g., the thermosensitive hydrogel (PEG-PLGA-PEG) was used as a TGF- β 1 gene delivery vehicle in Lee et al. Thermosensitive Hydrogel as a Tgf- β 1 Gene Delivery Vehicle Enhances Diabetic Wound Healing. *Pharmaceutical Research*, 2003 20(12): 1995-2000; as a controlled gene delivery system in Li et al. Controlled Gene Delivery System Based on Thermosensitive Biodegradable Hydrogel. *Pharmaceutical Research* 2003 20(6):884-888; and Chang et al., Non-ionic amphiphilic biodegradable PEG-PLGA-PEG copolymer enhances gene delivery efficiency in rat skeletal muscle. *J Controlled Release*. 2007 118:245-253, the contents of each of which are herein incorporated by reference in their entirety). The RNA (e.g., mRNA) vaccines of the present disclosure may be formulated in lipid nanoparticles comprising the PEG-PLGA-PEG block copolymer.

[0489] In some embodiments, the therapeutic nanoparticle may comprise a multiblock copolymer (see e.g., U.S. Pat. Nos. 8,263,665 and 8,287,910 and U.S. Patent Pub. No. US20130195987, the contents of each of which are herein incorporated by reference in their entirety).

[0490] In some embodiments, the block copolymers described herein may be included in a polyion complex comprising a non-polymeric micelle and the block copolymer. (see e.g., U.S. Publication No. 20120076836, the contents of which are herein incorporated by reference in their entirety).

[0491] In some embodiments, the therapeutic nanoparticle may comprise at least one acrylic polymer. Acrylic polymers include but are not limited to, acrylic acid, methacrylic acid, acrylic acid and methacrylic acid copolymers, methyl methacrylate copolymers, ethoxyethyl methacrylates, cyanoethyl

methacrylate, amino alkyl methacrylate copolymer, poly (acrylic acid), poly(methacrylic acid), polycyanoacrylates and combinations thereof.

[0492] In some embodiments, the therapeutic nanoparticles may comprise at least one poly(vinyl ester) polymer. The poly(vinyl ester) polymer may be a copolymer such as a random copolymer. As a non-limiting example, the random copolymer may have a structure such as those described in International Application No. WO2013032829 or U.S. Patent Publication No. US20130121954, the contents of each of which are herein incorporated by reference in their entirety. In some embodiments, the poly(vinyl ester) polymers may be conjugated to the polynucleotides described herein.

[0493] In some embodiments, the therapeutic nanoparticle may comprise at least one diblock copolymer. The diblock copolymer may be, but it not limited to, a poly(lactic) acid-poly(ethylene)glycol copolymer (see, e.g., International Patent Publication No. WO2013044219, the contents of which are herein incorporated by reference in their entirety). As a non-limiting example, the therapeutic nanoparticle may be used to treat cancer (see International publication No. WO2013044219, the contents of which are herein incorporated by reference in their entirety).

[0494] In some embodiments, the therapeutic nanoparticles may comprise at least one cationic polymer described herein and/or known in the art.

[0495] In some embodiments, the therapeutic nanoparticles may comprise at least one amine-containing polymer such as, but not limited to polylysine, polyethylene imine, poly(amidoamine) dendrimers, poly(beta-amino esters) (see, e.g., U.S. Pat. No. 8,287,849, the contents of which are herein incorporated by reference in their entirety) and combinations thereof.

[0496] In some embodiments, the nanoparticles described herein may comprise an amine cationic lipid such as those described in International Patent Application No. WO2013059496, the contents of which are herein incorporated by reference in their entirety. In some embodiments, the cationic lipids may have an amino-amine or an amino-amide moiety.

[0497] In some embodiments, the therapeutic nanoparticles may comprise at least one degradable polyester which may contain polycationic side chains. Degradable polyesters include, but are not limited to, poly(serine ester), poly(L-lactide-co-L-lysine), poly(4-hydroxy-L-proline ester), and combinations thereof. In some embodiments, the degradable polyesters may include a PEG conjugation to form a PEGylated polymer.

[0498] In some embodiments, the synthetic nanocarriers may contain an immunostimulatory agent to enhance the immune response from delivery of the synthetic nanocarrier. As a non-limiting example, the synthetic nanocarrier may comprise a Th1 immunostimulatory agent, which may enhance a Th1-based response of the immune system (see International Pub No. WO2010123569 and U.S. Publication No. US20110223201, the contents of each of which are herein incorporated by reference in their entirety).

[0499] In some embodiments, the synthetic nanocarriers may be formulated for targeted release. In some embodiments, the synthetic nanocarrier is formulated to release the polynucleotides at a specified pH and/or after a desired time interval. As a non-limiting example, the synthetic nanoparticle may be formulated to release the RNA (e.g., mRNA) vaccines after 24 hours and/or at a pH of 4.5 (see Interna-

tional Publication Nos. WO2010138193 and WO2010138194 and US Pub Nos. US20110020388 and US20110027217, each of which is herein incorporated by reference in their entirety).

[0500] In some embodiments, the synthetic nanocarriers may be formulated for controlled and/or sustained release of the polynucleotides described herein. As a non-limiting example, the synthetic nanocarriers for sustained release may be formulated by methods known in the art, described herein and/or as described in International Pub No. WO2010138192 and US Pub No. 20100303850, each of which is herein incorporated by reference in their entirety.

[0501] In some embodiments, the RNA (e.g., mRNA) vaccine may be formulated for controlled and/or sustained release wherein the formulation comprises at least one polymer that is a crystalline side chain (CYSC) polymer. CYSC polymers are described in U.S. Pat. No. 8,399,007, herein incorporated by reference in its entirety.

[0502] In some embodiments, the synthetic nanocarrier may be formulated for use as a vaccine. In some embodiments, the synthetic nanocarrier may encapsulate at least one polynucleotide which encode at least one antigen. As a non-limiting example, the synthetic nanocarrier may include at least one antigen and an excipient for a vaccine dosage form (see International Publication No. WO2011150264 and U.S. Publication No. US20110293723, the contents of each of which are herein incorporated by reference in their entirety). As another non-limiting example, a vaccine dosage form may include at least two synthetic nanocarriers with the same or different antigens and an excipient (see International Publication No. WO2011150249 and U.S. Publication No. US20110293701, the contents of each of which are herein incorporated by reference in their entirety). The vaccine dosage form may be selected by methods described herein, known in the art and/or described in International Publication No. WO2011150258 and U.S. Publication No. US20120027806, the contents of each of which are herein incorporated by reference in their entirety).

[0503] In some embodiments, the synthetic nanocarrier may comprise at least one polynucleotide which encodes at least one adjuvant. As non-limiting example, the adjuvant may comprise dimethyldioctadecylammonium-bromide, dimethyldioctadecylammonium-chloride, dimethyldioctadecylammonium-phosphate or dimethyldioctadecylammonium-acetate (DDA) and an apolar fraction or part of said apolar fraction of a total lipid extract of a mycobacterium (see, e.g., U.S. Pat. No. 8,241,610, the content of which is herein incorporated by reference in its entirety). In some embodiments, the synthetic nanocarrier may comprise at least one polynucleotide and an adjuvant. As a non-limiting example, the synthetic nanocarrier comprising and adjuvant may be formulated by the methods described in International Publication No. WO2011150240 and U.S. Publication No. US20110293700, the contents of each of which are herein incorporated by reference in their entirety.

[0504] In some embodiments, the synthetic nanocarrier may encapsulate at least one polynucleotide that encodes a peptide, fragment or region from a virus. As a non-limiting example, the synthetic nanocarrier may include, but is not limited to, any of the nanocarriers described in International Publication No. WO2012024621, WO201202629, WO2012024632 and U.S. Publication No. US20120064110,

US20120058153 and US20120058154, the contents of each of which are herein incorporated by reference in their entirety.

[0505] In some embodiments, the synthetic nanocarrier may be coupled to a polynucleotide which may be able to trigger a humoral and/or cytotoxic T lymphocyte (CTL) response (see, e.g., International Publication No. WO2013019669, the contents of which are herein incorporated by reference in their entirety).

[0506] In some embodiments, the RNA (e.g., mRNA) vaccine may be encapsulated in, linked to and/or associated with zwitterionic lipids. Non-limiting examples of zwitterionic lipids and methods of using zwitterionic lipids are described in U.S. Patent Publication No. US20130216607, the contents of which are herein incorporated by reference in their entirety. In some aspects, the zwitterionic lipids may be used in the liposomes and lipid nanoparticles described herein.

[0507] In some embodiments, the RNA (e.g., mRNA) vaccine may be formulated in colloid nanocarriers as described in U.S. Patent Publication No. US20130197100, the contents of which are herein incorporated by reference in their entirety.

[0508] In some embodiments, the nanoparticle may be optimized for oral administration. The nanoparticle may comprise at least one cationic biopolymer such as, but not limited to, chitosan or a derivative thereof. As a non-limiting example, the nanoparticle may be formulated by the methods described in U.S. Publication No. 20120282343, the contents of which are herein incorporated by reference in their entirety.

[0509] In some embodiments, LNPs comprise the lipid KL52 (an amino-lipid disclosed in U.S. Application Publication No. 2012/0295832, the contents of which are herein incorporated by reference in their entirety. Activity and/or safety (as measured by examining one or more of ALT/AST, white blood cell count and cytokine induction, for example) of LNP administration may be improved by incorporation of such lipids. LNPs comprising KL52 may be administered intravenously and/or in one or more doses. In some embodiments, administration of LNPs comprising KL52 results in equal or improved mRNA and/or protein expression as compared to LNPs comprising MC3.

[0510] In some embodiments, RNA (e.g., mRNA) vaccine may be delivered using smaller LNPs. Such particles may comprise a diameter from below 0.1 μm up to 100 nm such as, but not limited to, less than 0.1 μm , less than 1.0 μm , less than 5 μm , less than 10 μm , less than 15 μm , less than 20 μm , less than 25 μm , less than 30 μm , less than 35 μm , less than 40 μm , less than 50 μm , less than 55 μm , less than 60 μm , less than 65 μm , less than 70 μm , less than 75 μm , less than 80 μm , less than 85 μm , less than 90 μm , less than 95 μm , less than 100 μm , less than 125 μm , less than 150 μm , less than 175 μm , less than 200 μm , less than 225 μm , less than 250 μm , less than 275 μm , less than 300 μm , less than 325 μm , less than 350 μm , less than 375 μm , less than 400 μm , less than 425 μm , less than 450 μm , less than 475 μm , less than 500 μm , less than 525 μm , less than 550 μm , less than 575 μm , less than 600 μm , less than 625 μm , less than 650 μm , less than 675 μm , less than 700 μm , less than 725 μm , less than 750 μm , less than 775 μm , less than 800 μm , less than 825 μm , less than 850 μm , less than 875 μm , less than 900 μm , less than 925 μm , less than 950 μm , less than 975 μm , or less than 1000 μm .

[0511] In some embodiments, RNA (e.g., mRNA) vaccines may be delivered using smaller LNPs, which may comprise a diameter from about 1 nm to about 100 nm, from about 1 nm to about 10 nm, about 1 nm to about 20 nm, from about 1 nm to about 30 nm, from about 1 nm to about 40 nm, from about 1 nm to about 50 nm, from about 1 nm to about 60 nm, from about 1 nm to about 70 nm, from about 1 nm to about 80 nm, from about 1 nm to about 90 nm, from about 5 nm to about 100 nm, from about 5 nm to about 10 nm, about 5 nm to about 20 nm, from about 5 nm to about 30 nm, from about 5 nm to about 40 nm, from about 5 nm to about 50 nm, from about 5 nm to about 60 nm, from about 5 nm to about 70 nm, from about 5 nm to about 80 nm, from about 5 nm to about 90 nm, about 10 to about 50 nm, from about 20 to about 50 nm, from about 30 to about 50 nm, from about 40 to about 50 nm, from about 20 to about 60 nm, from about 30 to about 60 nm, from about 40 to about 60 nm, from about 20 to about 70 nm, from about 30 to about 70 nm, from about 40 to about 70 nm, from about 50 to about 70 nm, from about 60 to about 70 nm, from about 20 to about 80 nm, from about 30 to about 80 nm, from about 40 to about 80 nm, from about 50 to about 80 nm, from about 60 to about 80 nm, from about 20 to about 90 nm, from about 30 to about 90 nm, from about 40 to about 90 nm, from about 50 to about 90 nm, from about 60 to about 90 nm and/or from about 70 to about 90 nm.

[0512] In some embodiments, such LNPs are synthesized using methods comprising microfluidic mixers. Examples of microfluidic mixers may include, but are not limited to, a slit interdigital micromixer including, but not limited to those manufactured by Microinnova (Allerheiligen bei Wildon, Austria) and/or a staggered herringbone micromixer (SHM) (Zhigaltsev, I.V. et al., Bottom-up design and synthesis of limit size lipid nanoparticle systems with aqueous and triglyceride cores using millisecond microfluidic mixing have been published (Langmuir. 2012. 28:3633-40; Beliveau, N. M. et al., Microfluidic synthesis of highly potent limit-size lipid nanoparticles for in vivo delivery of siRNA. Molecular Therapy-Nucleic Acids. 2012. 1:e37; Chen, D. et al., Rapid discovery of potent siRNA-containing lipid nanoparticles enabled by controlled microfluidic formulation. J Am Chem Soc. 2012. 134(16):6948-51, the contents of each of which are herein incorporated by reference in their entirety). In some embodiments, methods of LNP generation comprising SHM, further comprise the mixing of at least two input streams wherein mixing occurs by microstructure-induced chaotic advection (MICA). According to this method, fluid streams flow through channels present in a herringbone pattern causing rotational flow and folding the fluids around each other. This method may also comprise a surface for fluid mixing wherein the surface changes orientations during fluid cycling. Methods of generating LNPs using SHM include those disclosed in U.S. Application Publication Nos. 2004/0262223 and 2012/0276209, the contents of each of which are herein incorporated by reference in their entirety.

[0513] In some embodiments, the RNA (e.g., mRNA) vaccine of the present disclosure may be formulated in lipid nanoparticles created using a micromixer such as, but not limited to, a Slit Interdigital Microstructured Mixer (SIMM-V2) or a Standard Slit Interdigital Micro Mixer (SSIMM) or Caterpillar (CPMM) or Impinging-jet (IJMM) from the Institut für Mikrotechnik Mainz GmbH, Mainz Germany).

[0514] In some embodiments, the RNA (e.g., mRNA) vaccines of the present disclosure may be formulated in lipid nanoparticles created using microfluidic technology (see, e.g., Whitesides, George M. The Origins and the Future of Microfluidics. Nature, 2006 442: 368-373; and Abraham et al. Chaotic Mixer for Microchannels. Science, 2002 295: 647-651; each of which is herein incorporated by reference in its entirety). As a non-limiting example, controlled microfluidic formulation includes a passive method for mixing streams of steady pressure-driven flows in micro channels at a low Reynolds number (see, e.g., Abraham et al. Chaotic Mixer for Microchannels. Science, 2002 295: 647-651, the contents of which are herein incorporated by reference in their entirety).

[0515] In some embodiments, the RNA (e.g., mRNA) vaccines of the present disclosure may be formulated in lipid nanoparticles created using a micromixer chip such as, but not limited to, those from Harvard Apparatus (Holliston, Mass.) or Dolomite Microfluidics (Royston, UK). A micromixer chip can be used for rapid mixing of two or more fluid streams with a split and recombine mechanism.

[0516] In some embodiments, the RNA (e.g., mRNA) vaccines of the disclosure may be formulated for delivery using the drug encapsulating microspheres described in International Patent Publication No. WO2013063468 or U.S. Pat. No. 8,440,614, the contents of each of which are herein incorporated by reference in their entirety. The microspheres may comprise a compound of the formula (I), (II), (III), (IV), (V) or (VI) as described in International Patent Publication No. WO2013063468, the contents of which are herein incorporated by reference in their entirety. In some embodiments, the amino acid, peptide, polypeptide, lipids (APPL) are useful in delivering the RNA (e.g., mRNA) vaccines of the disclosure to cells (see International Patent Publication No. WO2013063468, the contents of which are herein incorporated by reference in their entirety).

[0517] In some embodiments, the RNA (e.g., mRNA) vaccines of the disclosure may be formulated in lipid nanoparticles having a diameter from about 10 to about 100 nm such as, but not limited to, about 10 to about 20 nm, about 10 to about 30 nm, about 10 to about 40 nm, about 10 to about 50 nm, about 10 to about 60 nm, about 10 to about 70 nm, about 10 to about 80 nm, about 10 to about 90 nm, about 20 to about 30 nm, about 20 to about 40 nm, about 20 to about 50 nm, about 20 to about 60 nm, about 20 to about 70 nm, about 20 to about 80 nm, about 20 to about 90 nm, about 30 to about 40 nm, about 30 to about 50 nm, about 30 to about 60 nm, about 30 to about 70 nm, about 30 to about 80 nm, about 30 to about 90 nm, about 40 to about 50 nm, about 40 to about 60 nm, about 40 to about 70 nm, about 40 to about 80 nm, about 40 to about 90 nm, about 50 to about 60 nm, about 50 to about 70 nm, about 50 to about 80 nm, about 50 to about 90 nm, about 50 to about 100 nm, about 60 to about 70 nm, about 60 to about 80 nm, about 60 to about 90 nm, about 60 to about 100 nm, about 70 to about 80 nm, about 70 to about 90 nm, about 70 to about 100 nm, about 80 to about 90 nm, about 80 to about 100 nm and/or about 90 to about 100 nm.

[0518] In some embodiments, the lipid nanoparticles may have a diameter from about 10 to 500 nm.

[0519] In some embodiments, the lipid nanoparticle may have a diameter greater than 100 nm, greater than 150 nm, greater than 200 nm, greater than 250 nm, greater than 300

nm, greater than 350 nm, greater than 400 nm, greater than 450 nm, greater than 500 nm, greater than 550 nm, greater than 600 nm, greater than 650 nm, greater than 700 nm, greater than 750 nm, greater than 800 nm, greater than 850 nm, greater than 900 nm, greater than 950 nm or greater than 1000 nm.

[0520] In some embodiments, the lipid nanoparticle may be a limit size lipid nanoparticle described in International Patent Publication No. WO2013059922, the contents of which are herein incorporated by reference in their entirety. The limit size lipid nanoparticle may comprise a lipid bilayer surrounding an aqueous core or a hydrophobic core; where the lipid bilayer may comprise a phospholipid such as, but not limited to, diacylphosphatidylcholine, a diacylphosphatidylethanolamine, a ceramide, a sphingomyelin, a dihydrosphingomyelin, a cephalin, a cerebroside, a C8-C20 fatty acid diacylphosphatidylcholine, and 1-palmitoyl-2-oleoyl phosphatidylcholine (POPC). In some embodiments, the limit size lipid nanoparticle may comprise a polyethylene glycol-lipid such as, but not limited to, DLPE-PEG, DMPE-PEG, DPPC-PEG and DSPE-PEG.

[0521] In some embodiments, the RNA (e.g., mRNA) vaccines may be delivered, localized and/or concentrated in a specific location using the delivery methods described in International Patent Publication No. WO2013063530, the contents of which are herein incorporated by reference in their entirety. As a non-limiting example, a subject may be administered an empty polymeric particle prior to, simultaneously with or after delivering the RNA (e.g., mRNA) vaccines to the subject. The empty polymeric particle undergoes a change in volume once in contact with the subject and becomes lodged, embedded, immobilized or entrapped at a specific location in the subject.

[0522] In some embodiments, the RNA (e.g., mRNA) vaccines may be formulated in an active substance release system (see, e.g., U.S. Patent Publication No. US20130102545, the contents of which are herein incorporated by reference in their entirety). The active substance release system may comprise 1) at least one nanoparticle bonded to an oligonucleotide inhibitor strand which is hybridized with a catalytically active nucleic acid and 2) a compound bonded to at least one substrate molecule bonded to a therapeutically active substance (e.g., polynucleotides described herein), where the therapeutically active substance is released by the cleavage of the substrate molecule by the catalytically active nucleic acid.

[0523] In some embodiments, the RNA (e.g., mRNA) vaccines may be formulated in a nanoparticle comprising an inner core comprising a non-cellular material and an outer surface comprising a cellular membrane. The cellular membrane may be derived from a cell or a membrane derived from a virus. As a non-limiting example, the nanoparticle may be made by the methods described in International Patent Publication No. WO2013052167, the contents of which are herein incorporated by reference in their entirety. As another non-limiting example, the nanoparticle described in International Patent Publication No. WO2013052167, the contents of which are herein incorporated by reference in their entirety, may be used to deliver the RNA (e.g., mRNA) vaccines described herein.

[0524] In some embodiments, the RNA (e.g., mRNA) vaccines may be formulated in porous nanoparticle-supported lipid bilayers (protocells). Protocells are described in

International Patent Publication No. WO2013056132, the contents of which are herein incorporated by reference in their entirety.

[0525] In some embodiments, the RNA (e.g., mRNA) vaccines described herein may be formulated in polymeric nanoparticles as described in or made by the methods described in U.S. Pat. Nos. 8,420,123 and 8,518,963 and European Patent No. EP2073848B1, the contents of each of which are herein incorporated by reference in their entirety. As a non-limiting example, the polymeric nanoparticle may have a high glass transition temperature such as the nanoparticles described in or nanoparticles made by the methods described in U.S. Pat. No. 8,518,963, the contents of which are herein incorporated by reference in their entirety. As another non-limiting example, the polymer nanoparticle for oral and parenteral formulations may be made by the methods described in European Patent No. EP2073848B1, the contents of which are herein incorporated by reference in their entirety.

[0526] In some embodiments, the RNA (e.g., mRNA) vaccines described herein may be formulated in nanoparticles used in imaging. The nanoparticles may be liposome nanoparticles such as those described in U.S. Patent Publication No. US20130129636, herein incorporated by reference in its entirety. As a non-limiting example, the liposome may comprise gadolinium(III)-2-{4,7-bis-carboxymethyl-10-[(N,N-distearylamidomethyl-N'-amido-methyl]-1,4,7,10-tetra-azacyclododec-1-yl}-acetic acid and a neutral, fully saturated phospholipid component (see, e.g., U.S. Patent Publication No. US20130129636, the contents of which are herein incorporated by reference in their entirety).

[0527] In some embodiments, the nanoparticles which may be used in the present disclosure are formed by the methods described in U.S. Patent Application No. US20130130348, the contents of which are herein incorporated by reference in their entirety.

[0528] The nanoparticles of the present disclosure may further include nutrients such as, but not limited to, those which deficiencies can lead to health hazards from anemia to neural tube defects (see, e.g., the nanoparticles described in International Patent Publication No. WO2013072929, the contents of which are herein incorporated by reference in their entirety). As a non-limiting example, the nutrient may be iron in the form of ferrous, ferric salts or elemental iron, iodine, folic acid, vitamins or micronutrients.

[0529] In some embodiments, the RNA (e.g., mRNA) vaccines of the present disclosure may be formulated in a swellable nanoparticle. The swellable nanoparticle may be, but is not limited to, those described in U.S. Pat. No. 8,440,231, the contents of which are herein incorporated by reference in their entirety. As a non-limiting embodiment, the swellable nanoparticle may be used for delivery of the RNA (e.g., mRNA) vaccines of the present disclosure to the pulmonary system (see, e.g., U.S. Pat. No. 8,440,231, the contents of which are herein incorporated by reference in their entirety).

[0530] The RNA (e.g., mRNA) vaccines of the present disclosure may be formulated in polyanhydride nanoparticles such as, but not limited to, those described in U.S. Pat. No. 8,449,916, the contents of which are herein incorporated by reference in their entirety.

[0531] The nanoparticles and microparticles of the present disclosure may be geometrically engineered to modulate macrophage and/or the immune response. In some embodi-

ments, the geometrically engineered particles may have varied shapes, sizes and/or surface charges in order to incorporate the polynucleotides of the present disclosure for targeted delivery such as, but not limited to, pulmonary delivery (see, e.g., International Publication No. WO2013082111, the contents of which are herein incorporated by reference in their entirety). Other physical features the geometrically engineering particles may have include, but are not limited to, fenestrations, angled arms, asymmetry and surface roughness, charge which can alter the interactions with cells and tissues. As a non-limiting example, nanoparticles of the present disclosure may be made by the methods described in International Publication No. WO2013082111, the contents of which are herein incorporated by reference in their entirety.

[0532] In some embodiments, the nanoparticles of the present disclosure may be water soluble nanoparticles such as, but not limited to, those described in International Publication No. WO2013090601, the contents of which are herein incorporated by reference in their entirety. The nanoparticles may be inorganic nanoparticles which have a compact and zwitterionic ligand in order to exhibit good water solubility. The nanoparticles may also have small hydrodynamic diameters (HD), stability with respect to time, pH, and salinity and a low level of non-specific protein binding.

[0533] In some embodiments the nanoparticles of the present disclosure may be developed by the methods described in U.S. Patent Publication No. US20130172406, the contents of which are herein incorporated by reference in their entirety.

[0534] In some embodiments, the nanoparticles of the present disclosure are stealth nanoparticles or target-specific stealth nanoparticles such as, but not limited to, those described in U.S. Patent Publication No. US20130172406, the contents of which are herein incorporated by reference in their entirety. The nanoparticles of the present disclosure may be made by the methods described in U.S. Patent Publication No. US20130172406, the contents of which are herein incorporated by reference in their entirety.

[0535] In some embodiments, the stealth or target-specific stealth nanoparticles may comprise a polymeric matrix. The polymeric matrix may comprise two or more polymers such as, but not limited to, polyethylenes, polycarbonates, polyanhydrides, polyhydroxyacids, polypropylfumerates, polycaprolactones, polyamides, polyacetals, polyethers, polyesters, poly(orthoesters), polycyanoacrylates, polyvinyl alcohols, polyurethanes, polyphosphazenes, polyacrylates, polymethacrylates, polycyanoacrylates, polyureas, polystyrenes, polyamines, polyesters, polyanhydrides, polyethers, polyurethanes, polymethacrylates, polyacrylates, polycyanoacrylates or combinations thereof.

[0536] In some embodiments, the nanoparticle may be a nanoparticle-nucleic acid hybrid structure having a high density nucleic acid layer. As a non-limiting example, the nanoparticle-nucleic acid hybrid structure may be made by the methods described in U.S. Patent Publication No. US20130171646, the contents of which are herein incorporated by reference in their entirety. The nanoparticle may comprise a nucleic acid such as, but not limited to, polynucleotides described herein and/or known in the art.

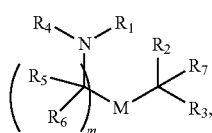
[0537] At least one of the nanoparticles of the present disclosure may be embedded in the core nanostructure

or coated with a low density porous 3-D structure or coating which is capable of carrying or associating with at least one payload within or on the surface of the nanostructure. Non-limiting examples of the nanostructures comprising at least one nanoparticle are described in International Patent Publication No. WO2013123523, the contents of which are herein incorporated by reference in their entirety.

[0538] In some embodiments the RNA (e.g., mRNA) vaccine may be associated with a cationic or polycationic compounds, including protamine, nucleoline, spermine or spermidine, or other cationic peptides or proteins, such as poly-L-lysine (PLL), polyarginine, basic polypeptides, cell penetrating peptides (CPPs), including HIV-binding peptides, HIV-1 Tat (HIV), Tat-derived peptides, Penetratin, VP²² derived or analog peptides, Pestivirus Ems, HSV, VP²² (Herpes simplex), MAP, KALA or protein transduction domains (PTDs), PpT620, prolin-rich peptides, arginine-rich peptides, lysine-rich peptides, MPG-peptide(s), Pep-1, L-oligomers, Calcitonin peptide(s), Antennapedia-derived peptides (particularly from *Drosophila antennapedia*), pAntp, plsl, FGF, Lactoferrin, Transportan, Buforin-2, Bac715-24, SynB, SynB(1), pVEC, hCT-derived peptides, SAP, histones, cationic polysaccharides, for example chitosan, polybrene, cationic polymers, e.g. polyethyleneimine (PEI), cationic lipids, e.g. DOTMA: [1-(2,3-sioleyloxy) propyl]-[N,N,N-trimethylammonium chloride, DMRIE, di-C14-amidine, DOTIM, SAINT, DC-Chol, BGTC, CTAP, DOPC, DODAP, DOPE: Dioleoyl phosphatidylethanolamine, DOSPA, DODAB, DOIC, DMEPC, DOGS: Dioctadecylamidoglycylspermin, DIMRI: Dimyristooxypropyl dimethyl hydroxyethyl ammonium bromide, DOTAP: dioleoyloxy-3-(trimethylammonio)propane, DC-6-14: O,O-ditetradecanoyl-N-.alpha.-trimethylammonioacetyl)diethanolamine chloride, CLIP 1: rac-[2,3-dioctadecyloxypropyl] (2-hydroxyethyl)-[dimethylammonium chloride, CLIP6: rac-[2(2,3-dihexadecyloxypropyloxymethoxy)ethyl]-trimethylammonium, CLIP9: rac-[2(2,3-dihexadecyloxypropyloxysuccinyloxy)ethyl]-trimethylammonium, oligofectamine, or cationic or polycationic polymers, e.g. modified polyaminoacids, such as beta-aminoacid-polymers or reversed polyamides, etc., modified polyethylenes, such as PVP (poly(N-ethyl-4-vinylpyridinium bromide)), etc., modified acrylates, such as pDMAEMA (poly(dimethylaminoethyl methylacrylate)), etc., modified amidoamines such as pAMAM (poly(amidoamine)), etc., modified polybetaminoester (PBAE), such as diamine end modified 1,4 butanediol diacrylate-co-5-amino-1-pentanol polymers, etc., dendrimers, such as polypropylamine dendrimers or pAMAM based dendrimers, etc., polyimine(s), such as PEI: poly(ethyleneimine), poly(propyleneimine), etc., polyallylamine, sugar backbone based polymers, such as cyclodextrin based polymers, dextran based polymers, chitosan, etc., silan backbone based polymers, such as PMOXA-PDMS copolymers, etc., blockpolymers consisting of a combination of one or more cationic blocks (e.g. selected from a cationic polymer as mentioned above) and of one or more hydrophilic or hydrophobic blocks (e.g. polyethyleneglycole), etc.

[0539] In other embodiments the RNA (e.g., mRNA) vaccine is not associated with a cationic or polycationic compounds.

[0540] In some embodiments, a nanoparticle comprises compounds of Formula (I):



(I)

[0541] or a salt or isomer thereof, wherein:

[0542] R_1 is selected from the group consisting of C_{5-30} alkyl, C_{5-20} alkenyl, $-R^*YR''$, $-YR''$, and $-R''M'R'$;

[0543] R_2 and R_3 are independently selected from the group consisting of H, C_{1-14} alkyl, C_{2-14} alkenyl, $-R^*YR''$, $-YR''$, and $-R^*OR''$, or R_2 and R_3 , together with the atom to which they are attached, form a heterocycle or carbocycle;

[0544] R_4 is selected from the group consisting of a C_{3-6} carbocycle, $-(CH_2)_nQ$, $-(CH_2)_nCHQR$,

[0545] $-CHQR$, $-CQ(R)_2$, and unsubstituted C_{1-6} alkyl, where Q is selected from a carbocycle, heterocycle, $-OR$, $-O(CH_2)_nN(R)_2$, $-C(O)OR$, $-OC(O)R$, $-CX_3$, $-CX_2H$, $-CXH_2$, $-CN$, $-N(R)_2$, $-C(O)N(R)_2$, $-N(R)C(O)R$, $-N(R)S(O)_2R$, $-N(R)C(O)N(R)_2$, $-(R)C(S)N(R)_2$, $-N(R)R_8$, $-O(CH_2)_nOR$, $-N(R)C(=NR_9)N(R)_2$, $-(R)C(=CHR_9)N(R)_2$, $-OC(O)N(R)_2$, $-N(R)C(O)OR$, $-N(OR)C(O)R$, $-N(OR)S(O)_2R$, $-N(OR)C(O)OR$, $-N(OR)C(O)N(R)_2$, $-(OR)C(S)N(R)_2$, $-N(OR)C(=NR_9)N(R)_2$, $-N(OR)C(=CHR_9)N(R)_2$, $-C(=NR_9)N(R)_2$, $-C(=NR_9)R$, $-C(O)N(R)OR$, and $-C(R)N(R)_2C(O)OR$, and each n is independently selected from 1, 2, 3, 4, and 5;

[0546] each R_5 is independently selected from the group consisting of C_{1-3} alkyl, C_{2-3} alkenyl, and H;

[0547] each R_6 is independently selected from the group consisting of C_{1-3} alkyl, C_{2-3} alkenyl, and H;

[0548] M and M' are independently selected from $-C(O)O-$, $-OC(O)-$, $-C(O)N(R')-$, $-N(R')C(O)-$, $-C(O)-$, $-C(S)-$, $-C(S)S-$, $-SC(S)-$, $-CH(OH)-$, $-P(O)(OR')O-$, $-S(O)_2-$, $-S-S-$, an aryl group, and a heteroaryl group;

[0549] R_7 is selected from the group consisting of C_{1-3} alkyl, C_{2-3} alkenyl, and H;

[0550] R_8 is selected from the group consisting of C_{3-6} carbocycle and heterocycle;

[0551] R_9 is selected from the group consisting of H, CN, NO_2 , C_{1-6} alkyl, $-OR$, $-S(O)_2R$, $-S(O)_2N(R)_2$, C_{2-6} alkenyl, C_{3-6} carbocycle and heterocycle;

[0552] each R is independently selected from the group consisting of C_{1-3} alkyl, C_{2-3} alkenyl, and H;

[0553] each R' is independently selected from the group consisting of C_{1-18} alkyl, C_{2-18} alkenyl, $-R^*YR''$, $-YR''$, and H;

[0554] each R'' is independently selected from the group consisting of C_{3-14} alkyl and C_{3-14} alkenyl;

[0555] each R^* is independently selected from the group consisting of C_{1-12} alkyl and C_{2-12} alkenyl;

[0556] each Y is independently a C_{3-6} carbocycle;

[0557] each X is independently selected from the group consisting of F, Cl, Br, and I; and

[0558] m is selected from 5, 6, 7, 8, 9, 10, 11, 12, and 13.

[0559] In some embodiments, a subset of compounds of Formula (I) includes those in which when R_4 is $-(CH_2)_nQ$,

$-(CH_2)_nCHQR$, $-CHQR$, or $-CQ(R)_2$, then (i) Q is not $-N(R)_2$ when n is 1, 2, 3, 4 or 5, or (ii) Q is not 5, 6, or 7-membered heterocycloalkyl when n is 1 or 2.

[0560] In some embodiments, another subset of compounds of Formula (I) includes those in which

[0561] R_1 is selected from the group consisting of C_{5-30} alkyl, C_{5-20} alkenyl, $-R^*YR''$, $-YR''$, and $-R''M'R'$;

[0562] R_2 and R_3 are independently selected from the group consisting of H, C_{1-14} alkyl, C_{2-14} alkenyl, $-R^*YR''$, $-YR''$, and $-R^*OR''$, or R_2 and R_3 , together with the atom to which they are attached, form a heterocycle or carbocycle;

[0563] R_4 is selected from the group consisting of a C_{3-6} carbocycle, $-(CH_2)_nQ$, $-(CH_2)_nCHQR$,

[0564] $-CHQR$, $-CQ(R)_2$, and unsubstituted C_{1-6} alkyl, where Q is selected from a C_{3-6} carbocycle, a 5- to 14-membered heteroaryl having one or more heteroatoms selected from N, O, and S, $-OR$,

[0565] $-O(CH_2)_nN(R)_2$, $-C(O)OR$, $-OC(O)R$, $-CX_3$, $-CX_2H$, $-CXH_2$, $-CN$, $-C(O)N(R)_2$, $-N(R)C(O)R$, $-N(R)S(O)_2R$, $-N(R)C(O)N(R)_2$, $-N(R)C(S)N(R)_2$, $-CRN(R)_2C(O)OR$, $-N(R)R_8$, $-O(CH_2)_nOR$, $-N(R)C(=NR_9)N(R)_2$, $-N(R)C(=CHR_9)N(R)_2$, $-OC(O)N(R)_2$, $-N(R)C(O)OR$, $-N(OR)C(O)R$, $-N(OR)C(O)N(R)_2$, $-N(OR)C(S)N(R)_2$, $-N(OR)C(=NR_9)N(R)_2$, $-N(OR)C(=CHR_9)N(R)_2$, $-C(=NR_9)N(R)_2$, $-C(=NR_9)R$, $-C(O)N(R)OR$, and a 5- to 14-membered heterocycloalkyl having one or more heteroatoms selected from N, O, and S which is substituted with one or more substituents selected from oxo ($=O$), OH, amino, mono- or di-alkylamino, and C_{1-3} alkyl, and each n is independently selected from 1, 2, 3, 4, and 5;

[0566] each R_6 is independently selected from the group consisting of C_{1-3} alkyl, C_{2-3} alkenyl, and H;

[0567] each R_7 is independently selected from the group consisting of C_{1-3} alkyl, C_{2-3} alkenyl, and H;

[0568] M and M' are independently selected from $-C(O)O-$, $-OC(O)-$, $-C(O)N(R')-$, $-N(R')C(O)-$, $-C(O)-$, $-C(S)-$, $-C(S)S-$, $-SC(S)-$, $-CH(OH)-$, $-P(O)(OR')O-$, $-S(O)_2-$, $-S-S-$, an aryl group, and a heteroaryl group;

[0569] R_7 is selected from the group consisting of C_{1-3} alkyl, C_{2-3} alkenyl, and H;

[0570] R_8 is selected from the group consisting of C_{3-6} carbocycle and heterocycle;

[0571] R_9 is selected from the group consisting of H, CN, NO_2 , C_{1-6} alkyl, $-OR$, $-S(O)_2R$, $-S(O)_2N(R)_2$, C_{2-6} alkenyl, C_{3-6} carbocycle and heterocycle;

[0572] each R is independently selected from the group consisting of C_{1-3} alkyl, C_{2-3} alkenyl, and H;

[0573] each R' is independently selected from the group consisting of C_{1-18} alkyl, C_{2-18} alkenyl, $-R^*YR''$, $-YR''$, and H;

[0574] each R'' is independently selected from the group consisting of C_{3-14} alkyl and C_{3-14} alkenyl;

[0575] each R^* is independently selected from the group consisting of C_{1-12} alkyl and C_{2-12} alkenyl;

[0576] each Y is independently a C_{3-6} carbocycle;

[0577] each X is independently selected from the group consisting of F, Cl, Br, and I; and

[0578] m is selected from 5, 6, 7, 8, 9, 10, 11, 12, and 13, or salts or isomers thereof.

[0579] In some embodiments, another subset of compounds of Formula (I) includes those in which

[0580] R_1 is selected from the group consisting of C_{5-30} alkyl, C_{5-20} alkenyl, $-R^*YR''$, $-YR''$, and $-R''M'R'$;

[0581] R_2 and R_3 are independently selected from the group consisting of H, C_{1-14} alkyl, C_{2-14} alkenyl, $-R^*YR''$, $-YR''$, and $-R^*OR''$, or R_2 and R_3 , together with the atom to which they are attached, form a heterocycle or carbocycle;

[0582] R_4 is selected from the group consisting of a C_{3-6} carbocycle, $-(CH_2)_nQ$, $-(CH_2)_nCHQR$,

[0583] $-CHQR$, $-CQ(R)_2$, and unsubstituted C_{1-6} alkyl, where Q is selected from a C_{3-6} carbocycle, a 5- to 14-membered heterocycle having one or more heteroatoms selected from N, O, and S, $-OR$,

[0584] $-O(CH_2)_nN(R)_2$, $-C(O)OR$, $-OC(O)R$, $-CX_3$, $-CX_2H$, $-CXH_2$, $-CN$, $-C(O)N(R)_2$, $-N(R)C(O)R$, $-N(R)S(O)_2R$, $-N(R)C(O)N(R)_2$, $-N(R)C(S)N(R)_2$, $-CRN(R)_2C(O)OR$, $-N(R)R_8$,

[0585] $-O(CH_2)_nOR$, $-N(R)C(=NR_9)N(R)_2$, $-N(R)C(=CHR_9)N(R)_2$, $-OC(O)N(R)_2$, $-N(R)C(O)OR$, $-N(OR)C(O)R$, $-N(OR)S(O)_2R$, $-N(OR)C(O)OR$, $-N(OR)C(O)N(R)_2$, $-N(OR)C(S)N(R)_2$, $-N(OR)C(=NR_9)N(R)_2$, $-N(OR)C(=CHR_9)N(R)_2$, $-C(=NR_9)R$, $-C(O)N(R)OR$, and $-C(=NR_9)N(R)_2$, and each n is independently selected from 1, 2, 3, 4, and 5; and when Q is a 5- to 14-membered heterocycle and (i) R_4 is $-(CH_2)_nQ$ in which n is 1 or 2, or (ii) R_4 is $-(CH_2)_nCHQR$ in which n is 1, or (iii) R_4 is $-CHQR$, and $-CQ(R)_2$, then Q is either a 5- to 14-membered heteroaryl or 8- to 14-membered heterocycloalkyl;

[0586] each R_5 is independently selected from the group consisting of C_{1-3} alkyl, C_{2-3} alkenyl, and H;

[0587] each R_6 is independently selected from the group consisting of C_{1-3} alkyl, C_{2-3} alkenyl, and H;

[0588] M and M' are independently selected from $-C(O)O-$, $-OC(O)-$, $-C(O)N(R')$, $-N(R')C(O)-$, $-C(O)-$, $-C(S)-$, $-C(S)S-$, $-SC(S)-$, $-CH(OH)-$, $-P(O)(OR')O-$, $-S(O)_2-$, $-S-S-$, an aryl group, and a heteroaryl group;

[0589] R_7 is selected from the group consisting of C_{1-3} alkyl, C_{2-3} alkenyl, and H;

[0590] R_8 is selected from the group consisting of C_{3-6} carbocycle and heterocycle;

[0591] R_9 is selected from the group consisting of H, CN, NO_2 , C_{1-6} alkyl, $-OR$, $-S(O)_2R$, $-S(O)_2N(R)_2$, C_{2-6} alkenyl, C_{3-6} carbocycle and heterocycle;

[0592] each R is independently selected from the group consisting of C_{1-3} alkyl, C_{2-3} alkenyl, and H;

[0593] each R' is independently selected from the group consisting of C_{1-18} alkyl, C_{2-18} alkenyl, $-R^*YR''$, $-YR''$, and H;

[0594] each R'' is independently selected from the group consisting of C_{3-14} alkyl and C_{3-14} alkenyl;

[0595] each R^* is independently selected from the group consisting of C_{1-12} alkyl and C_{2-12} alkenyl;

[0596] each Y is independently a C_{3-6} carbocycle;

[0597] each X is independently selected from the group consisting of F, Cl, Br, and I; and

[0598] m is selected from 5, 6, 7, 8, 9, 10, 11, 12, and 13,

[0599] or salts or isomers thereof.

[0600] In some embodiments, another subset of compounds of Formula (I) includes those in which

[0601] R_1 is selected from the group consisting of C_{5-30} alkyl, C_{5-20} alkenyl, $-R^*YR''$, $-YR''$, and $-R''M'R'$;

[0602] R_2 and R_3 are independently selected from the group consisting of H, C_{1-14} alkyl, C_{2-14} alkenyl, $-R^*YR''$,

$-YR''$, and $-R^*OR''$, or R_2 and R_3 , together with the atom to which they are attached, form a heterocycle or carbocycle;

[0603] R_4 is selected from the group consisting of a C_{3-6} carbocycle, $-(CH_2)_nQ$, $-(CH_2)_nCHQR$,

[0604] $-CHQR$, $-CQ(R)_2$, and unsubstituted C_{1-6} alkyl, where Q is selected from a C_{3-6} carbocycle, a 5- to 14-membered heteroaryl having one or more heteroatoms selected from N, O, and S, $-OR$,

[0605] $-O(CH_2)_nN(R)_2$, $-C(O)OR$, $-OC(O)R$, $-CX_3$, $-CX_2H$, $-CXH_2$, $-CN$, $-C(O)N(R)_2$, $-N(R)C(O)R$, $-N(R)S(O)_2R$, $-N(R)C(O)N(R)_2$, $-N(R)C(S)N(R)_2$, $-CRN(R)_2C(O)OR$, $-N(R)R_8$, $-O(CH_2)_nOR$, $-N(R)C(=NR_9)N(R)_2$, $-N(R)C(=CHR_9)N(R)_2$, $-OC(O)N(R)_2$, $-N(R)C(O)OR$, $-N(OR)C(O)R$, $-N(OR)S(O)_2R$, $-N(OR)C(O)OR$, $-N(OR)C(O)N(R)_2$, $-N(OR)C(S)N(R)_2$, $-N(OR)C(=NR_9)N(R)_2$, $-N(OR)C(=CHR_9)N(R)_2$, $-C(=NR_9)R$, $-C(O)N(R)OR$, and $-C(=NR_9)N(R)_2$, and each n is independently selected from 1, 2, 3, 4, and 5;

[0606] each R_5 is independently selected from the group consisting of C_{1-3} alkyl, C_{2-3} alkenyl, and H;

[0607] each R_6 is independently selected from the group consisting of C_{1-3} alkyl, C_{2-3} alkenyl, and H;

[0608] M and M' are independently selected from $-C(O)O-$, $-OC(O)-$, $-C(O)N(R')$, $-N(R')C(O)-$, $-C(O)-$, $-C(S)-$, $-C(S)S-$, $-SC(S)-$, $-CH(OH)-$, $-P(O)(OR')O-$, $-S(O)_2-$, $-S-S-$, an aryl group, and a heteroaryl group;

[0609] R_7 is selected from the group consisting of C_{1-3} alkyl, C_{2-3} alkenyl, and H;

[0610] R_8 is selected from the group consisting of C_{3-6} carbocycle and heterocycle;

[0611] R_9 is selected from the group consisting of H, CN, NO_2 , C_{1-6} alkyl, $-OR$, $-S(O)_2R$, $-S(O)_2N(R)_2$, C_{2-6} alkenyl, C_{3-6} carbocycle and heterocycle;

[0612] each R is independently selected from the group consisting of C_{1-3} alkyl, C_{2-3} alkenyl, and H;

[0613] each R' is independently selected from the group consisting of C_{1-18} alkyl, C_{2-18} alkenyl, $-R^*YR''$, $-YR''$, and H;

[0614] each R'' is independently selected from the group consisting of C_{3-14} alkyl and C_{3-14} alkenyl;

[0615] each R^* is independently selected from the group consisting of C_{1-12} alkyl and C_{2-12} alkenyl;

[0616] each Y is independently a C_{3-6} carbocycle;

[0617] each X is independently selected from the group consisting of F, Cl, Br, and I; and

[0618] m is selected from 5, 6, 7, 8, 9, 10, 11, 12, and 13,

[0619] or salts or isomers thereof.

[0620] In some embodiments, another subset of compounds of Formula (I) includes those in which

[0621] R_1 is selected from the group consisting of C_{5-30} alkyl, C_{5-20} alkenyl, $-R^*YR''$, $-YR''$, and $-R''M'R'$;

[0622] R_2 and R_3 are independently selected from the group consisting of H, C_{2-14} alkyl, C_{2-14} alkenyl, $-R^*YR''$, $-YR''$, and $-R^*OR''$, or R_2 and R_3 , together with the atom to which they are attached, form a heterocycle or carbocycle;

[0623] R_4 is $-(CH_2)_nQ$ or $-(CH_2)_nCHQR$, where Q is $-N(R)_2$, and n is selected from 3, 4, and 5;

[0624] each R_5 is independently selected from the group consisting of C_{1-3} alkyl, C_{2-3} alkenyl, and H;

[0625] each R_6 is independently selected from the group consisting of C_{1-3} alkyl, C_{2-3} alkenyl, and H;

[0626] M and M' are independently selected from $-C(O)O-$, $-OC(O)-$, $-C(O)N(R')$, $-N(R')C(O)-$,

—C(O)—, —C(S)—, —C(S)S—, —SC(S)—, —CH(OH)—, —P(O)(OR')O—, —S(O)₂—, —S—S—, an aryl group, and a heteroaryl group;

[0627] R₇ is selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

[0628] each R is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

[0629] each R' is independently selected from the group consisting of C₁₋₁₈ alkyl, C₂₋₁₈ alkenyl, —R*YR'', —YR'', and H;

[0630] each R'' is independently selected from the group consisting of C₃₋₁₄ alkyl and C₃₋₁₄ alkenyl;

[0631] each R* is independently selected from the group consisting of C₁₋₁₂ alkyl and C₁₋₁₂ alkenyl;

[0632] each Y is independently a C₃₋₆ carbocycle;

[0633] each X is independently selected from the group consisting of F, Cl, Br, and I; and

[0634] m is selected from 5, 6, 7, 8, 9, 10, 11, 12, and 13,

[0635] or salts or isomers thereof.

[0636] In some embodiments, another subset of compounds of Formula (I) includes those in which

[0637] R₁ is selected from the group consisting of C₅₋₃₀ alkyl, C₅₋₂₀ alkenyl, —R*YR'', —YR'', and —R''MR';

[0638] R₂ and R₃ are independently selected from the group consisting of C₁₋₁₄ alkyl, C₂₋₁₄ alkenyl, —R*YR'', —YR'', and —R*OR'', or R₂ and R₃, together with the atom to which they are attached, form a heterocycle or carbocycle;

[0639] R₄ is selected from the group consisting of —(CH₂)_nQ, —(CH₂)_nCHQR, —CHQR, and 13 CQ(R)₂, where Q is —N(R)₂, and n is selected from 1, 2, 3, 4, and 5;

[0640] each R₅ is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H; each R₆ is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

[0641] M and M' are independently selected from —C(O)O—, —OC(O)—, —C(O)N(R')—, —N(R')C(O)—, —C(O)—, —C(S)—, —C(S)S—, —SC(S)—, —CH(OH)—, —P(O)(OR')O—, —S(O)₂—, —S—S—, an aryl group, and a heteroaryl group;

[0642] R₇ is selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

[0643] each R is independently selected from the group consisting of C₁₋₃ alkyl, C₂₋₃ alkenyl, and H;

[0644] each R' is independently selected from the group consisting of C₁₋₁₈ alkyl, C₂₋₁₈ alkenyl, —R*YR'', —YR'', and H;

[0645] each R'' is independently selected from the group consisting of C₃₋₁₄ alkyl and C₃₋₁₄ alkenyl;

[0646] each R* is independently selected from the group consisting of C₁₋₁₂ alkyl and C₁₋₁₂ alkenyl;

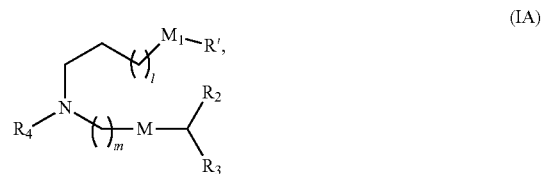
[0647] each Y is independently a C₃₋₆ carbocycle;

[0648] each X is independently selected from the group consisting of F, Cl, Br, and I; and

[0649] m is selected from 5, 6, 7, 8, 9, 10, 11, 12, and 13,

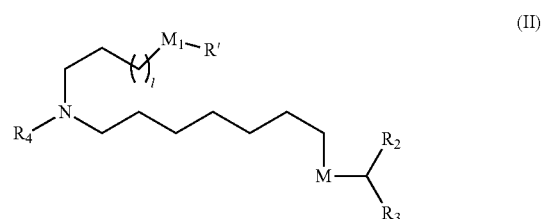
[0650] or salts or isomers thereof.

[0651] In some embodiments, a subset of compounds of Formula (I) includes those of Formula (IA):



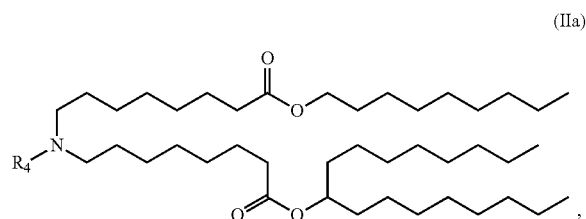
[0652] or a salt or isomer thereof, wherein l is selected from 1, 2, 3, 4, and 5; m is selected from 5, 6, 7, 8, and 9; M₁ is a bond or M'; R₄ is unsubstituted C₁₋₃ alkyl, or —(CH₂)_nQ, in which Q is OH, —NHC(S)N(R)₂, —NHC(O)N(R)₂, —N(R)C(O)R, —N(R)S(O)₂R, —N(R)R₈, —NHC(=NR₉)N(R)₂, —NHC(=CHR₉)N(R)₂, —OC(O)N(R)₂, —N(R)C(O)OR, heteroaryl or heterocycloalkyl; M and M' are independently selected from —C(O)O—, —OC(O)—, —C(O)N(R')—, —P(O)(OR')O—, —S—S—, an aryl group, and a heteroaryl group; and R₂ and R₃ are independently selected from the group consisting of H, C₁₋₁₄ alkyl, and C₂₋₁₄ alkenyl.

[0653] In some embodiments, a subset of compounds of Formula (I) includes those of Formula (II):

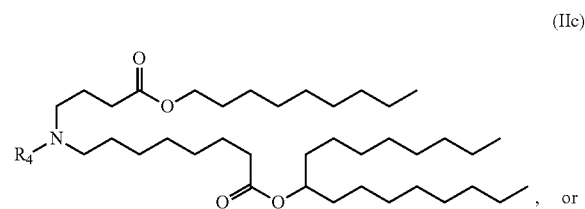
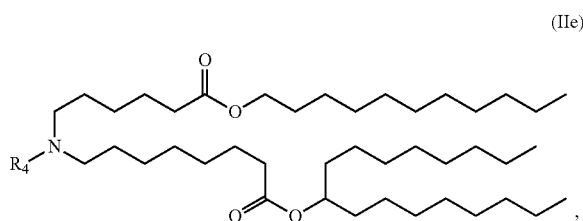
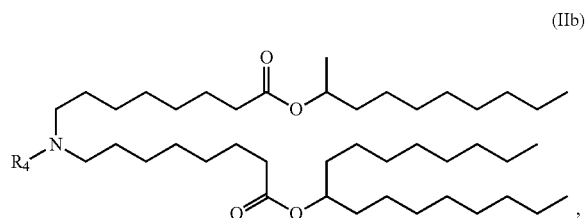
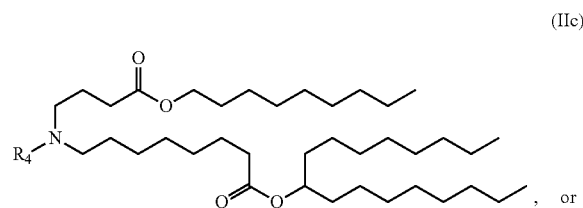
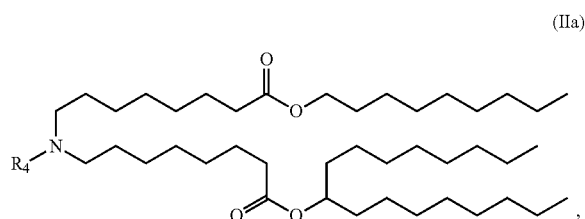
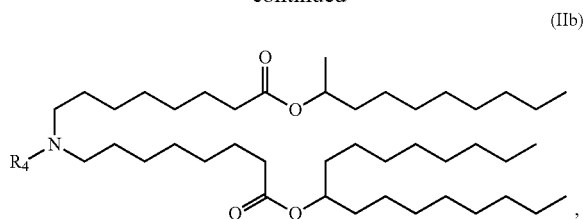


or a salt or isomer thereof, wherein l is selected from 1, 2, 3, 4, and 5; M₁ is a bond or M'; R₄ is unsubstituted C₁₋₃ alkyl, or —(CH₂)_nQ, in which n is 2, 3, or 4, and Q is OH, —NHC(S)N(R)₂, —NHC(O)N(R)₂, —N(R)C(O)R, —N(R)S(O)₂R, —N(R)R₈, —NHC(=NR₉)N(R)₂, —NHC(=CHR₉)N(R)₂, —OC(O)N(R)₂, —N(R)C(O)OR, heteroaryl or heterocycloalkyl; M and M' are independently selected from —C(O)O—, —OC(O)—, —C(O)N(R')—, —P(O)(OR')O—, —S—S—, an aryl group, and a heteroaryl group; and R₂ and R₃ are independently selected from the group consisting of H, C₁₋₁₄ alkyl, and C₂₋₁₄ alkenyl.

[0654] In some embodiments, a subset of compounds of Formula (I) includes those of Formula (IIa), (IIb), (IIc), or (Ile):

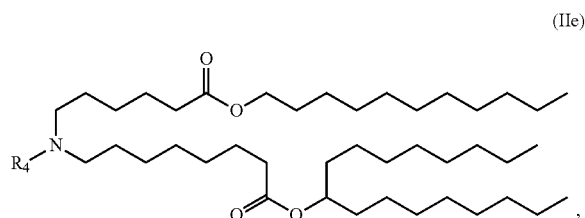


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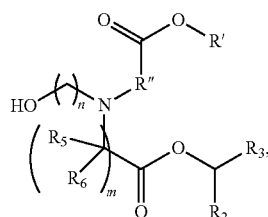
[0655] or a salt or isomer thereof, wherein R_4 is as described herein.

[0656] In some embodiments, a subset of compounds of Formula (I) includes those of Formula (IIa);



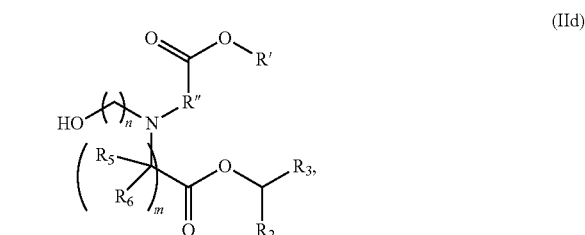
[0659] or a salt or isomer thereof, wherein R_4 is as described herein.

[0660] In some embodiments, a subset of compounds of Formula (I) includes those of Formula (IIa);



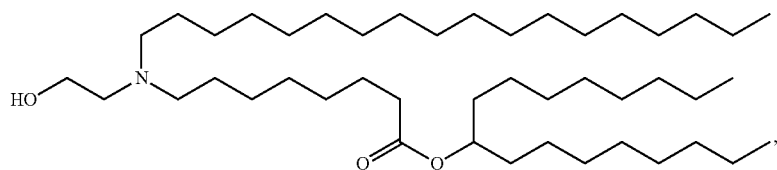
[0657] or a salt or isomer thereof, wherein n is 2, 3, or 4; and m , R' , R'' , and R_2 through R_6 are as described herein. For example, each of R_2 and R_3 may be independently selected from the group consisting of C_{5-14} alkyl and C_{5-14} alkenyl.

[0658] In some embodiments, a subset of compounds of Formula (I) includes those of Formula (IIa), (IIb), (IIc), or (IIe);

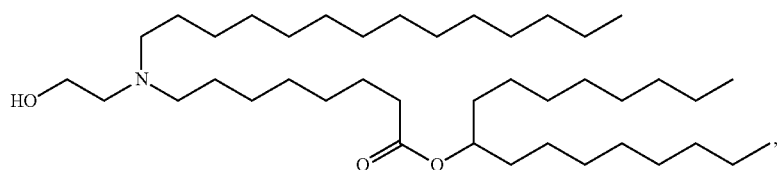


[0661] or a salt or isomer thereof, wherein n is 2, 3, or 4; and m , R' , R'' , and R_2 through R_6 are as described herein. For example, each of R_2 and R_3 may be independently selected from the group consisting of C_{5-14} alkyl and C_{5-14} alkenyl.

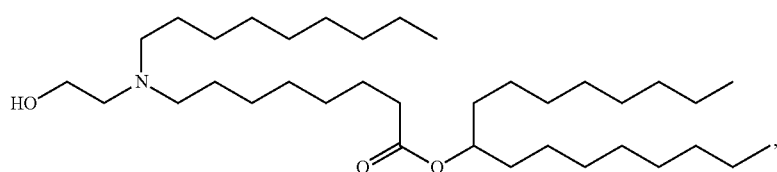
[0662] In some embodiments, the compound of Formula (I) is selected from the group consisting of:



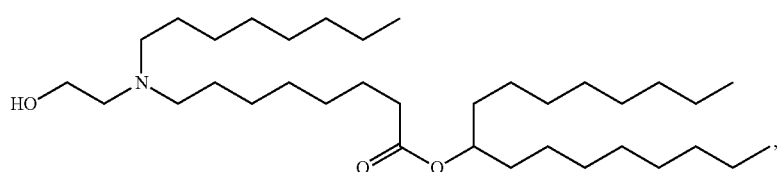
(Compound 1)



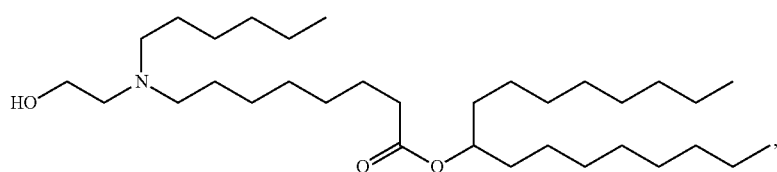
(Compound 2)



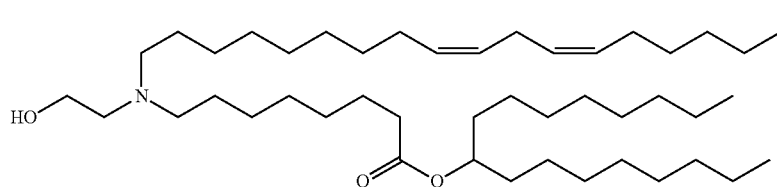
(Compound 3)



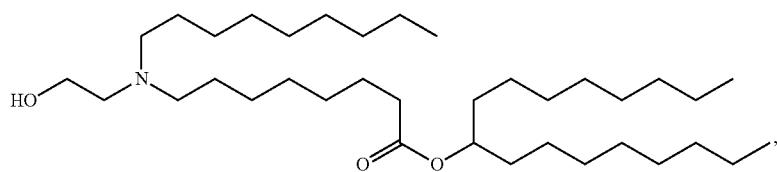
(Compound 4)



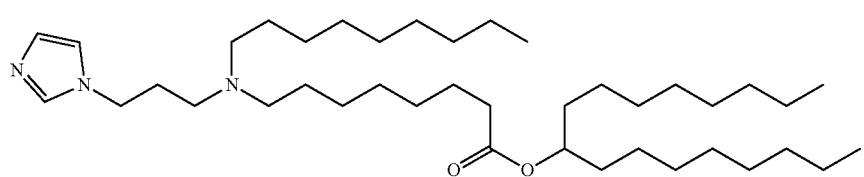
(Compound 5)



(Compound 6)



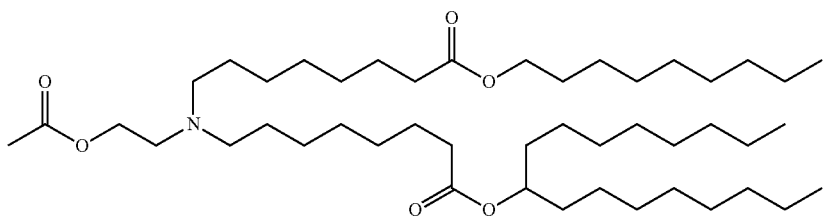
(Compound 7)



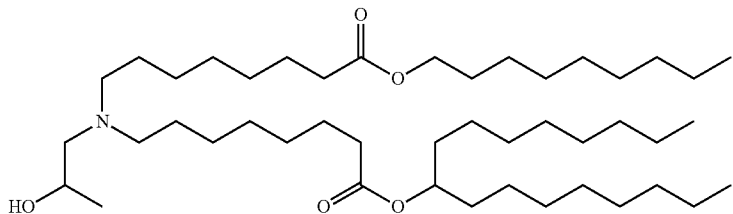
(Compound 8)

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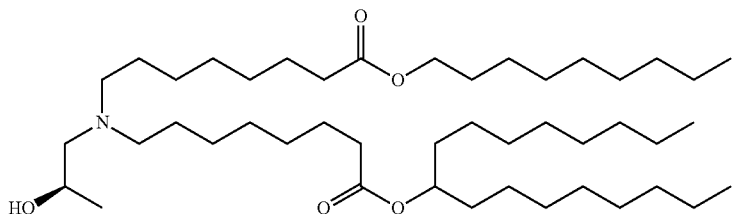
(Compound 9)



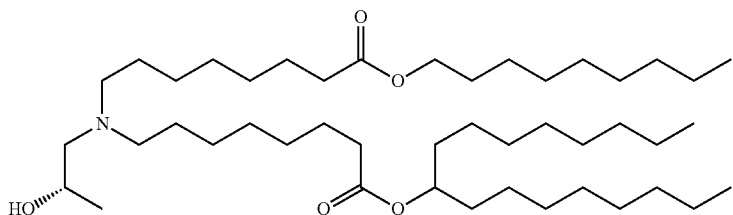
(Compound 10)



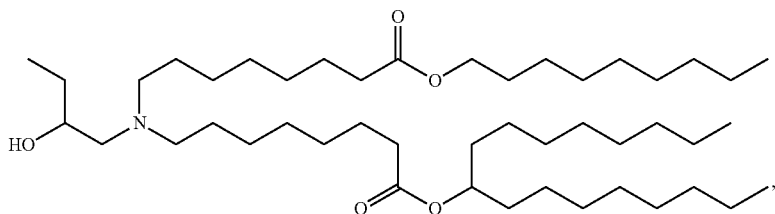
(Compound 11)



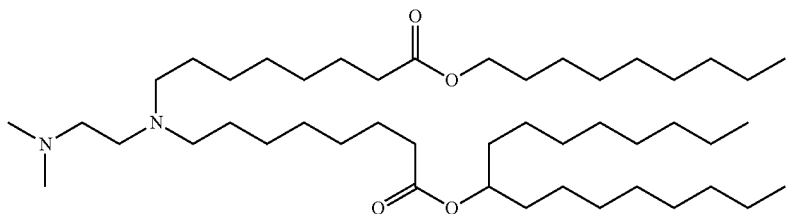
(Compound 12)



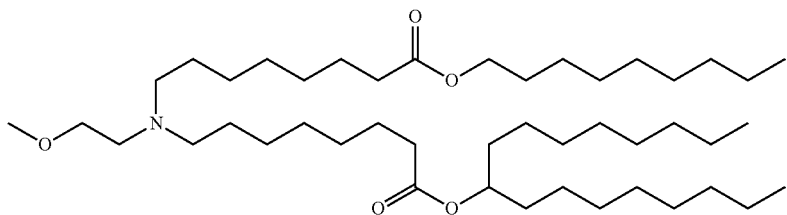
(Compound 13)



(Compound 14)

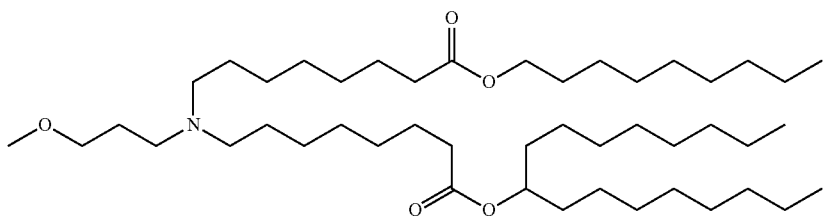


(Compound 15)

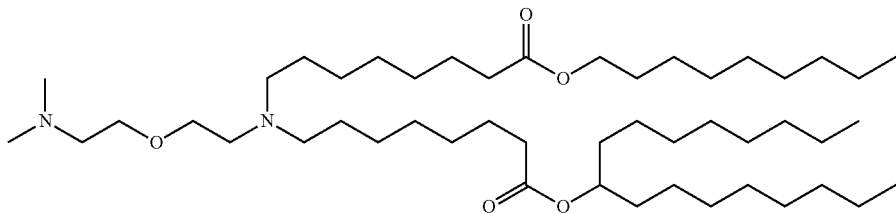


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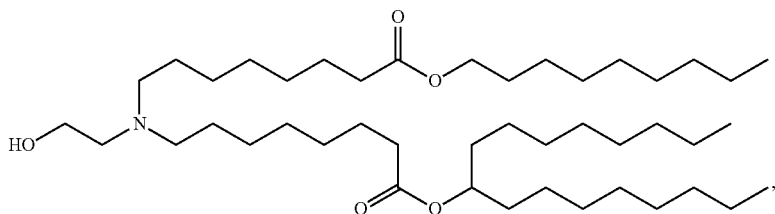
(Compound 16)



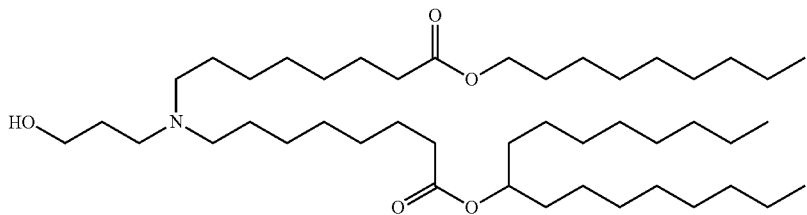
(Compound 17)



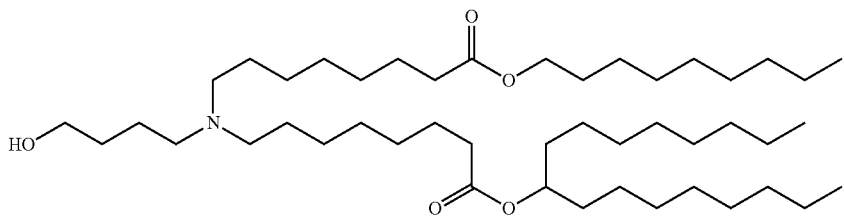
(Compound 18)



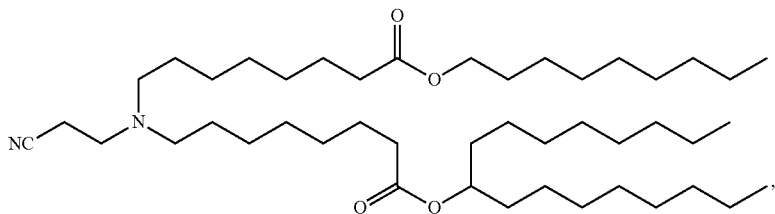
(Compound 19)



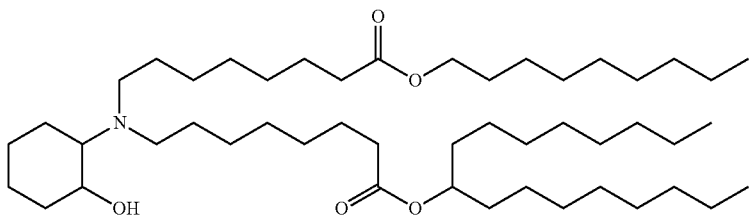
(Compound 20)



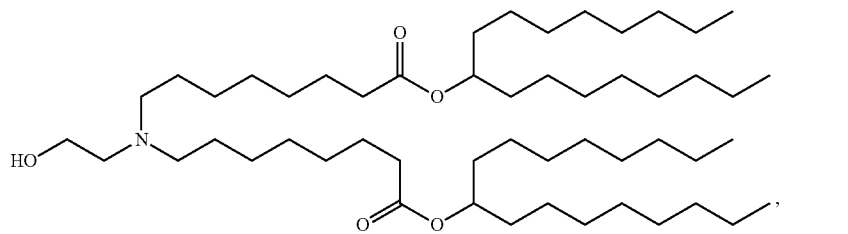
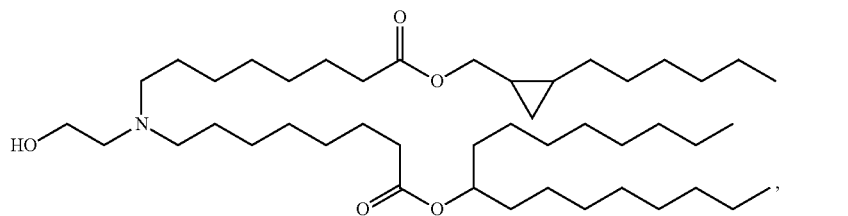
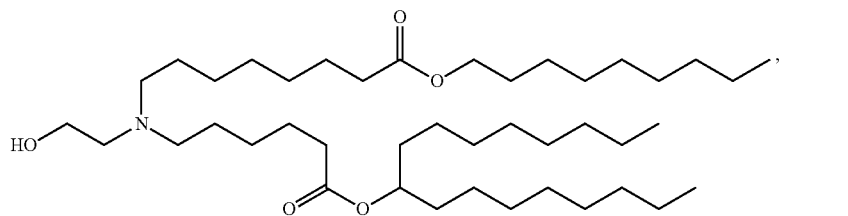
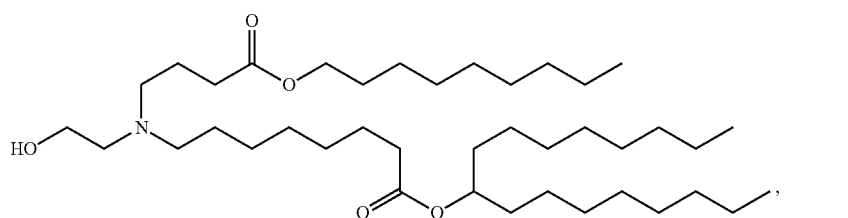
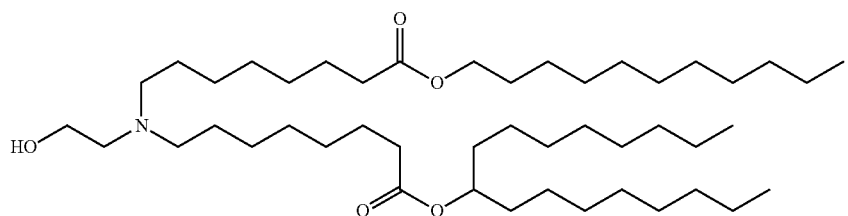
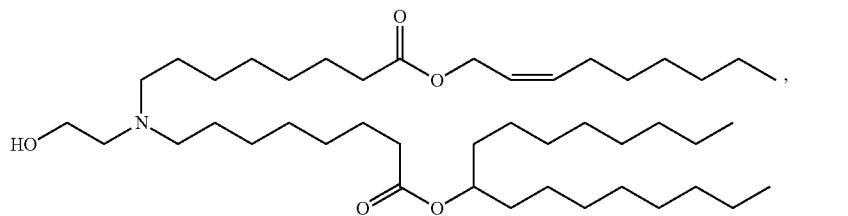
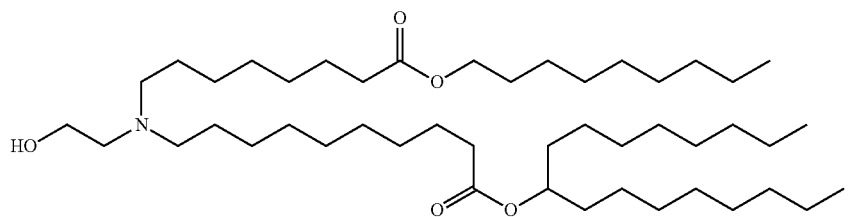
(Compound 21)



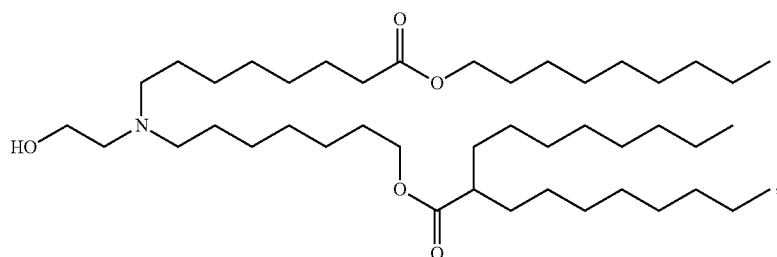
(Compound 22)



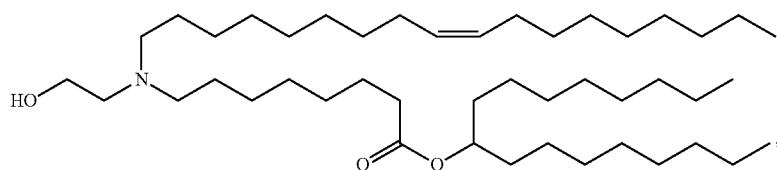
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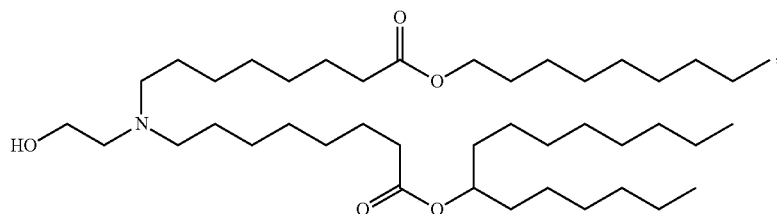
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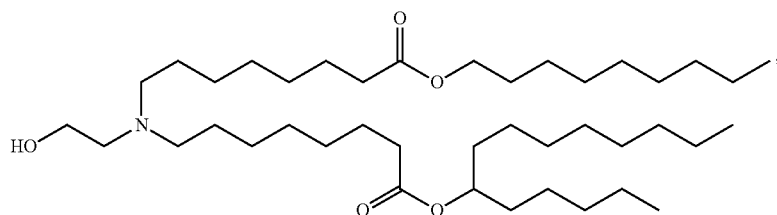
(Compound 30)



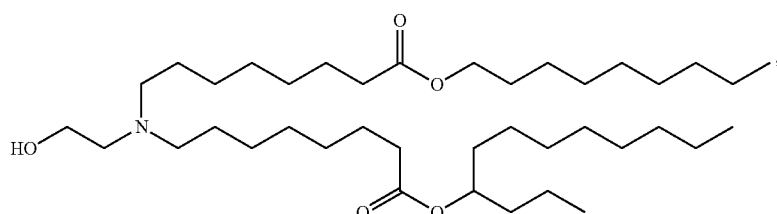
(Compound 31)



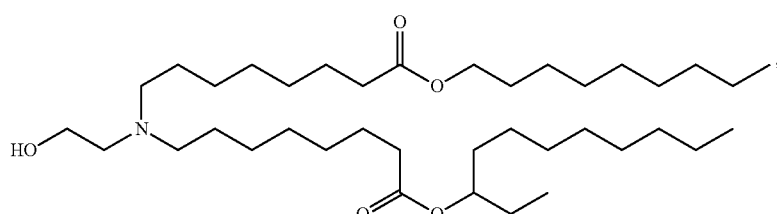
(Compound 32)



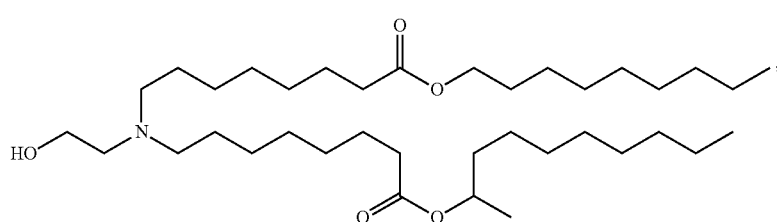
(Compound 33)



(Compound 34)

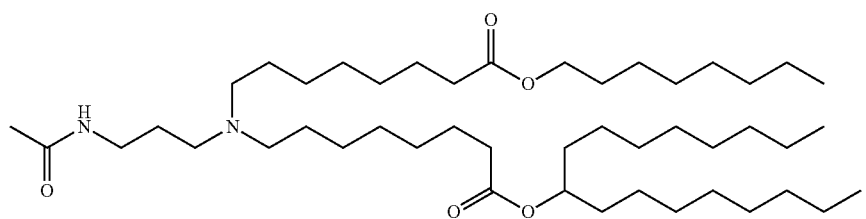


(Compound 35)

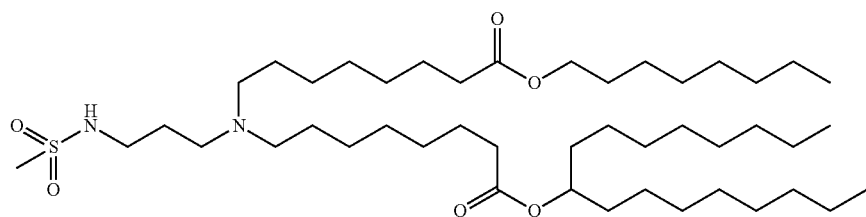


(Compound 36)

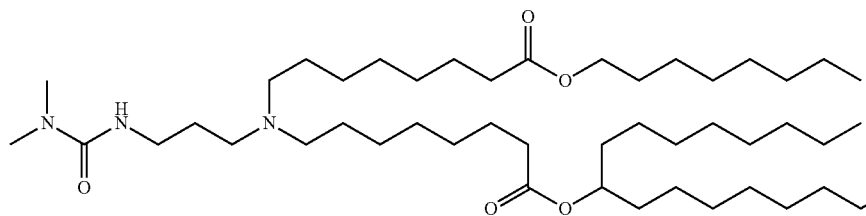
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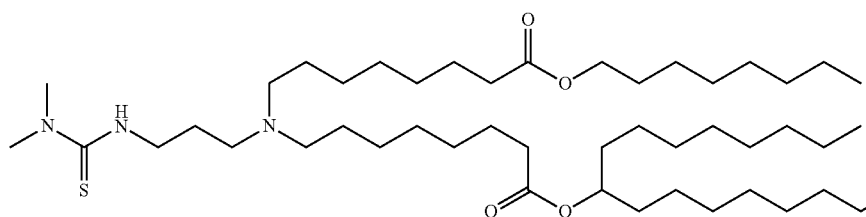
(Compound 37)



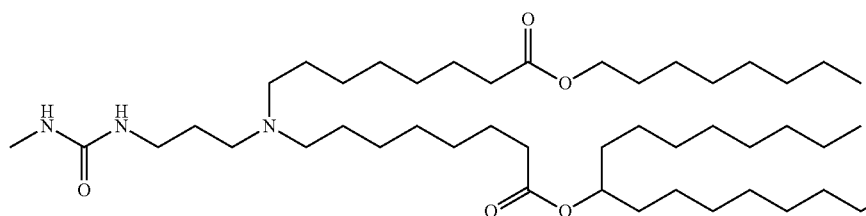
(Compound 38)



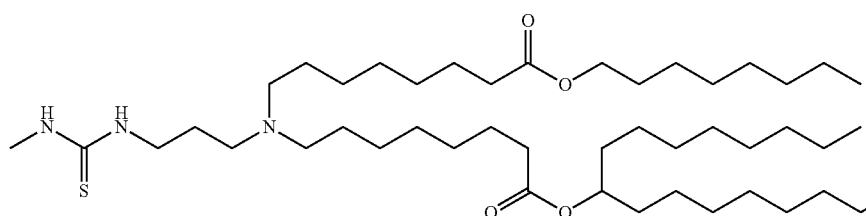
(Compound 39)



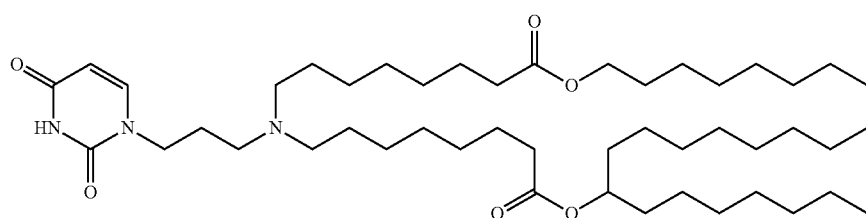
(Compound 40)



(Compound 41)

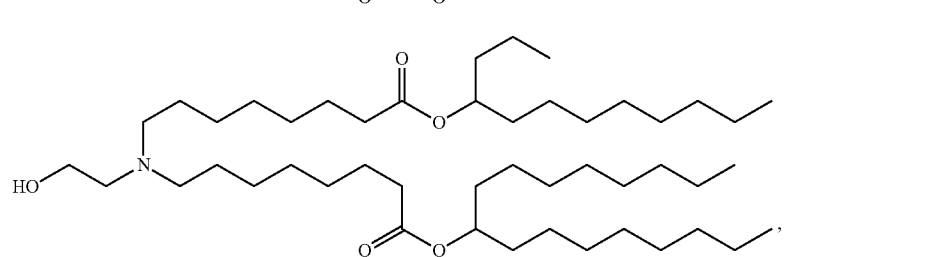
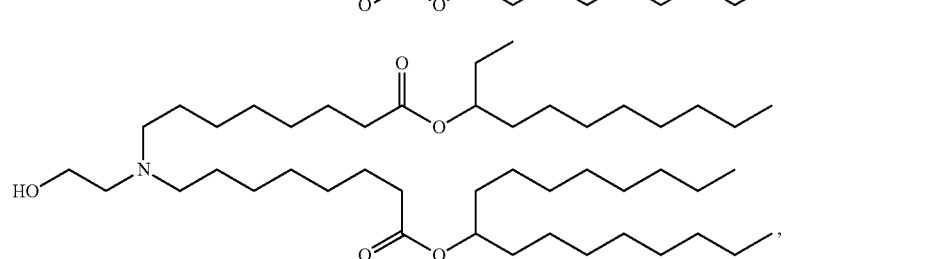
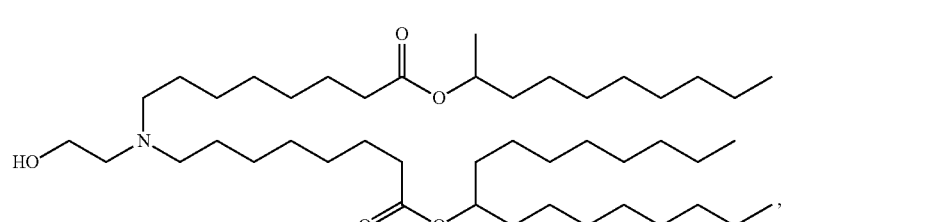
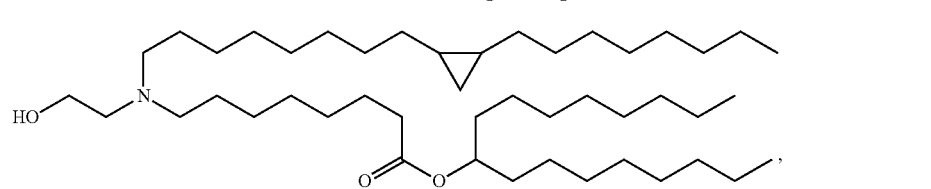
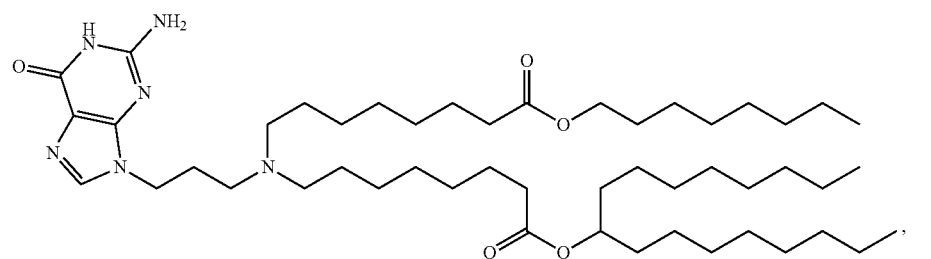
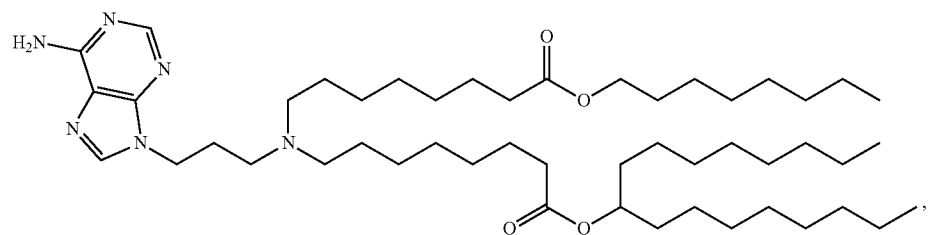
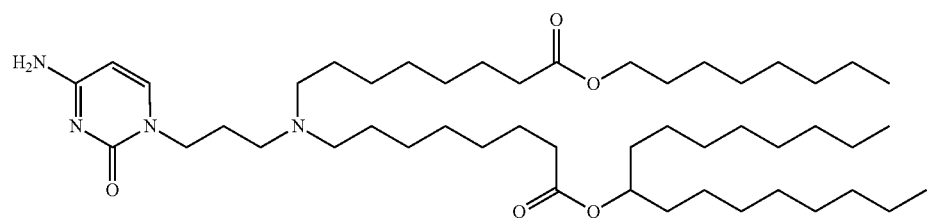


(Compound 42)

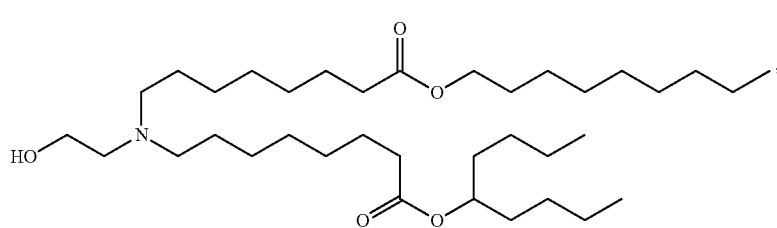
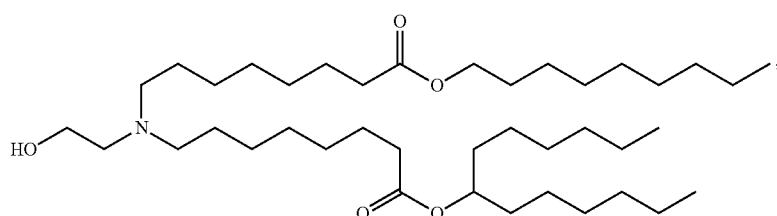
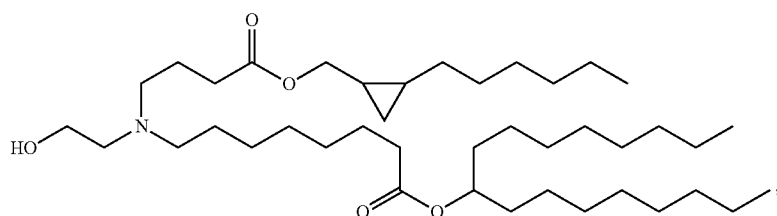
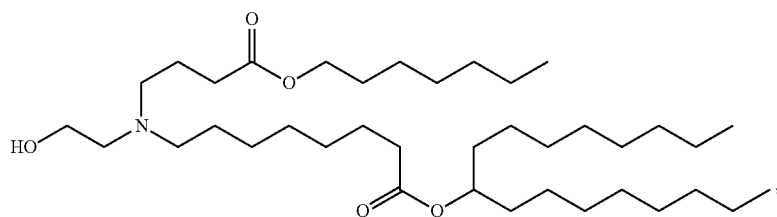
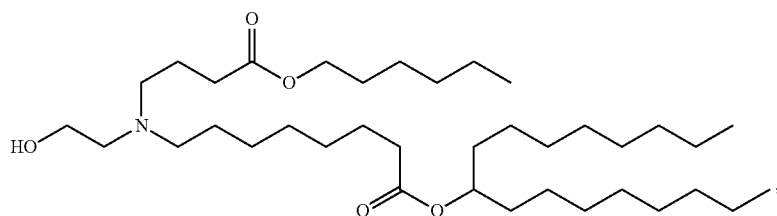
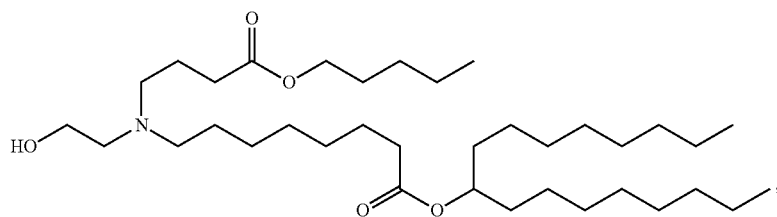
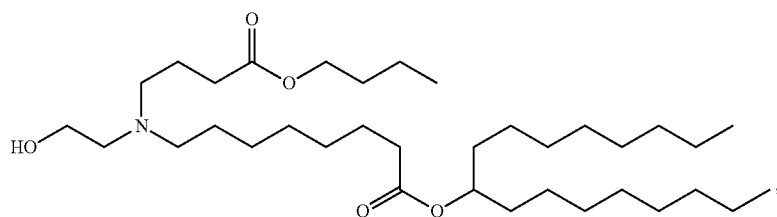


(Compound 43)

-continued

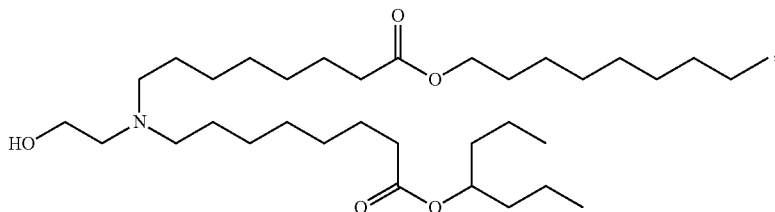


-continued

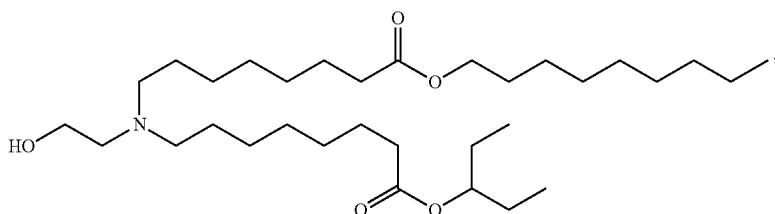


-continued

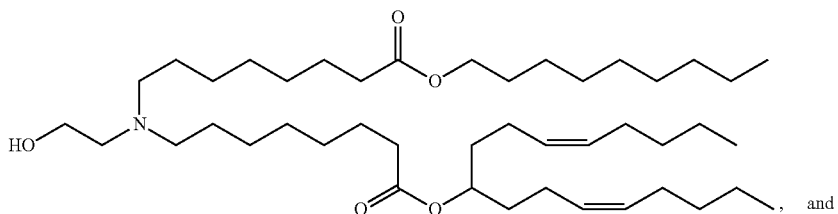
(Compound 58)



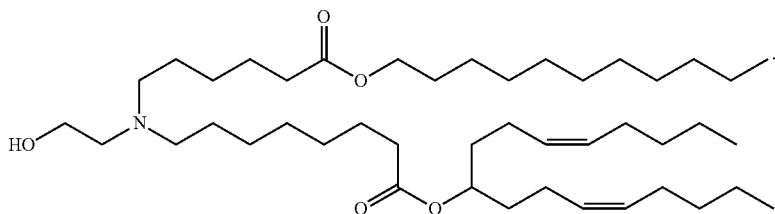
(Compound 59)



(Compound 60)



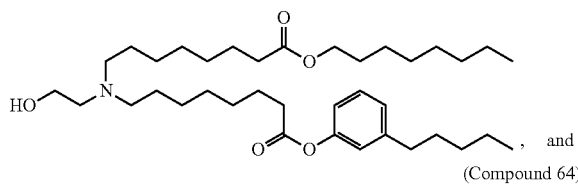
(Compound 61)



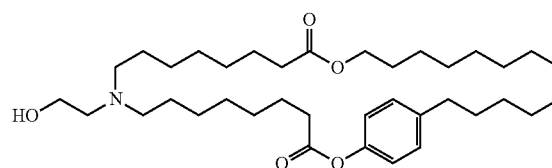
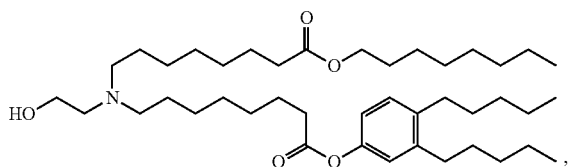
[0663] In further embodiments, the compound of Formula (I) is selected from the group consisting of:

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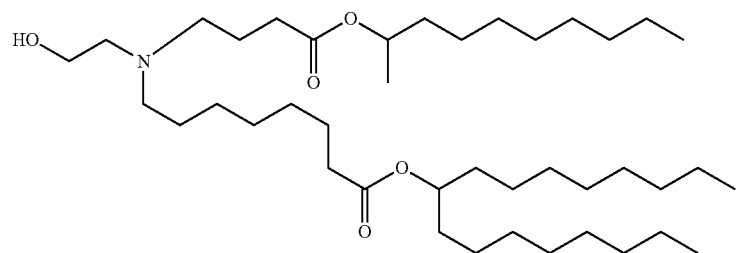
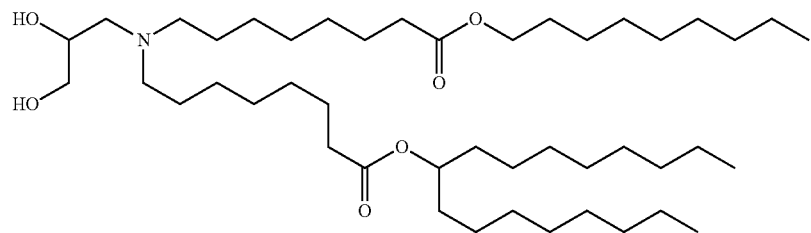
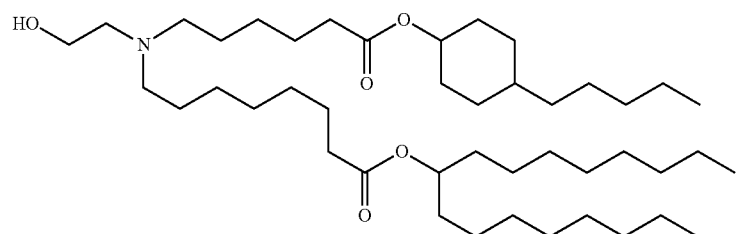
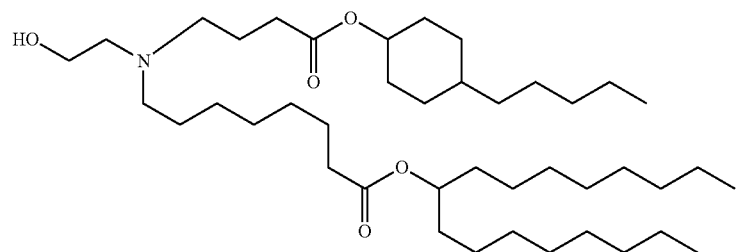
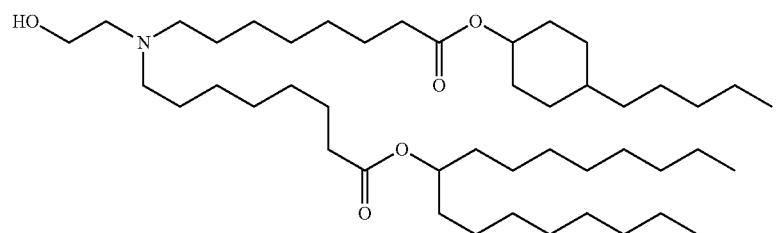
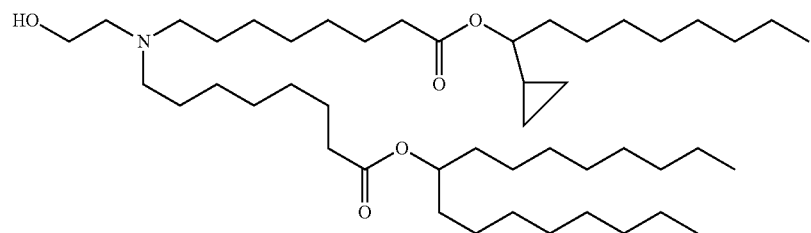
(Compound 63)



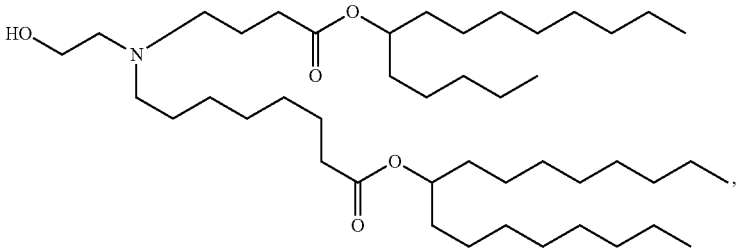
(Compound 62)



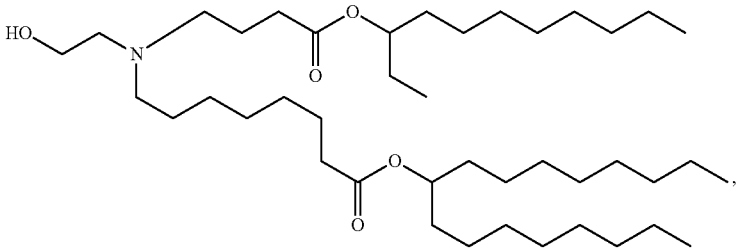
[0664] In some embodiments, the compound of Formula (I) is selected from the group consisting of:



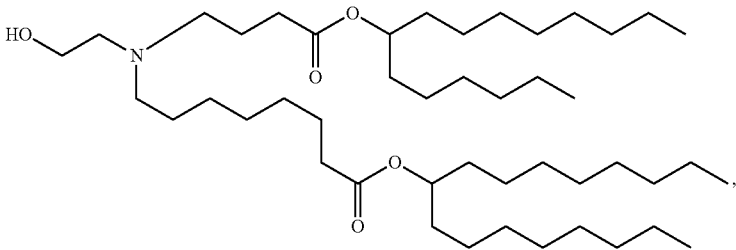
-continued



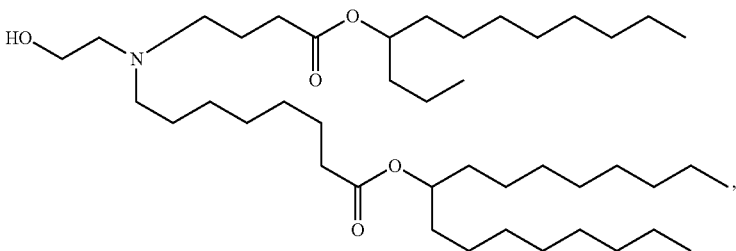
(Compound 71)



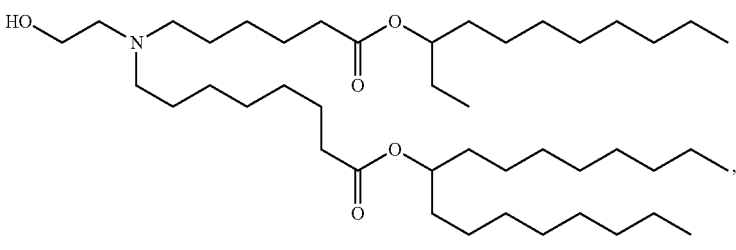
(Compound 72)



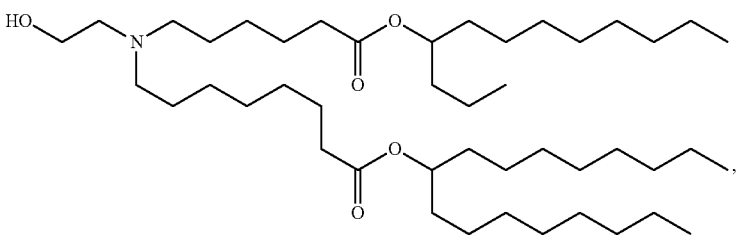
(Compound 73)



(Compound 74)

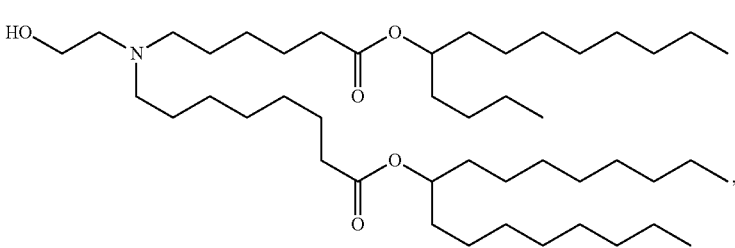


(Compound 75)

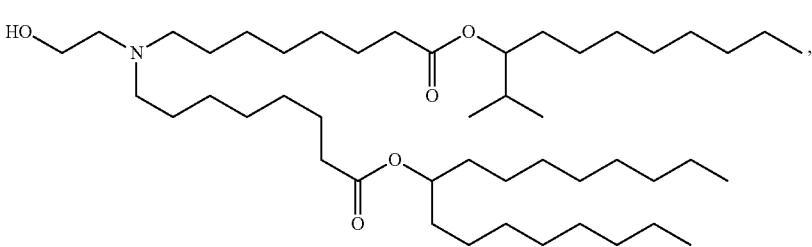


(Compound 76)

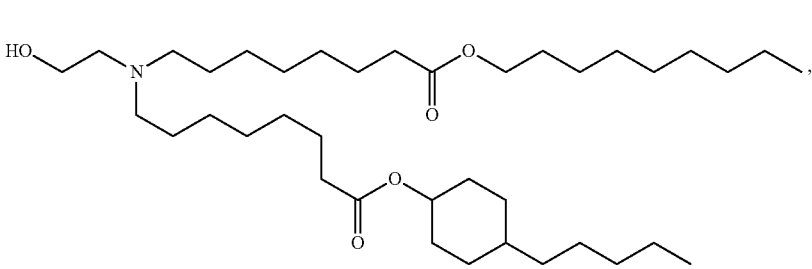
-continued



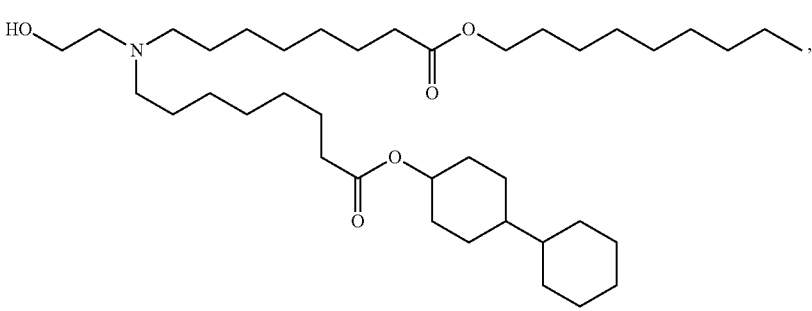
(Compound 77)



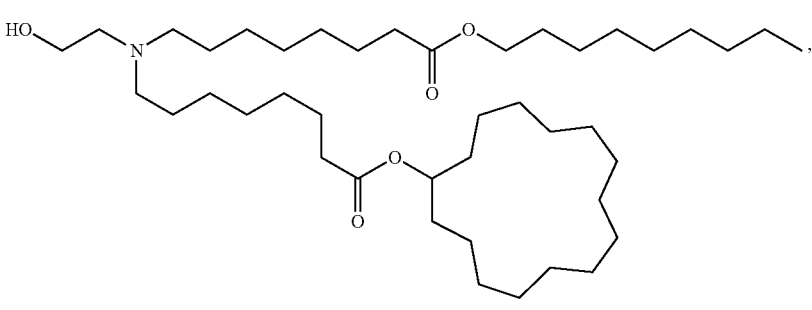
(Compound 78)



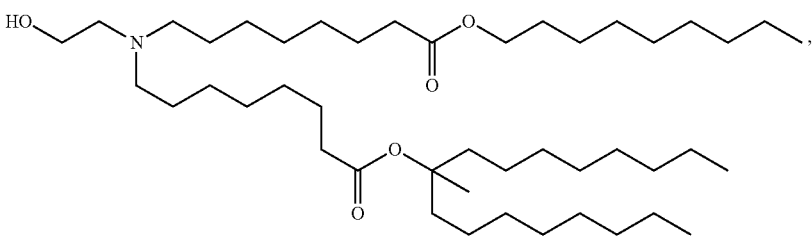
(Compound 79)



(Compound 80)

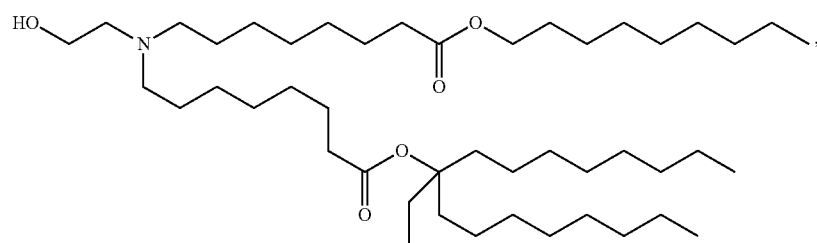


(Compound 81)

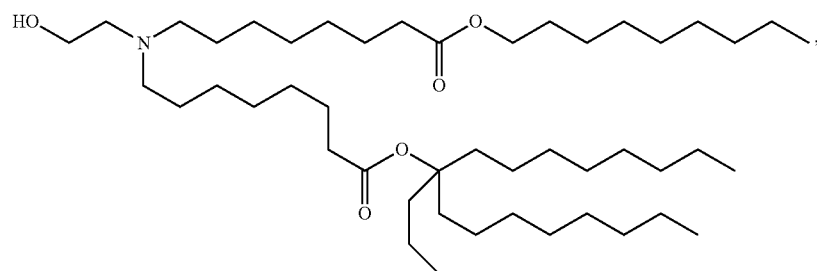


(Compound 82)

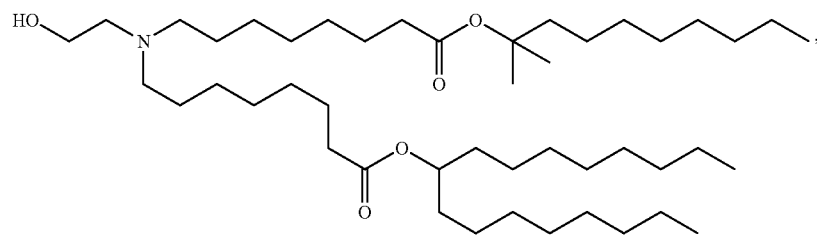
-continued



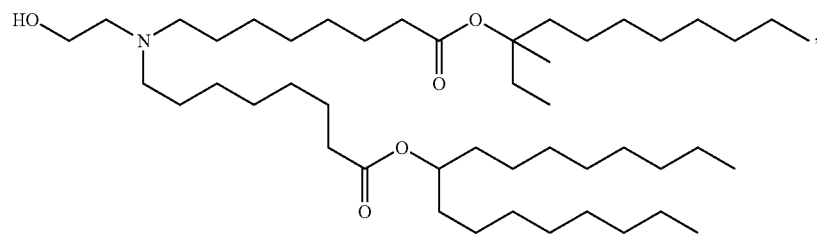
(Compound 83)



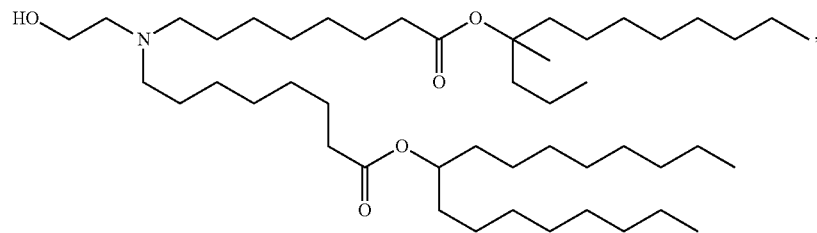
(Compound 84)



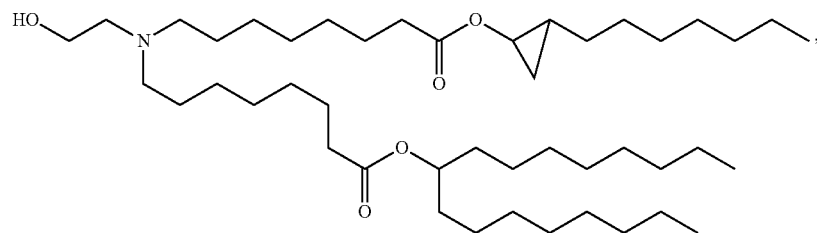
(Compound 85)



(Compound 86)

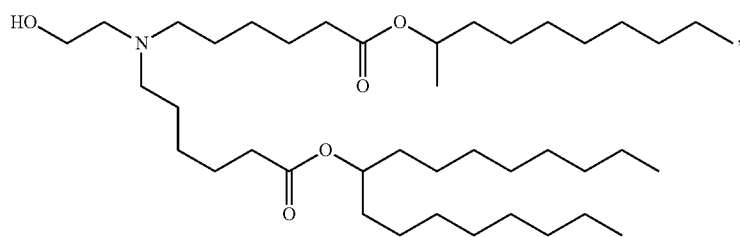


(Compound 87)

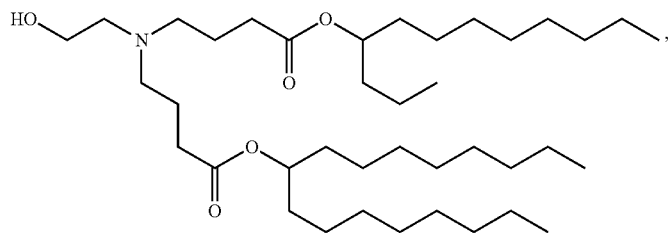


(Compound 88)

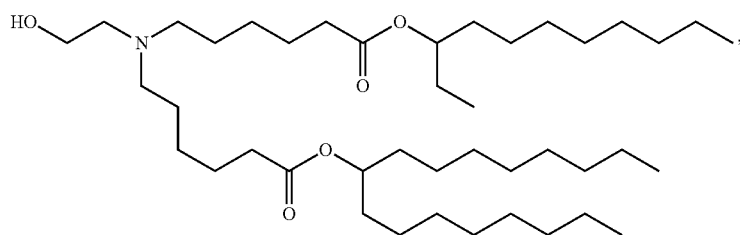
-continued



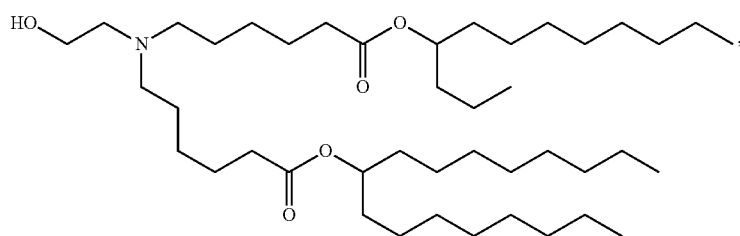
(Compound 89)



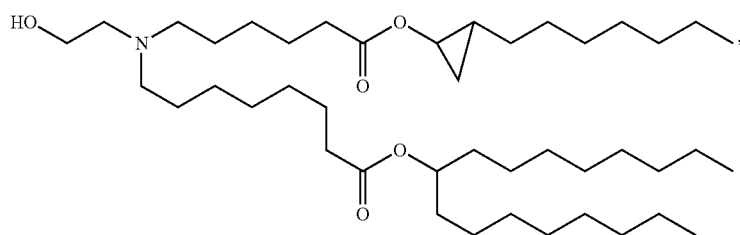
(Compound 90)



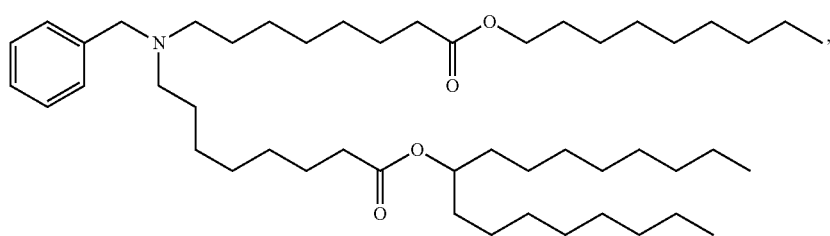
(Compound 91)



(Compound 92)

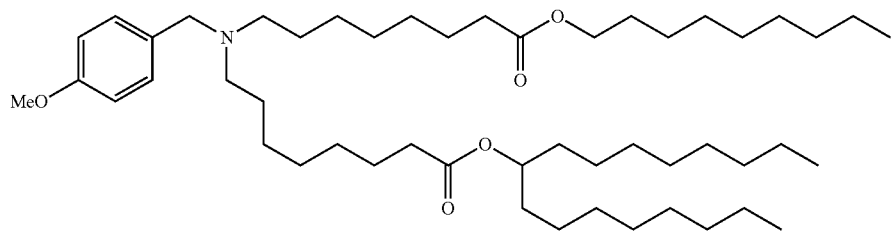


(Compound 93)

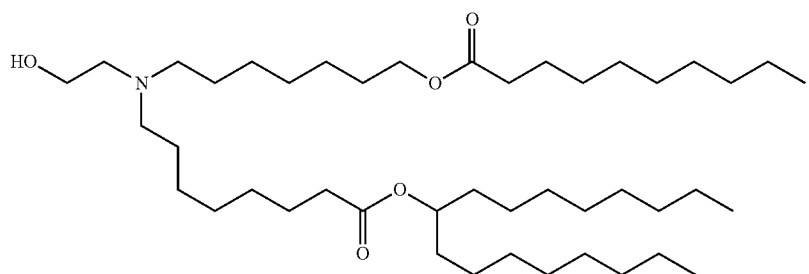


(Compound 94)

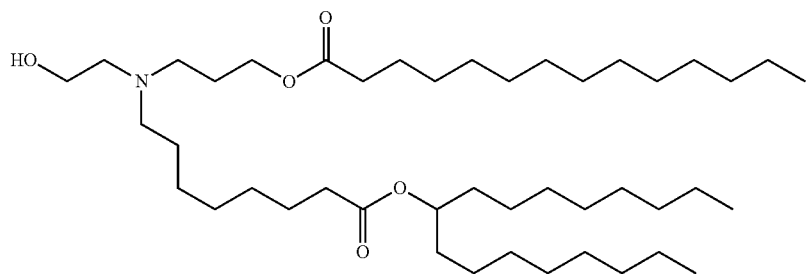
-continued



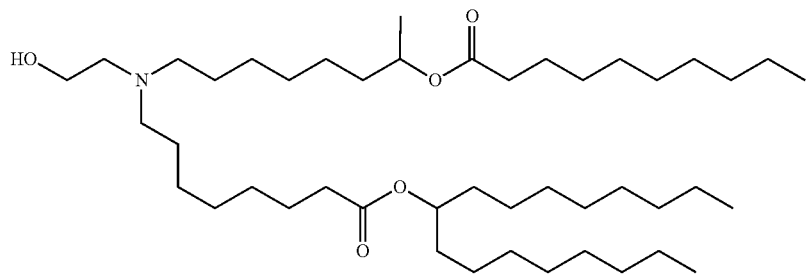
(Compound 95)



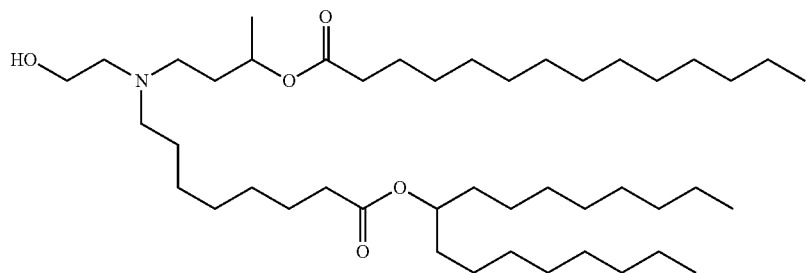
(Compound 96)



(Compound 97)



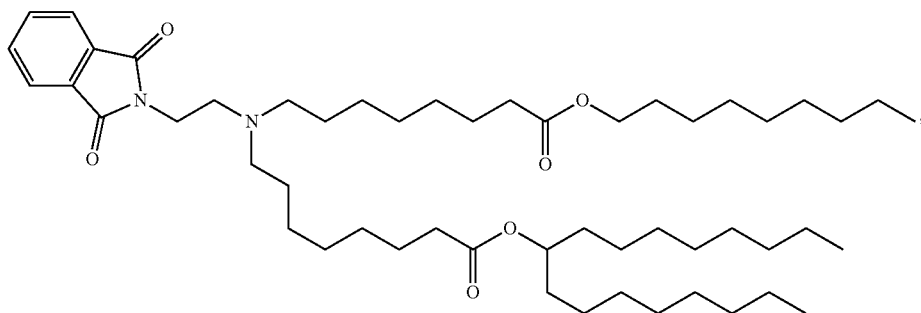
(Compound 98)



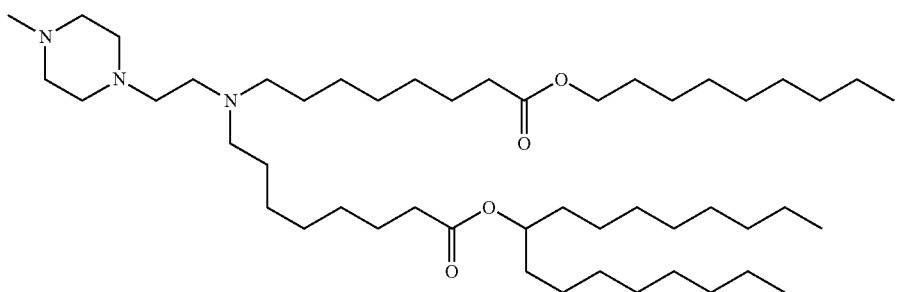
(Compound 99)

-continued

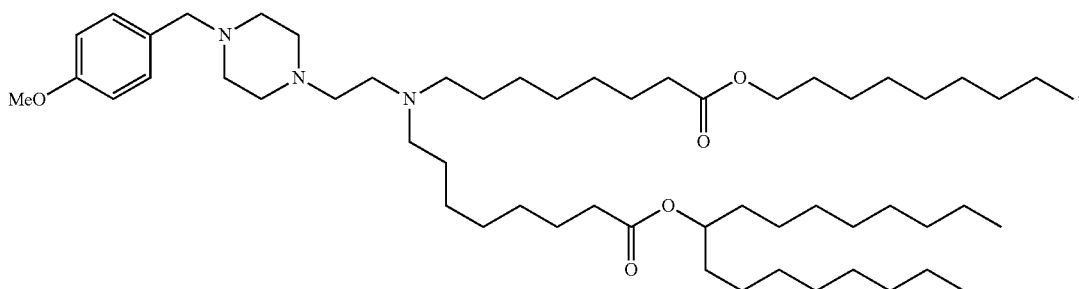
(Compound 100)



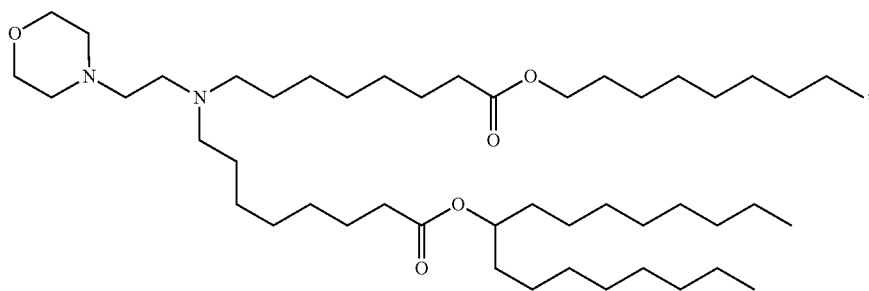
(Compound 101)



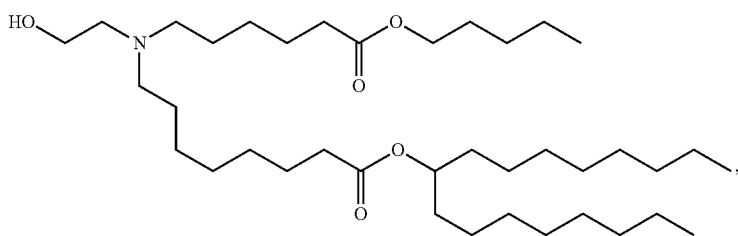
(Compound 102)



(Compound 103)

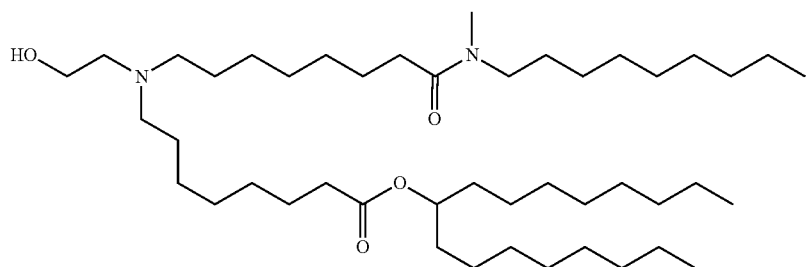


(Compound 104)

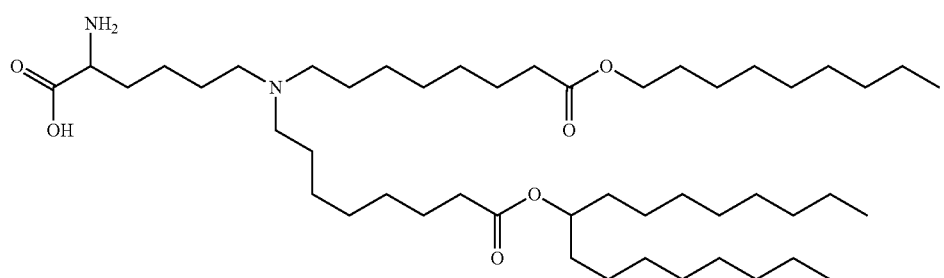


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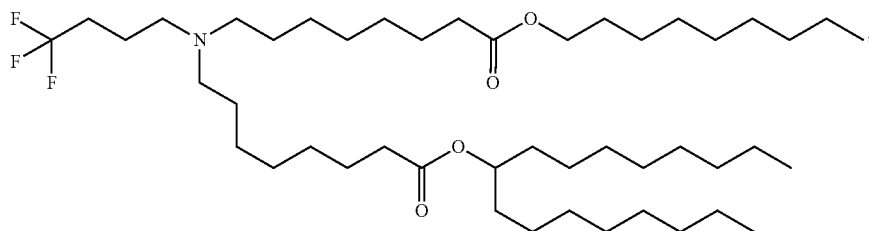
(Compound 105)



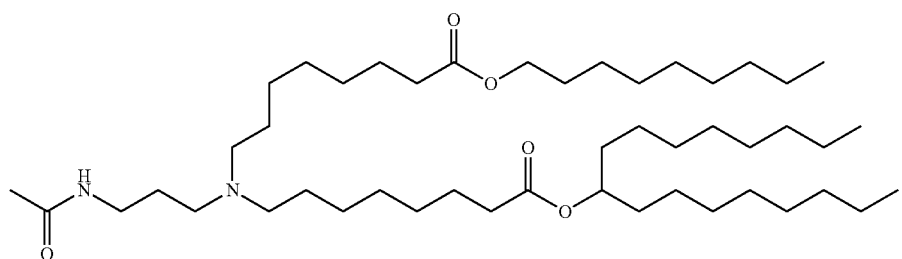
(Compound 106)



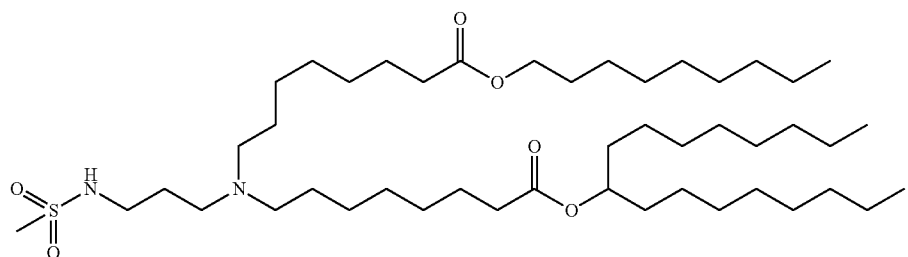
(Compound 107)



(Compound 108)

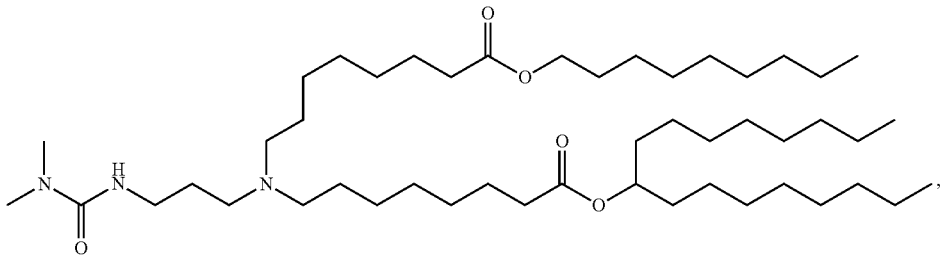


(Compound 109)

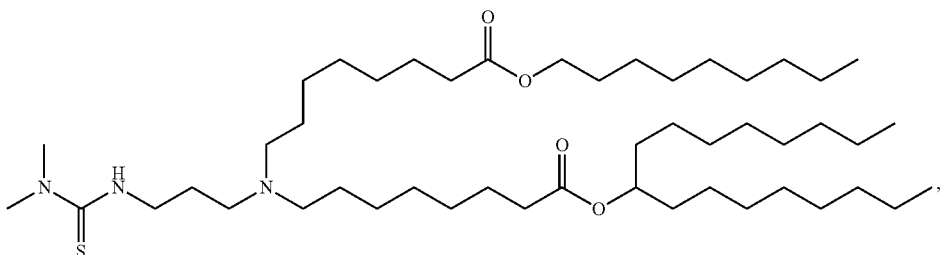


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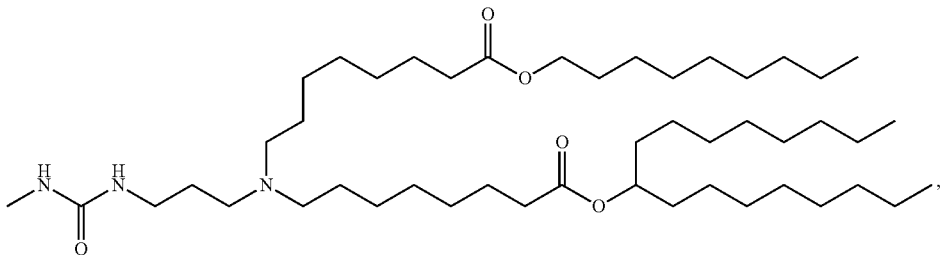
(Compound 110)



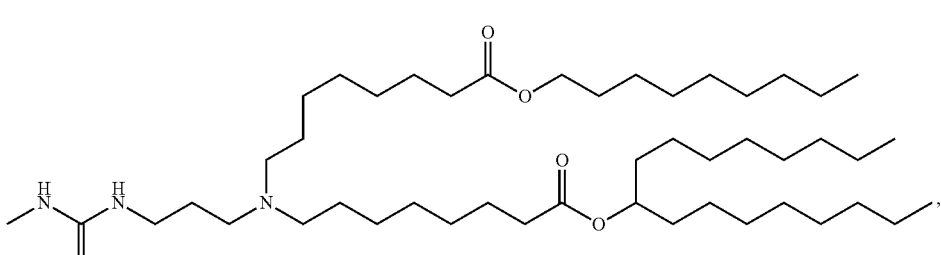
(Compound 111)



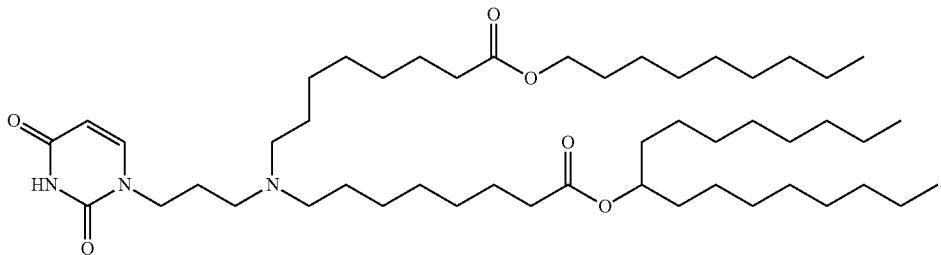
(Compound 112)



(Compound 113)

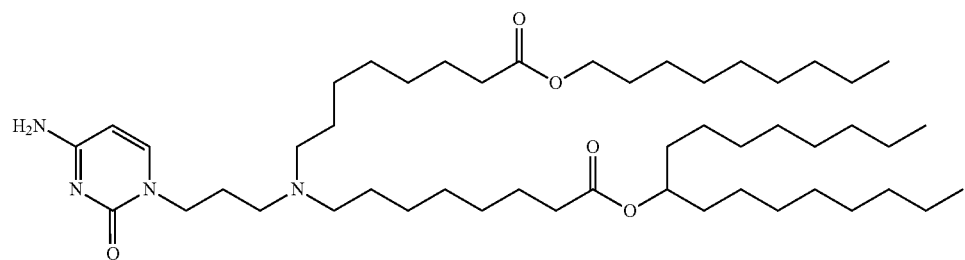


(Compound 114)

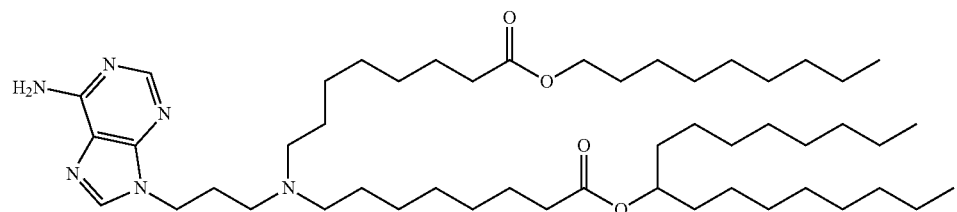


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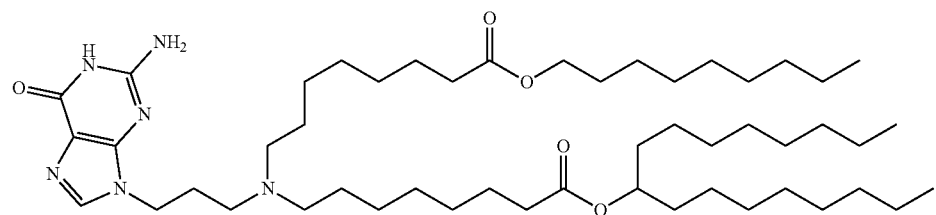
(Compound 115)



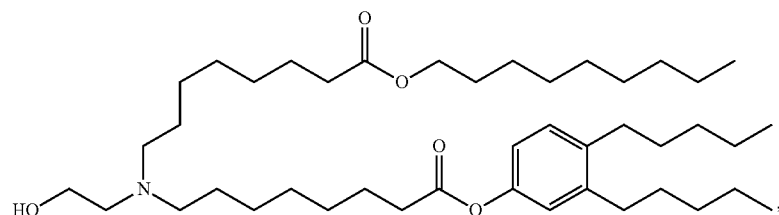
(Compound 116)



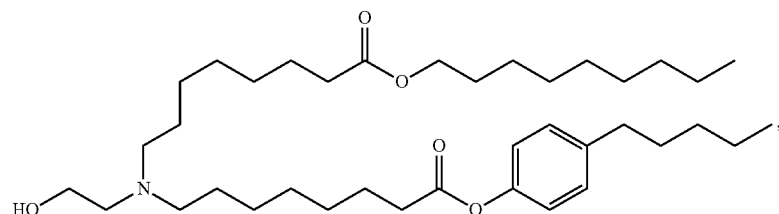
(Compound 117)



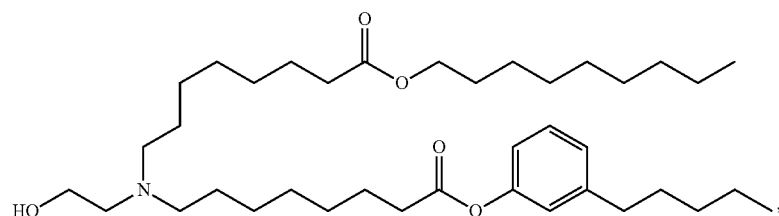
(Compound 118)



(Compound 119)

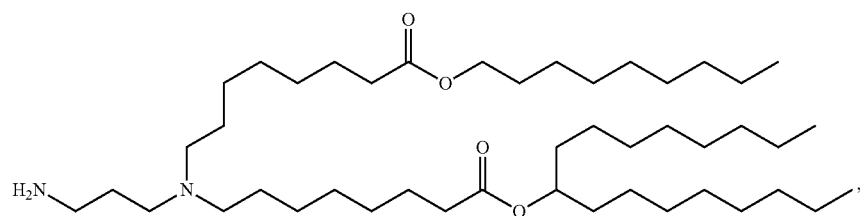


(Compound 120)

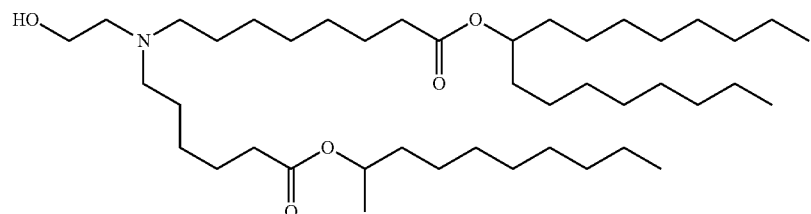


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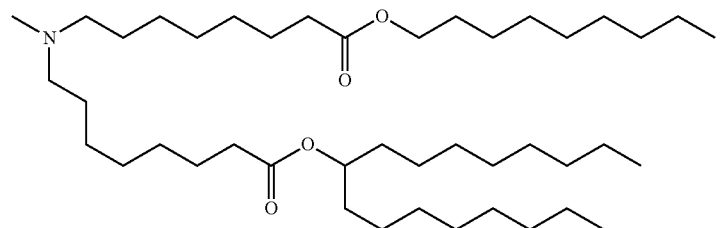
(Compound 121)



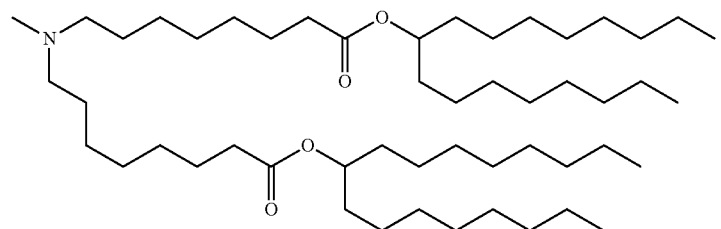
(Compound 122)



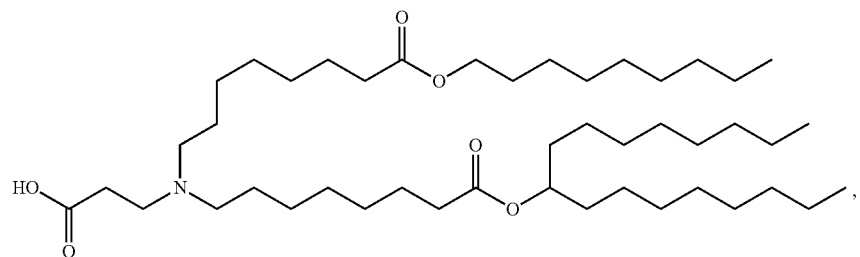
(Compound 123)



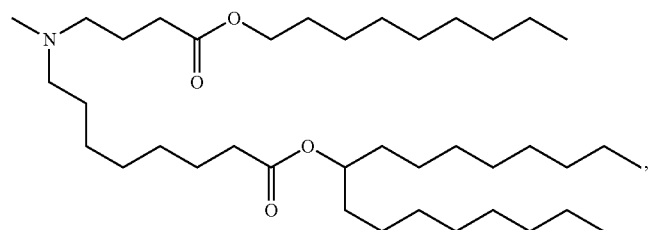
(Compound 124)



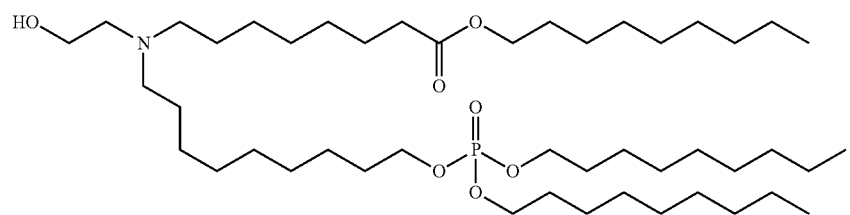
(Compound 125)



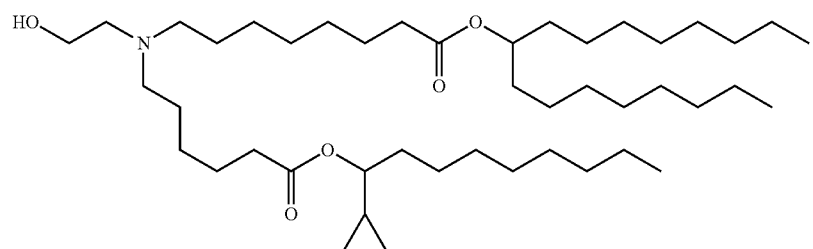
(Compound 126)



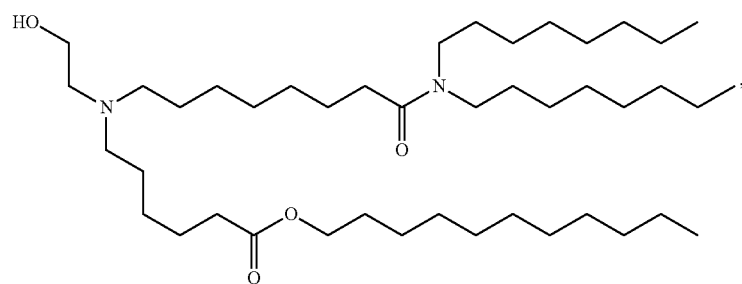
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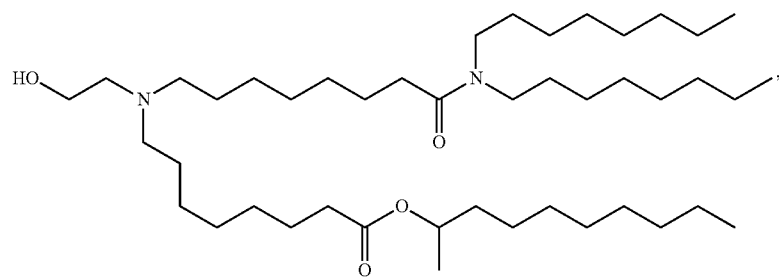
(Compound 127)



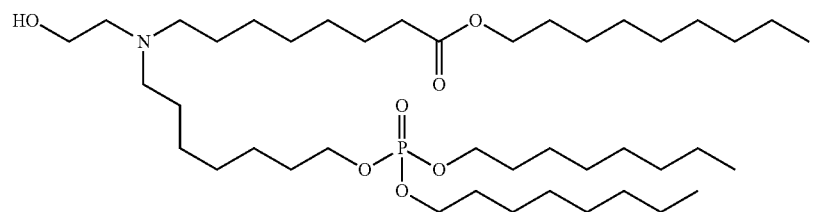
(Compound 128)



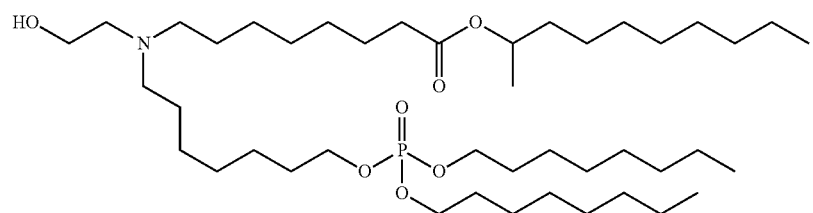
(Compound 129)



(Compound 130)



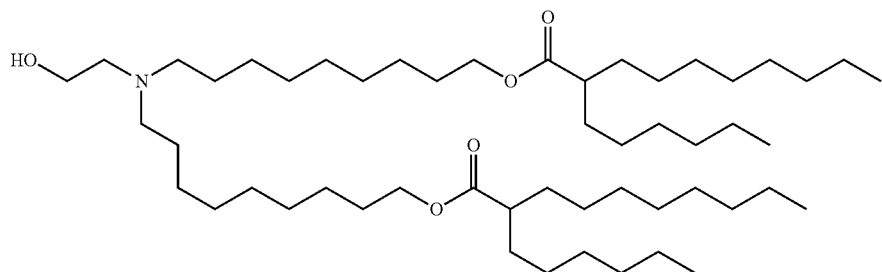
(Compound 131)



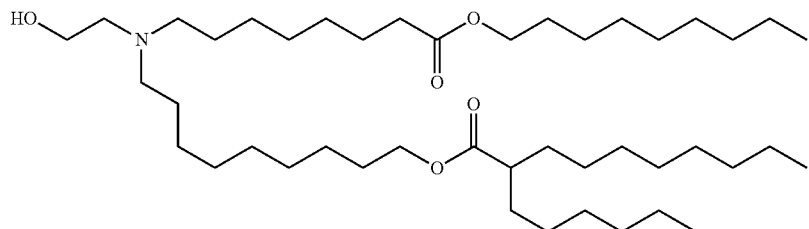
(Compound 132)

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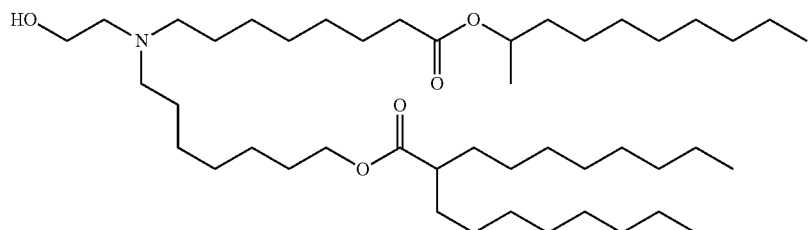
(Compound 133)



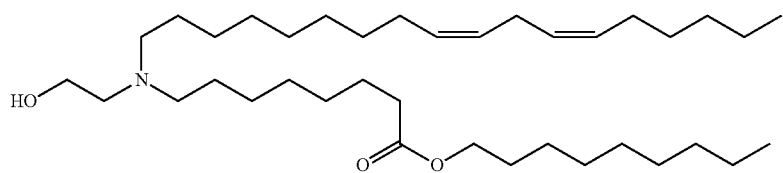
(Compound 134)



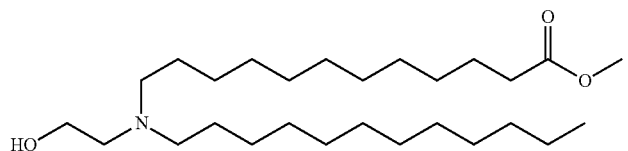
(Compound 135)



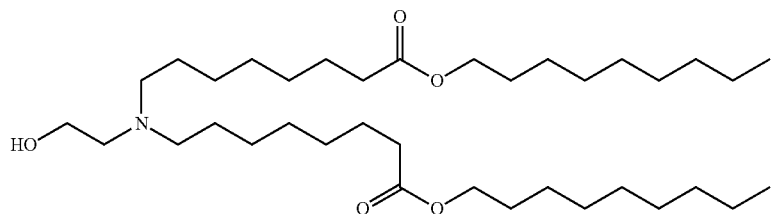
(Compound 136)



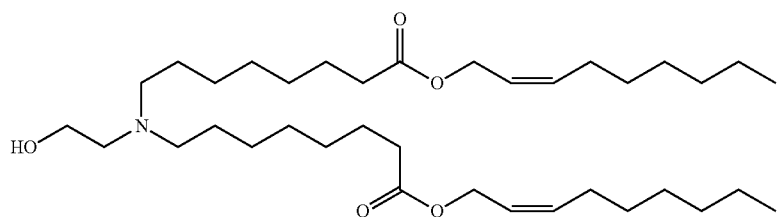
(Compound 137)



(Compound 138)

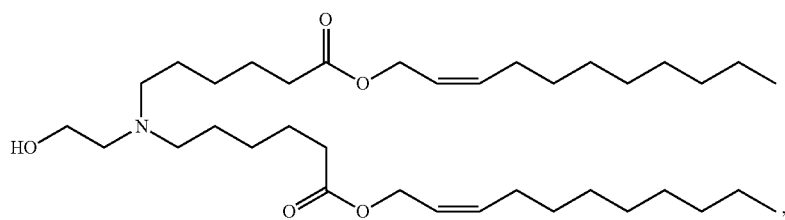


(Compound 139)

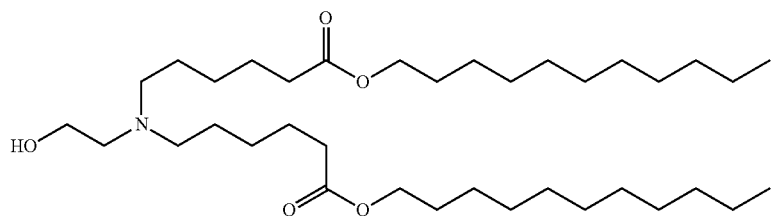


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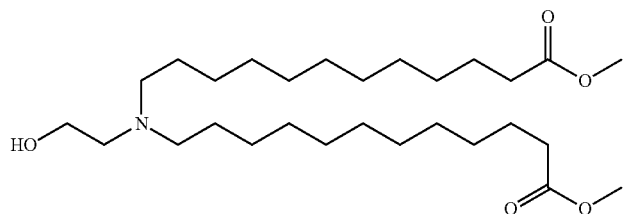
(Compound 140)



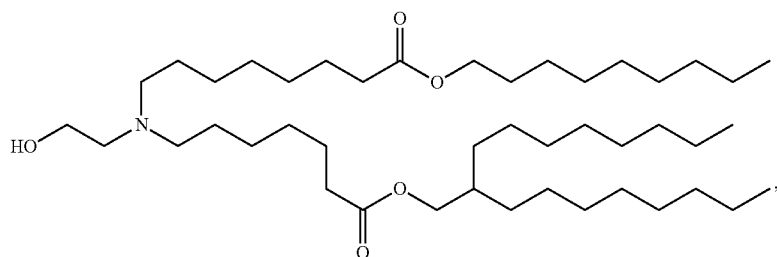
(Compound 141)



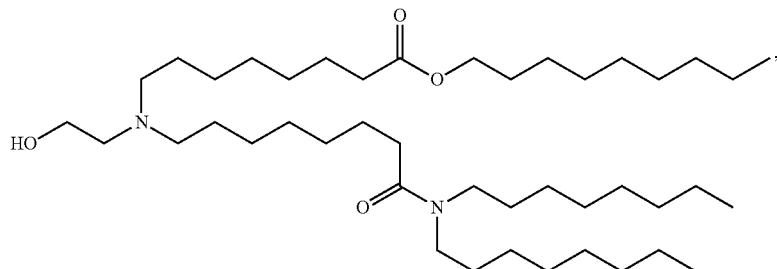
(Compound 142)



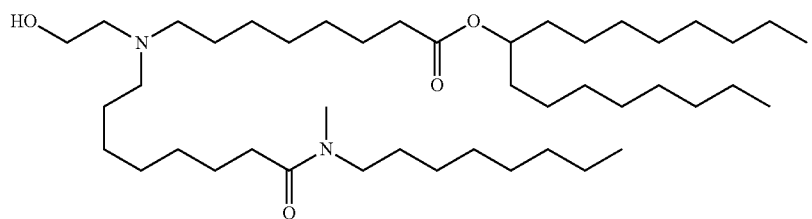
(Compound 143)



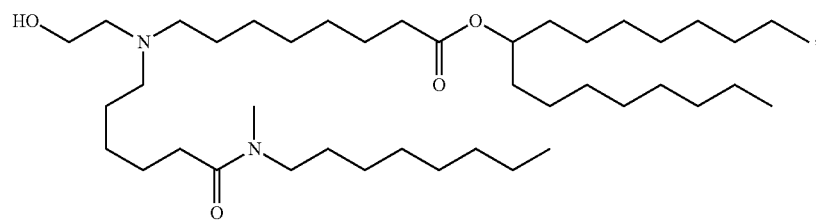
(Compound 144)



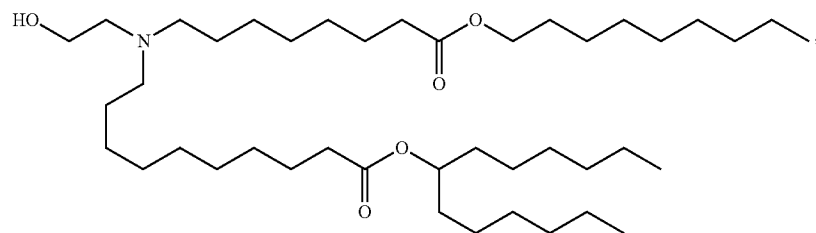
(Compound 145)



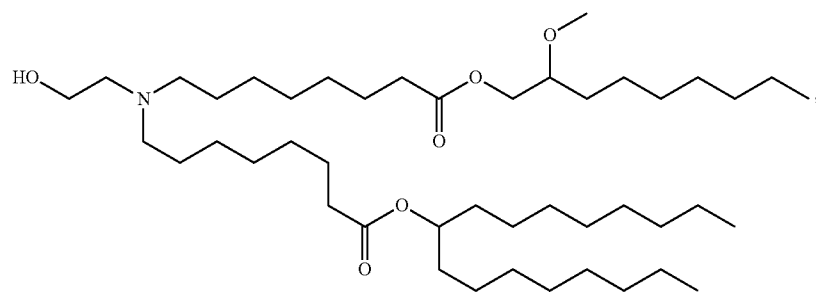
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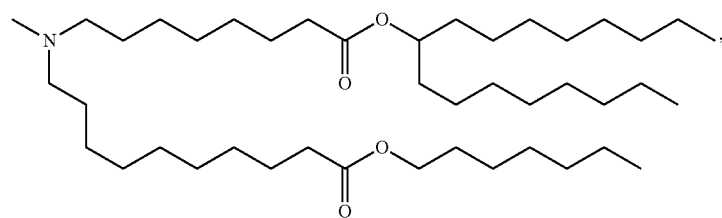
(Compound 146)



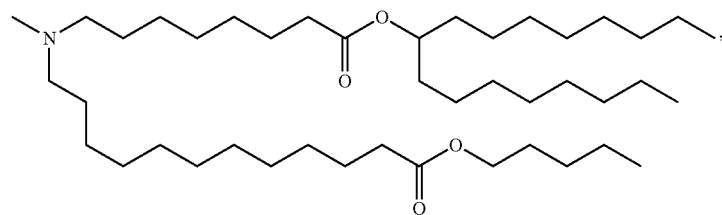
(Compound 147)



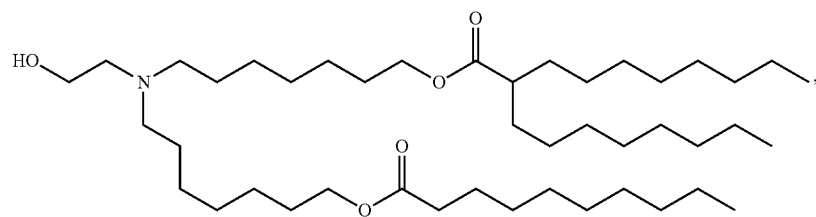
(Compound 148)



(Compound 149)



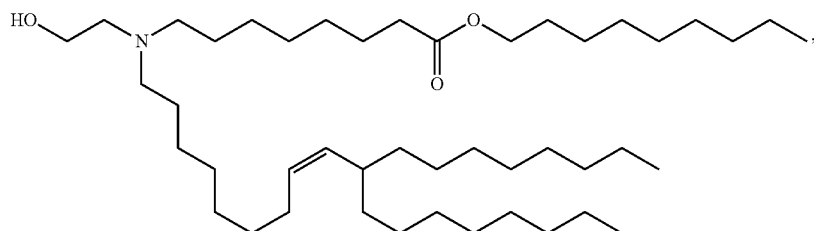
(Compound 150)



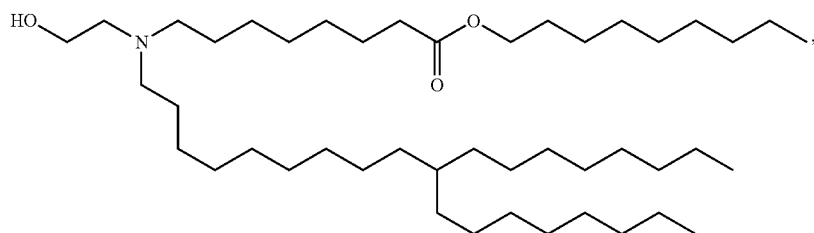
(Compound 151)

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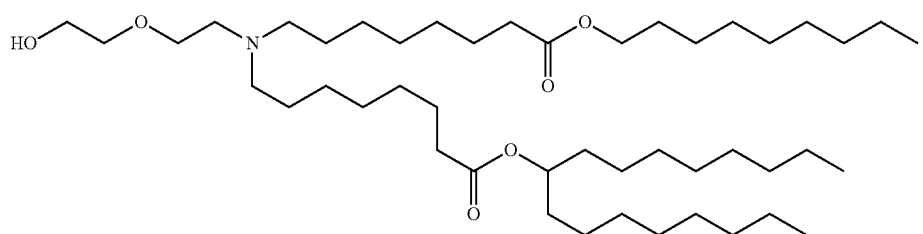
(Compound 152)



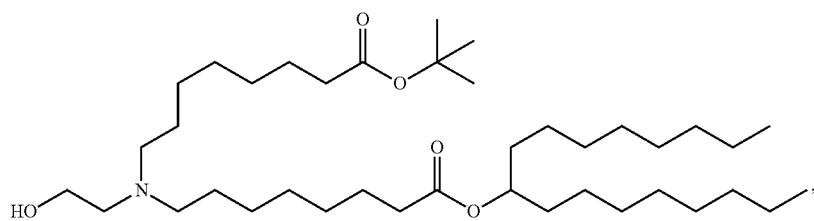
(Compound 153)



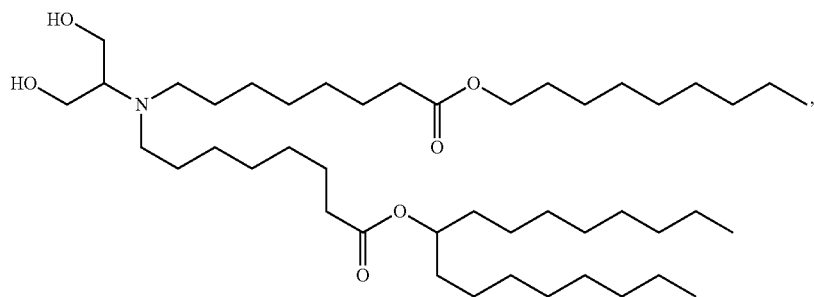
(Compound 154)



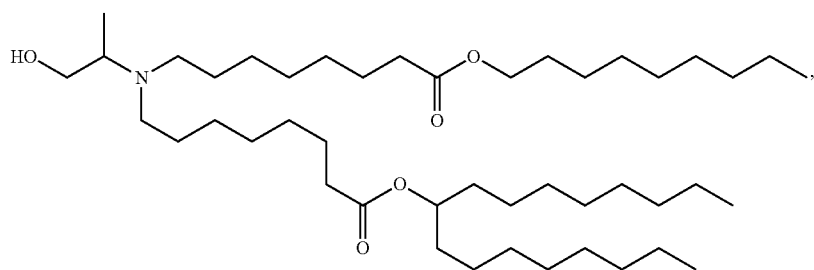
(Compound 155)



(Compound 156)

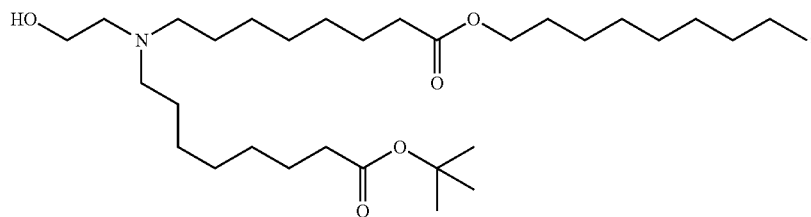


(Compound 157)

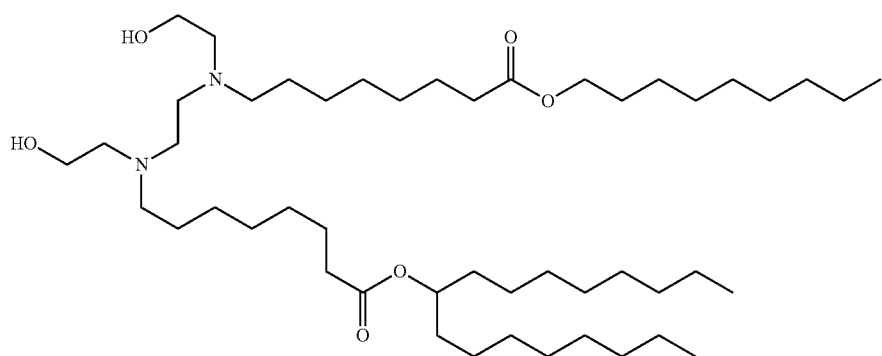


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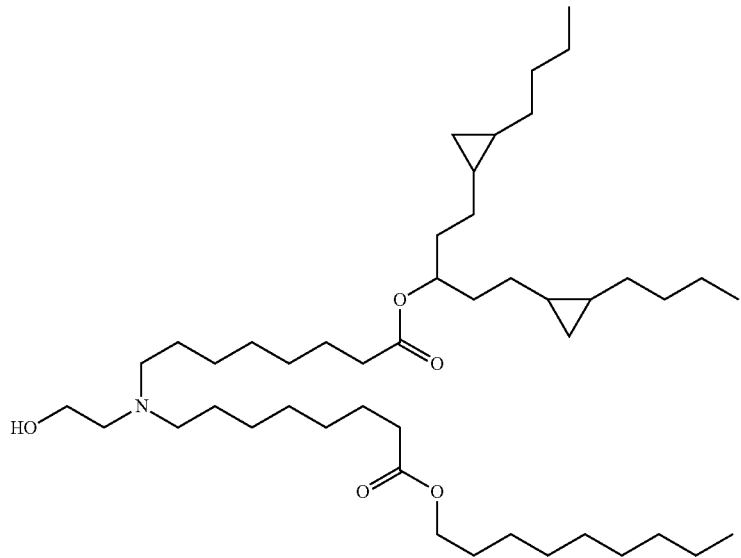
(Compound 158)



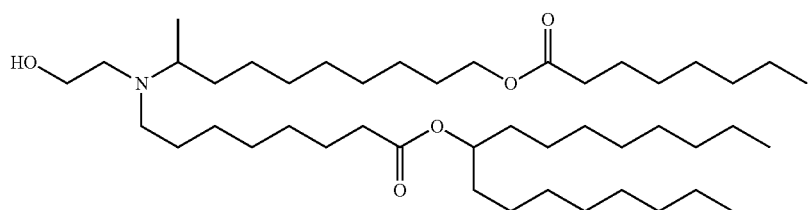
(Compound 159)



(Compound 160)

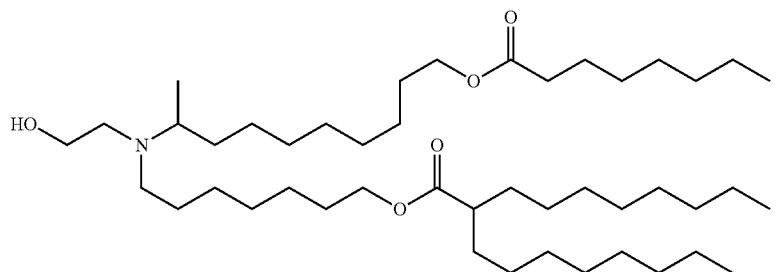


(Compound 161)

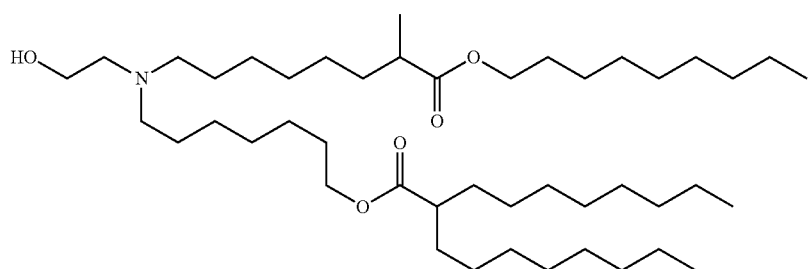


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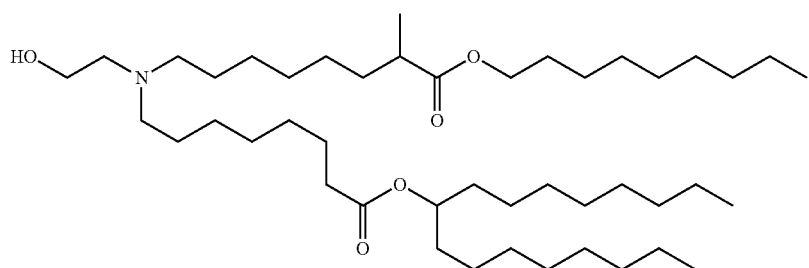
(Compound 162)



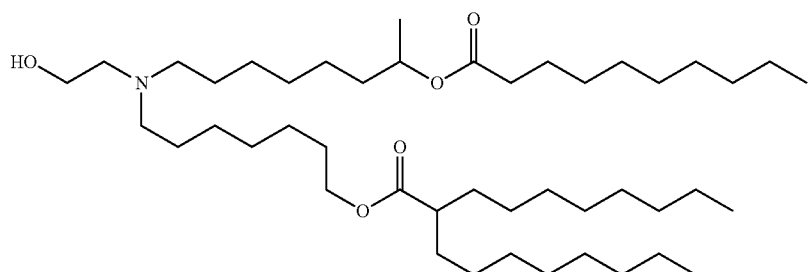
(Compound 163)



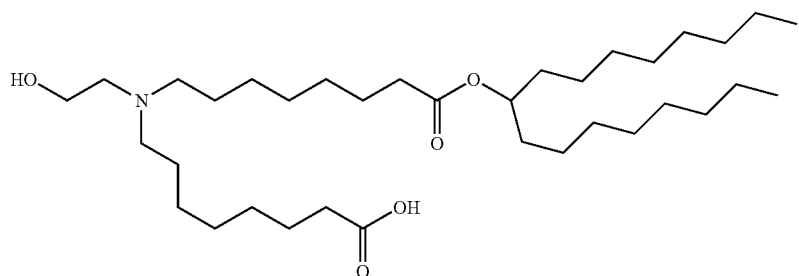
(Compound 164)



(Compound 165)

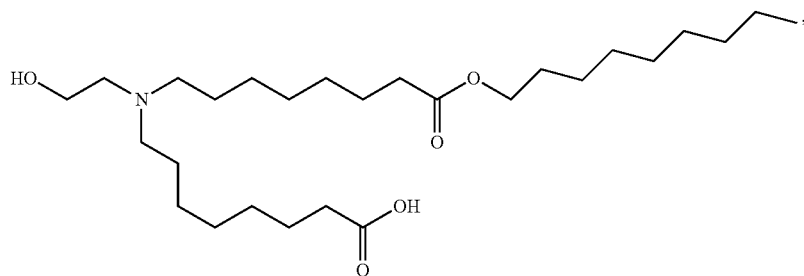


(Compound 166)

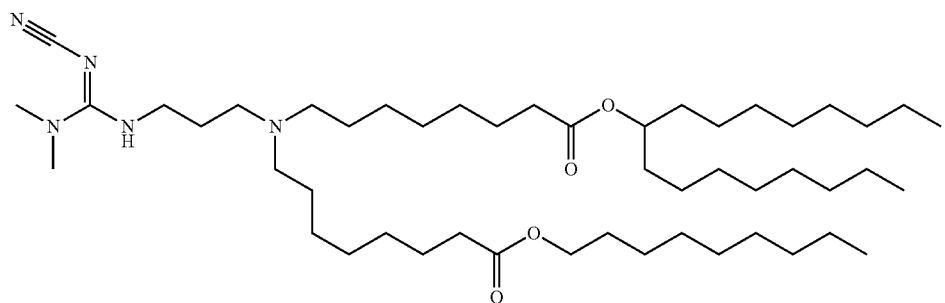


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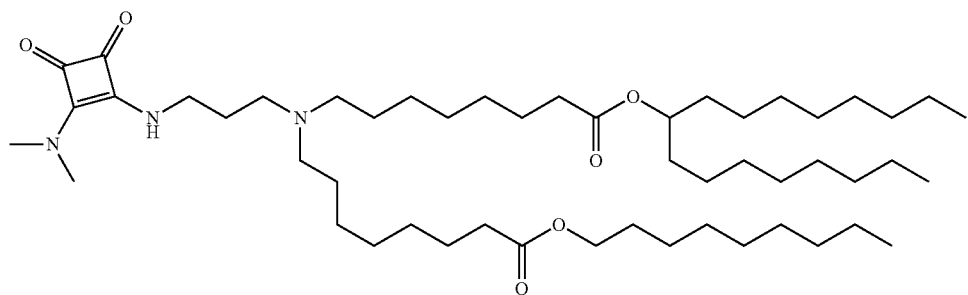
(Compound 167)



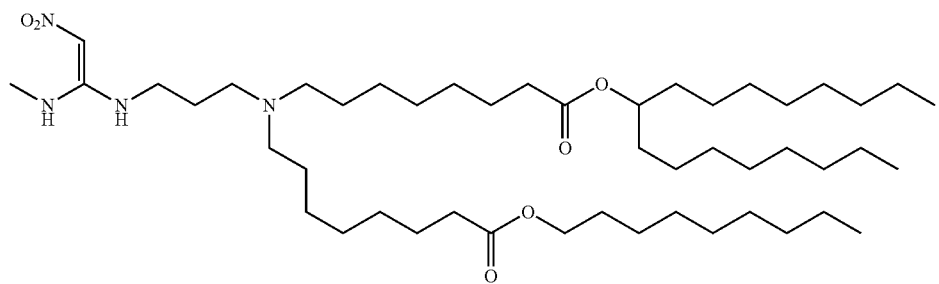
(Compound 168)



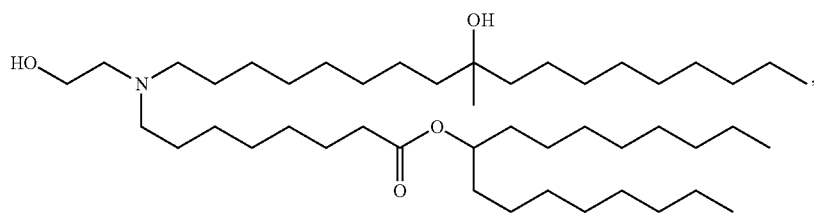
(Compound 169)



(Compound 170)

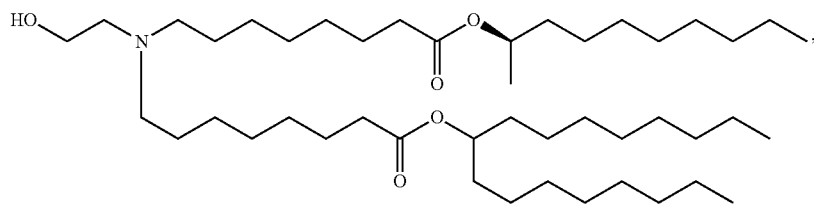


(Compound 171)

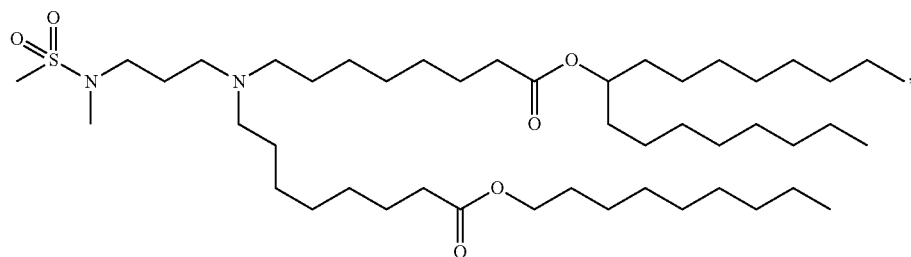


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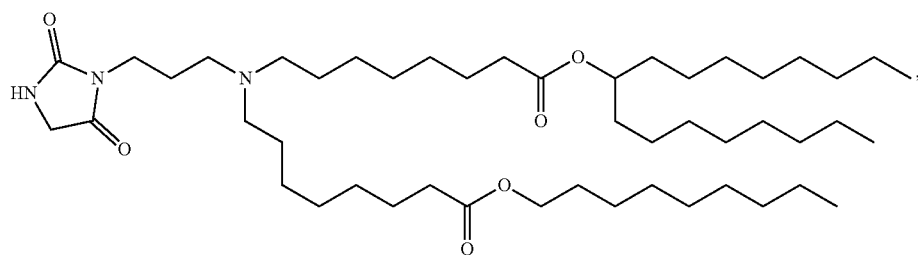
(Compound 172)



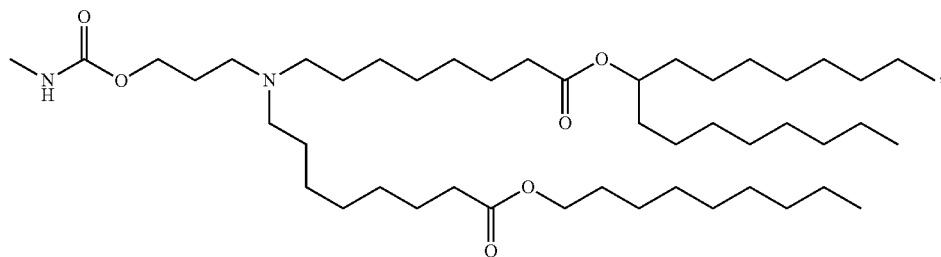
(Compound 173)



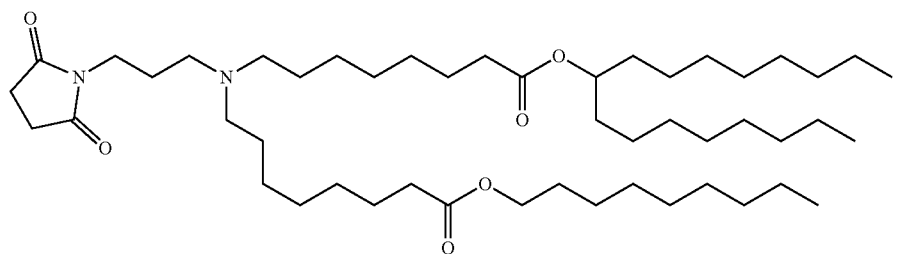
(Compound 174)



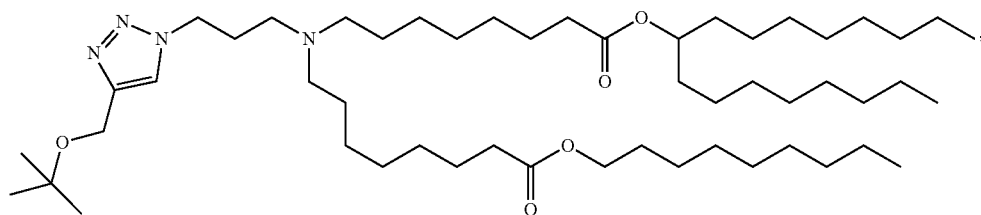
(Compound 175)



(Compound 176)

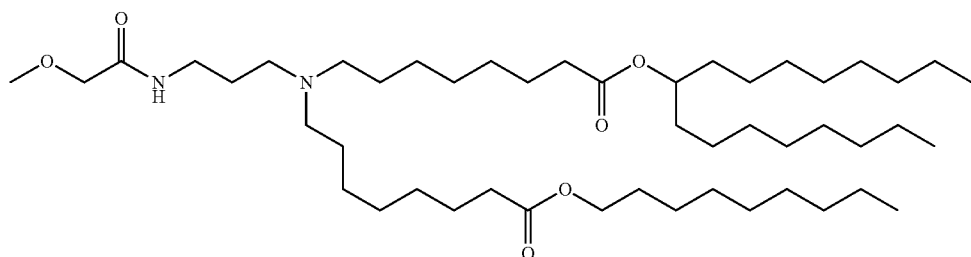


(Compound 177)

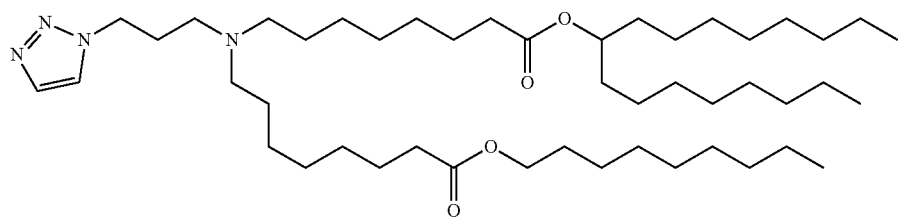


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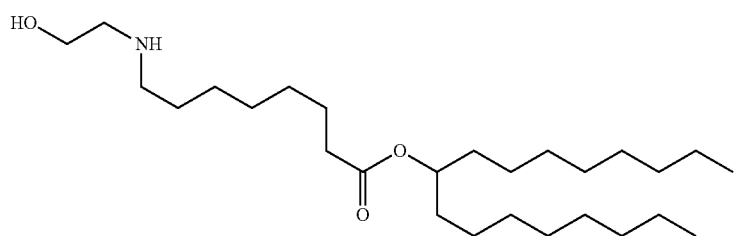
(Compound 178)



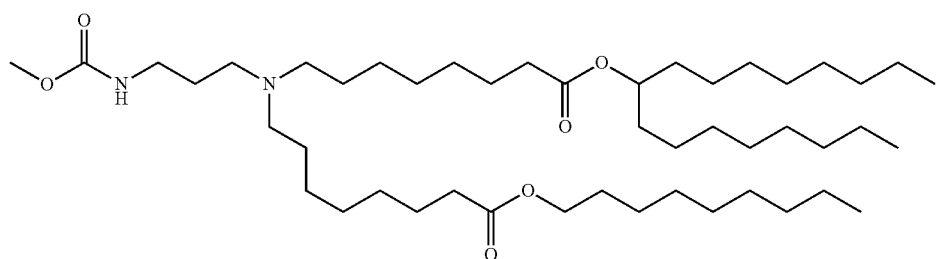
(Compound 179)



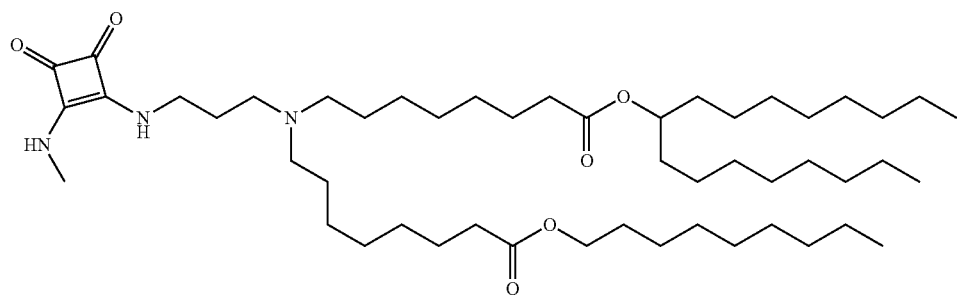
(Compound 180)



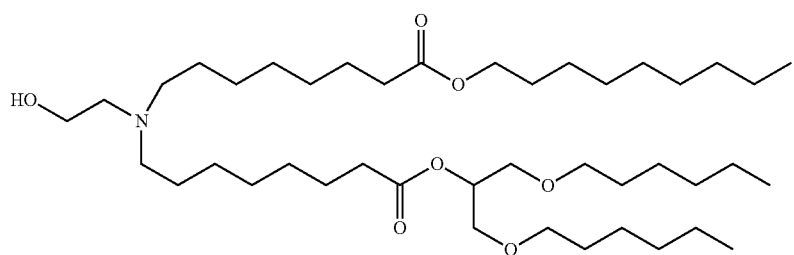
(Compound 181)



(Compound 182)

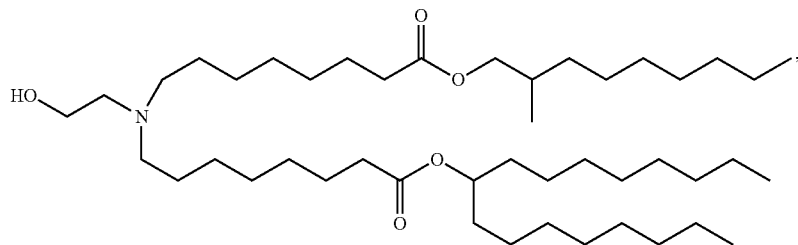


(Compound 183)

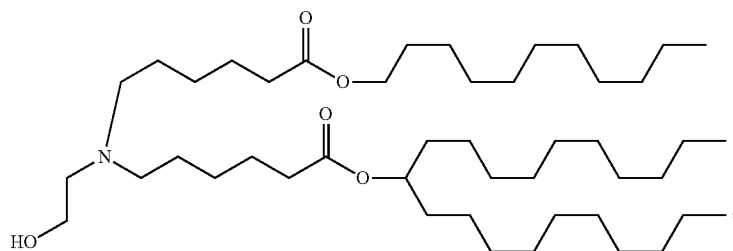


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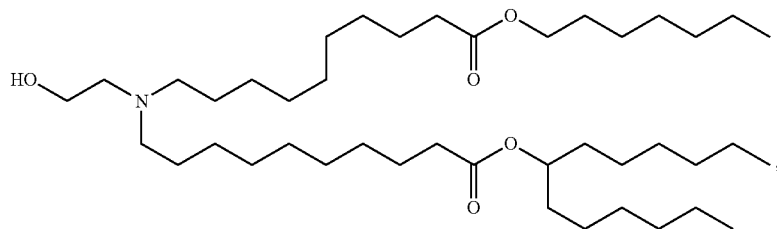
(Compound 184)



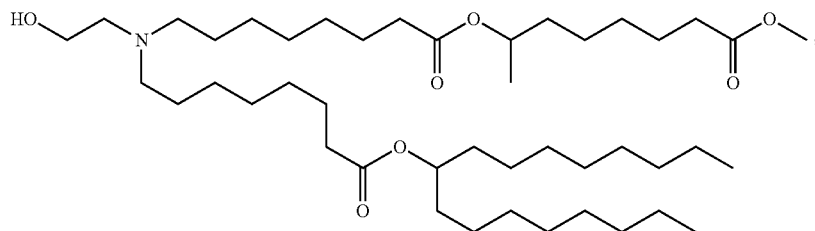
(Compound 185)



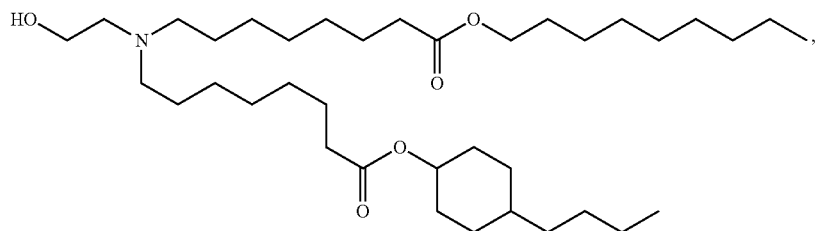
(Compound 186)



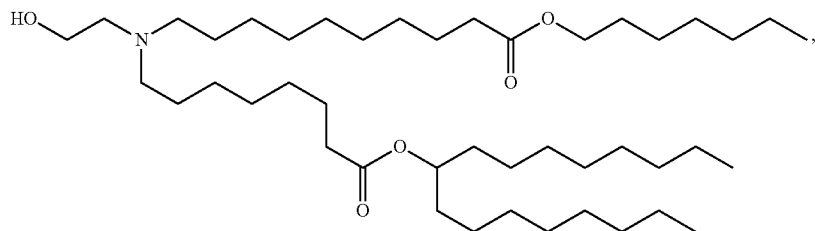
(Compound 187)



(Compound 188)

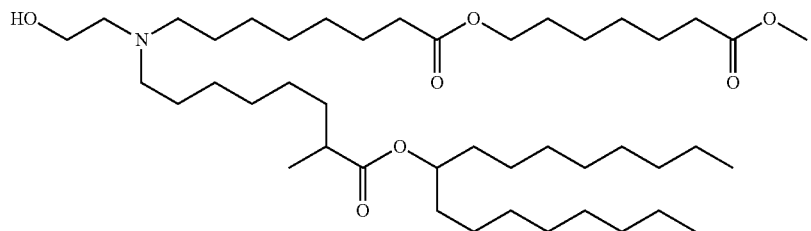


(Compound 189)

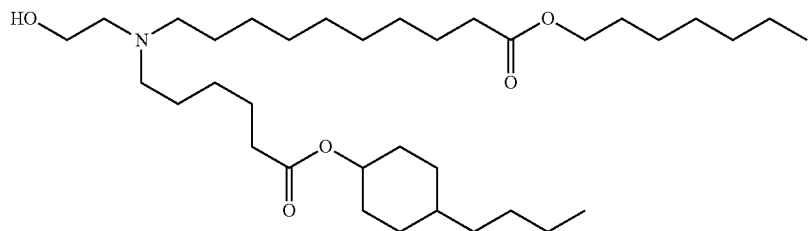


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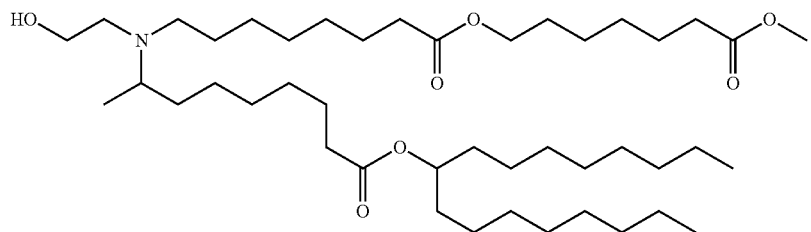
(Compound 190)



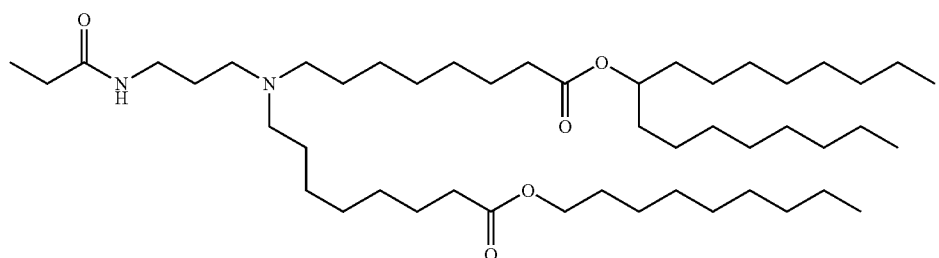
(Compound 191)



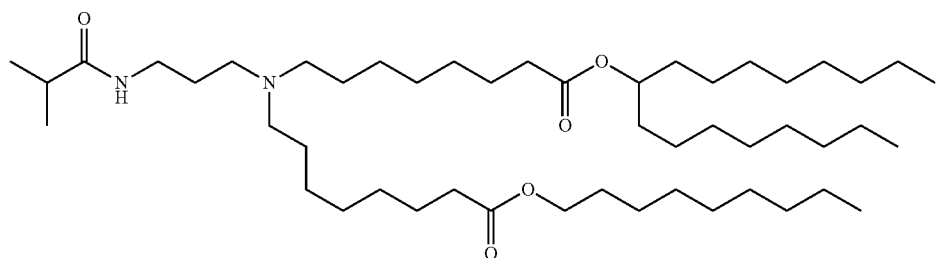
(Compound 192)



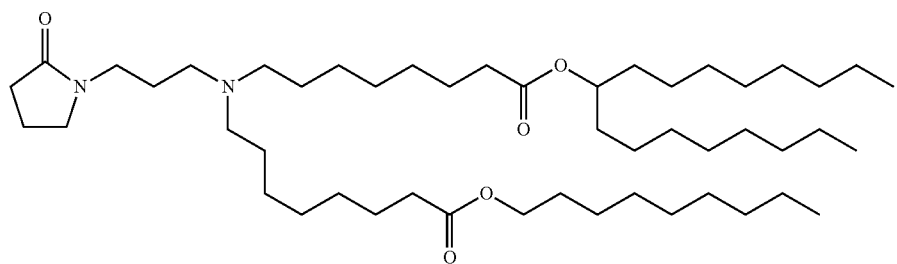
(Compound 193)



(Compound 194)

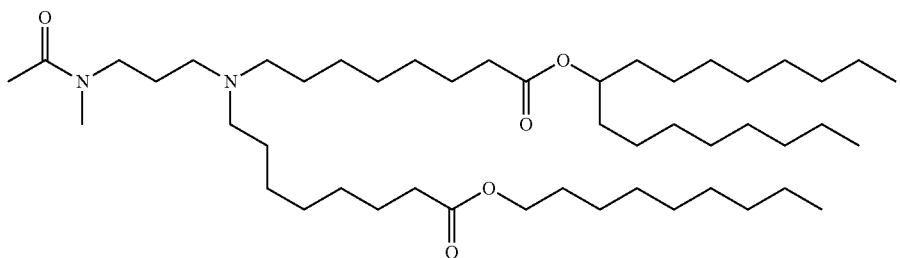


(Compound 195)

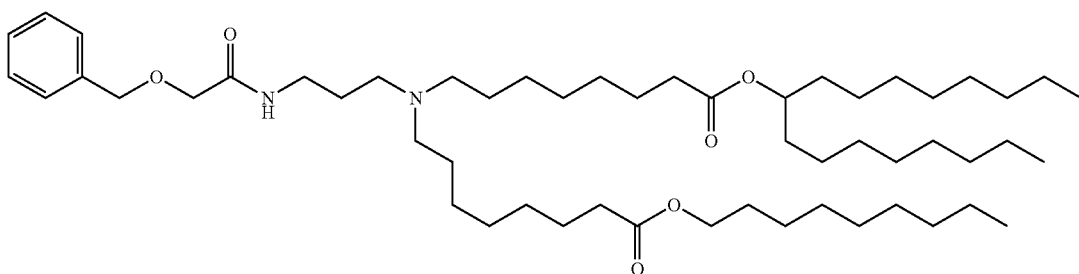


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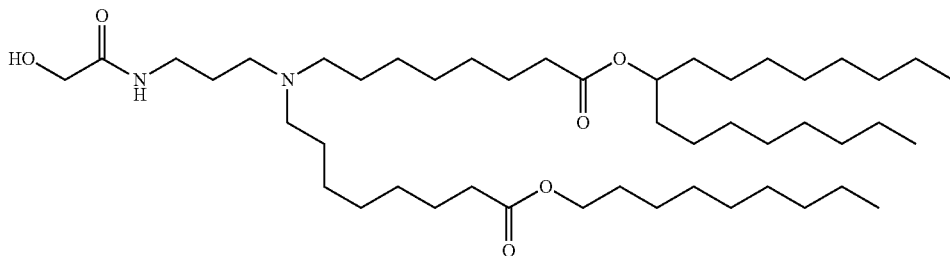
(Compound 196)



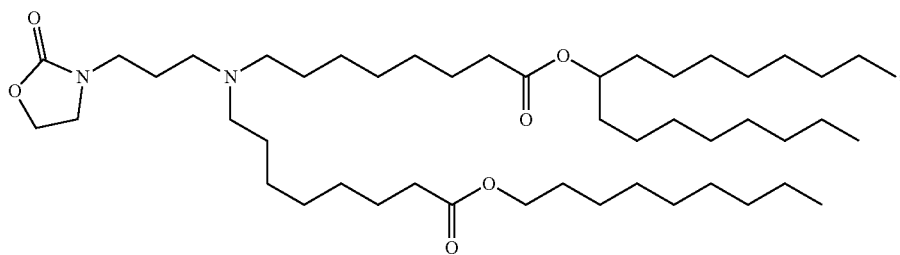
(Compound 197)



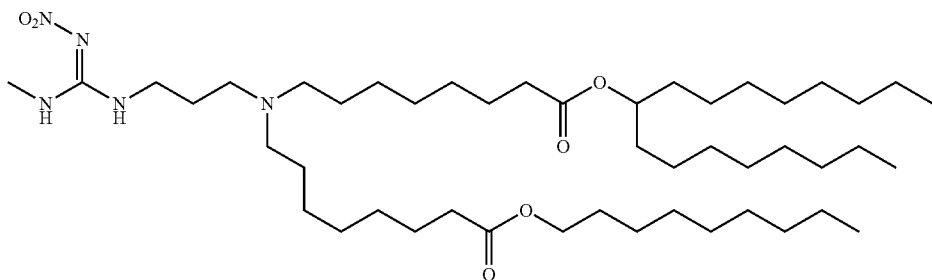
(Compound 198)



(Compound 199)

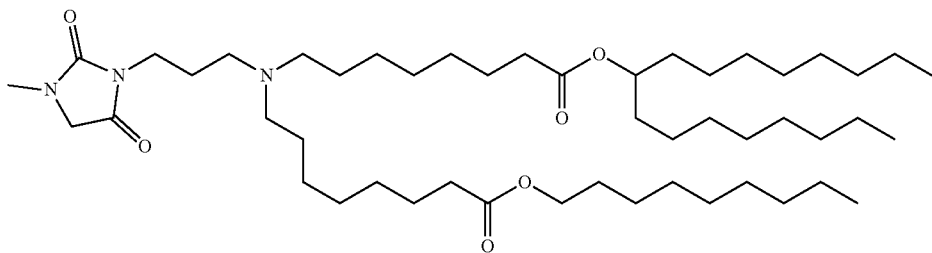


(Compound 200)

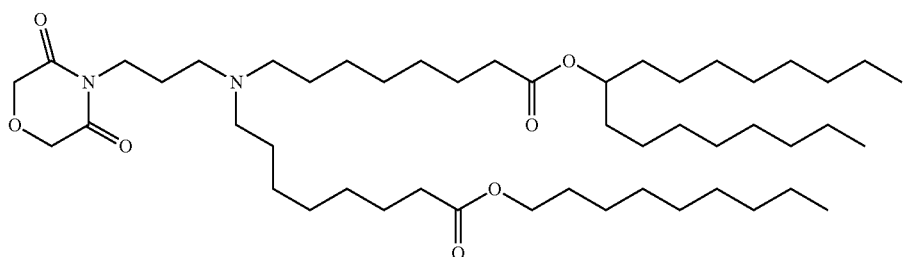


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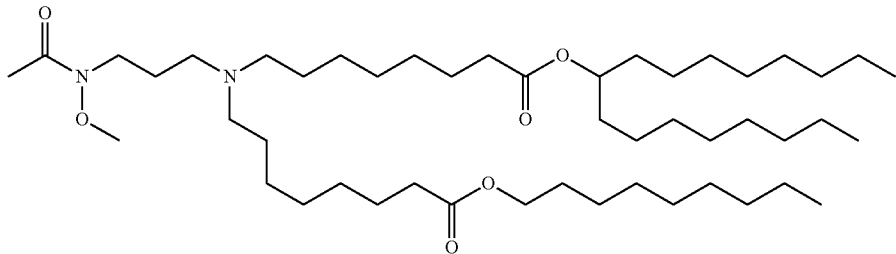
(Compound 201)



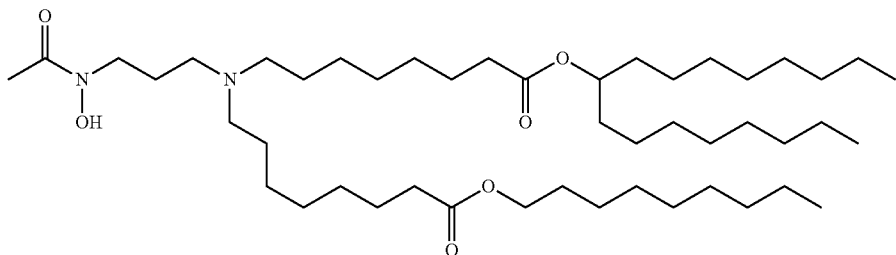
(Compound 202)



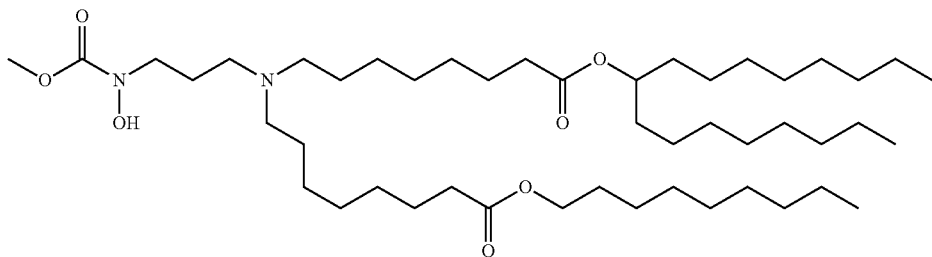
(Compound 203)



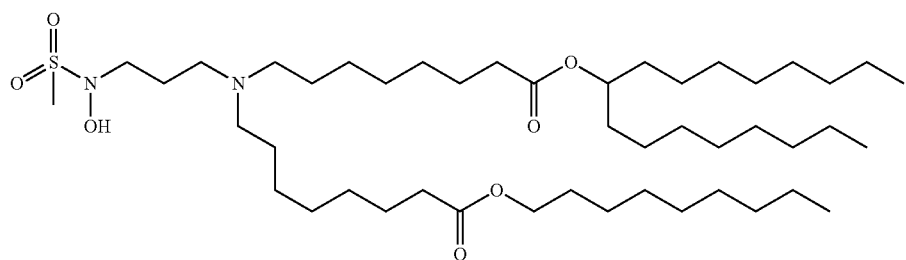
(Compound 204)



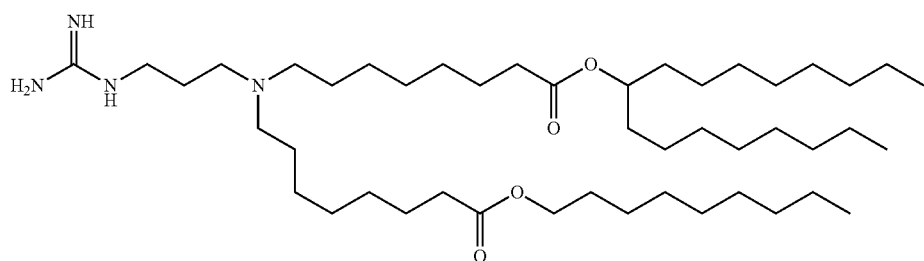
(Compound 205)



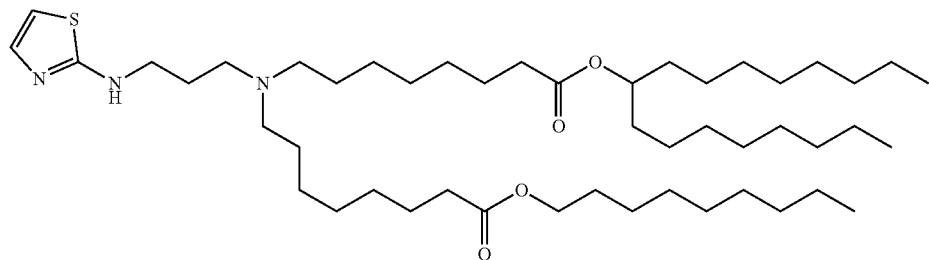
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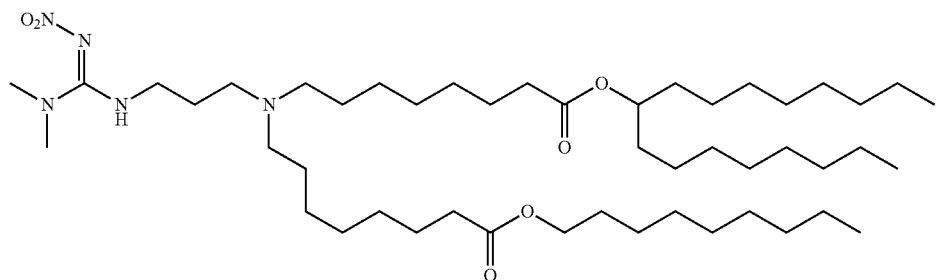
(Compound 206)



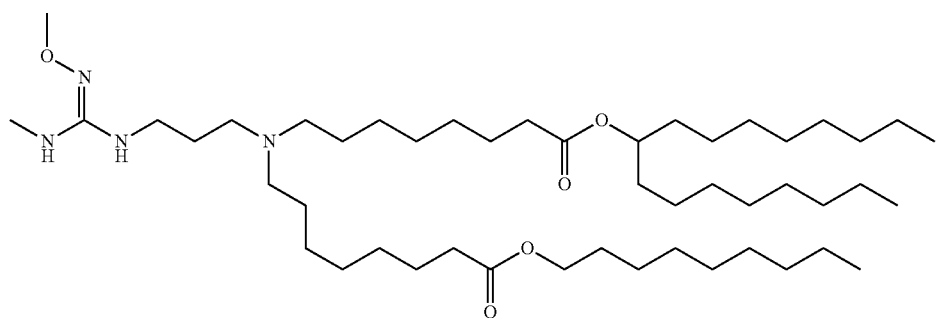
(Compound 207)



(Compound 208)



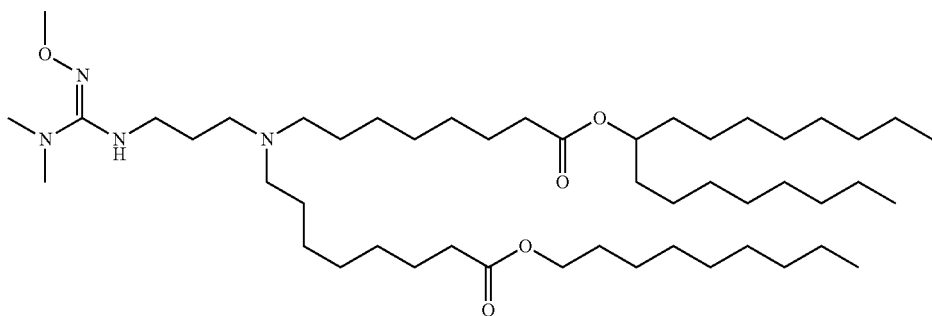
(Compound 209)



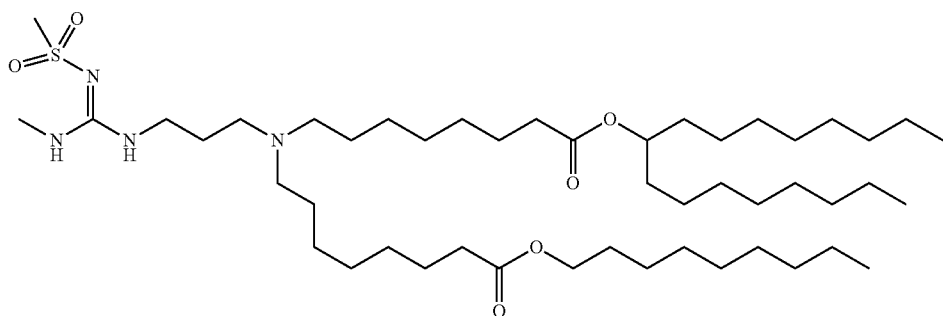
(Compound 210)

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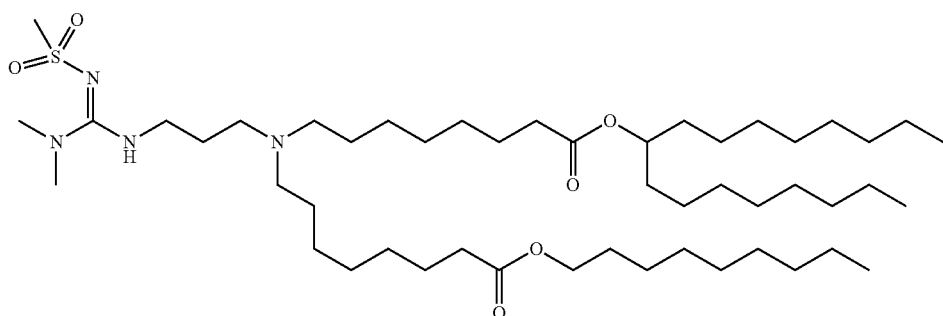
(Compound 211)



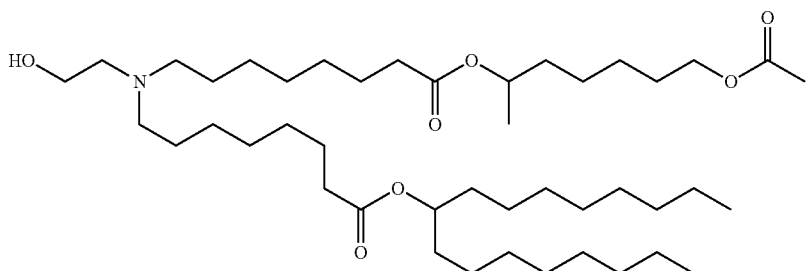
(Compound 212)



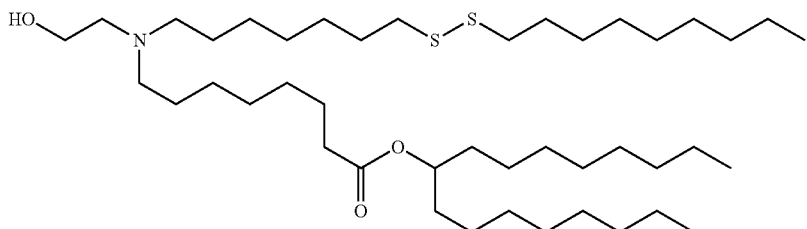
(Compound 213)



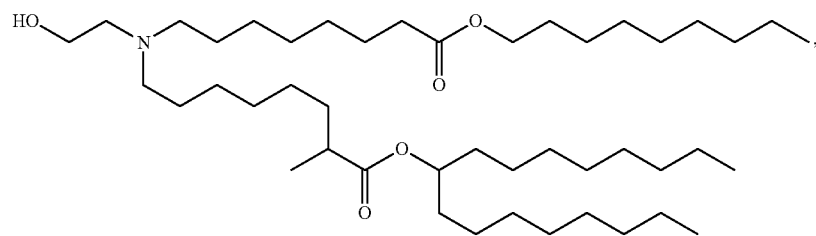
(Compound 214)



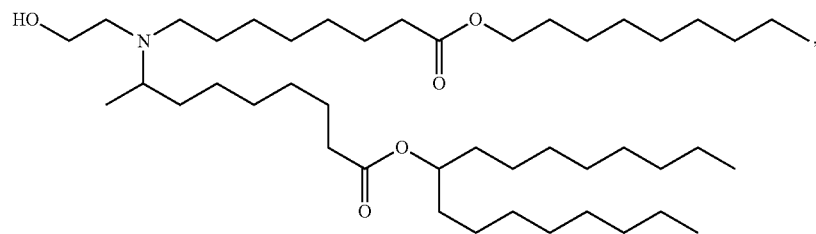
(Compound 215)



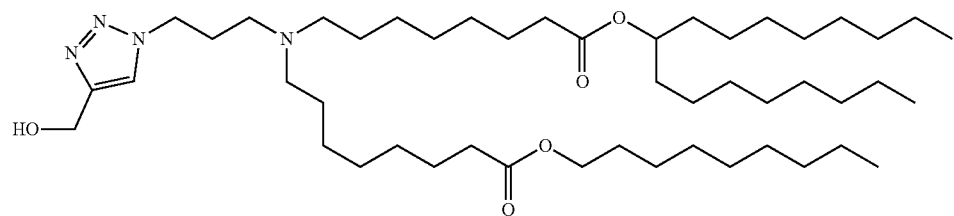
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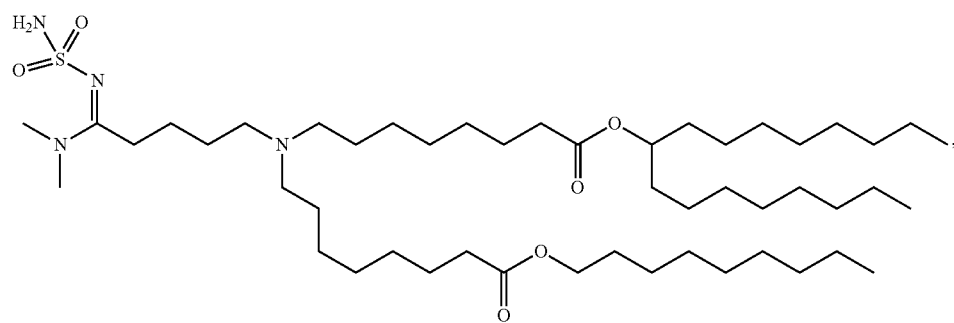
(Compound 216)



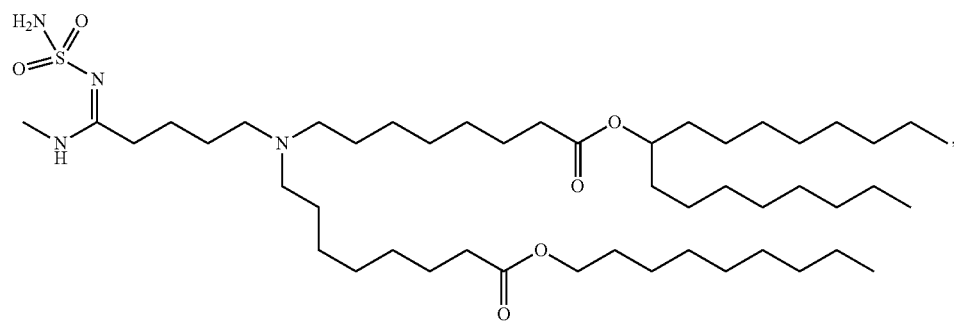
(Compound 217)



(Compound 218)



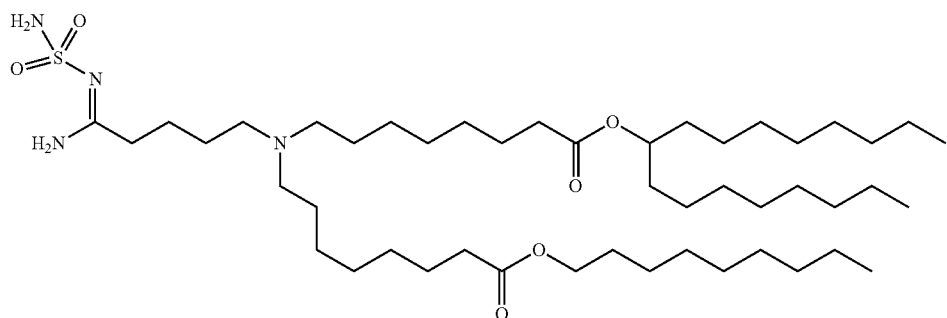
(Compound 219)



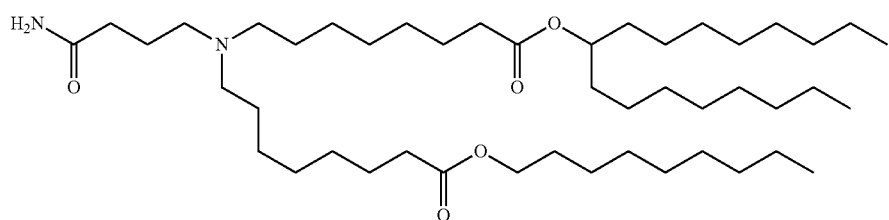
(Compound 220)

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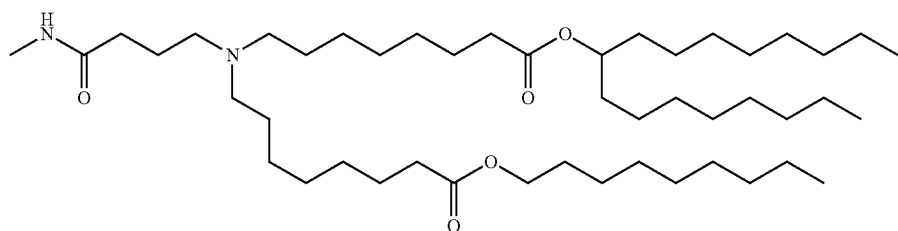
(Compound 221)



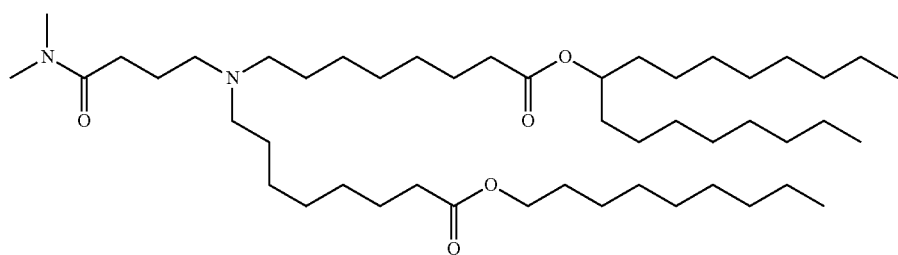
(Compound 222)



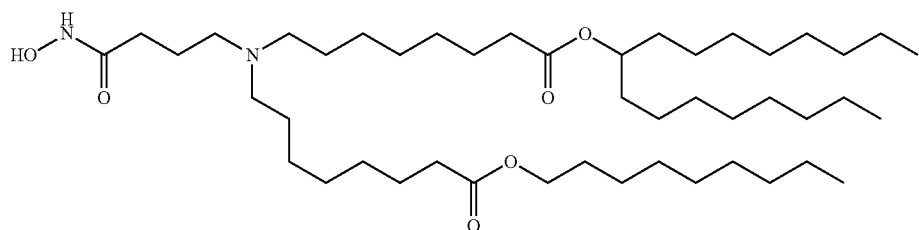
(Compound 223)



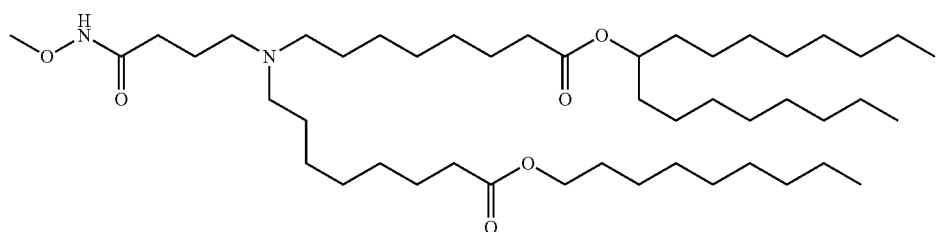
(Compound 224)



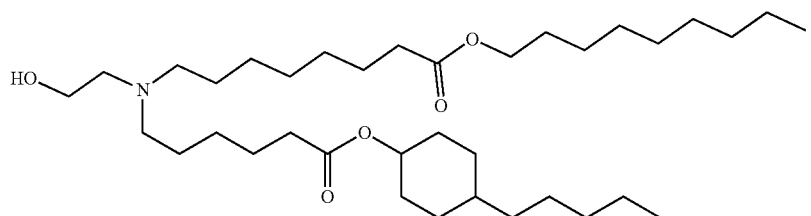
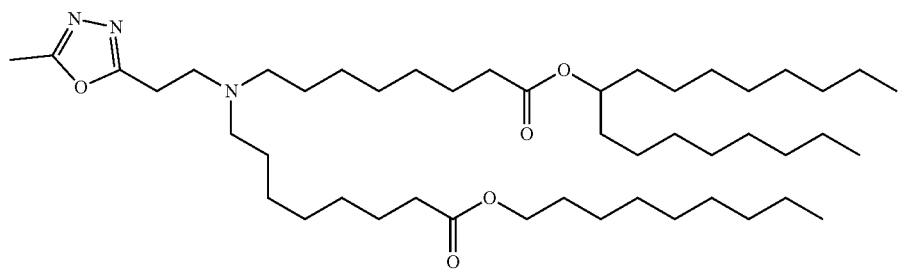
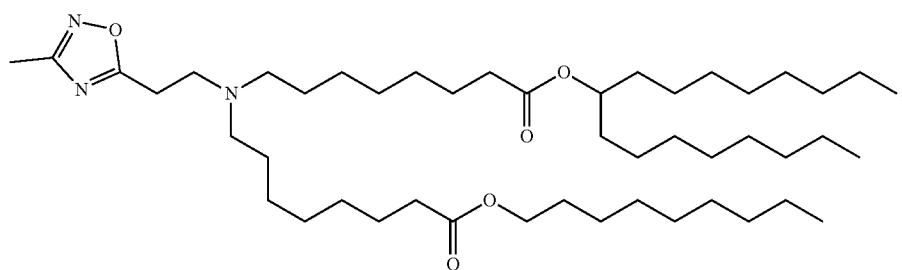
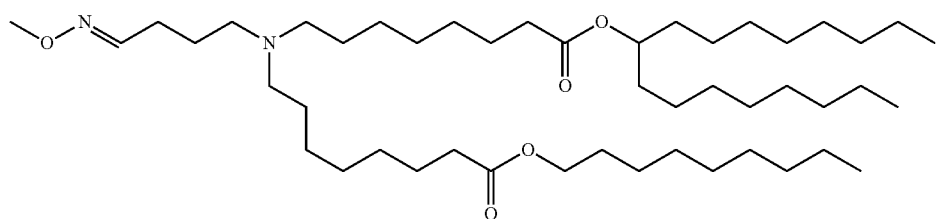
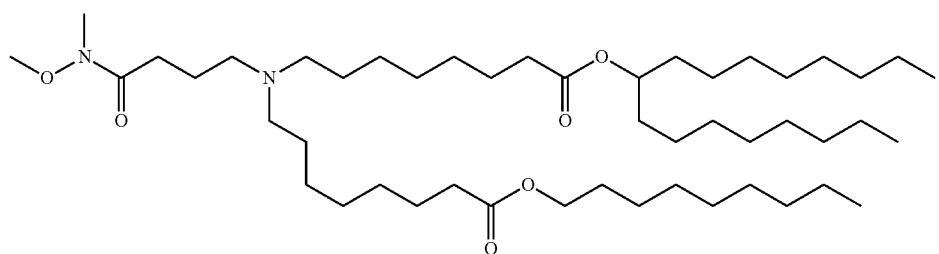
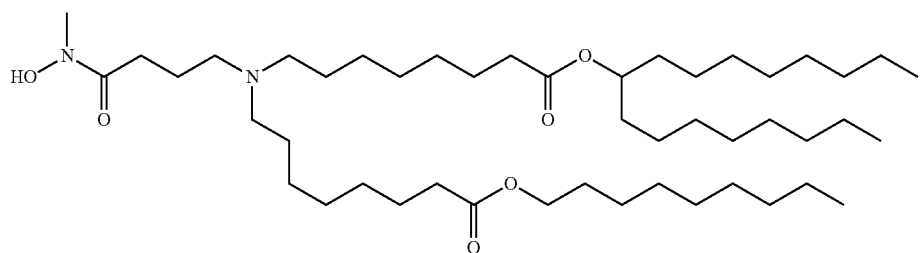
(Compound 225)



(Compound 226)

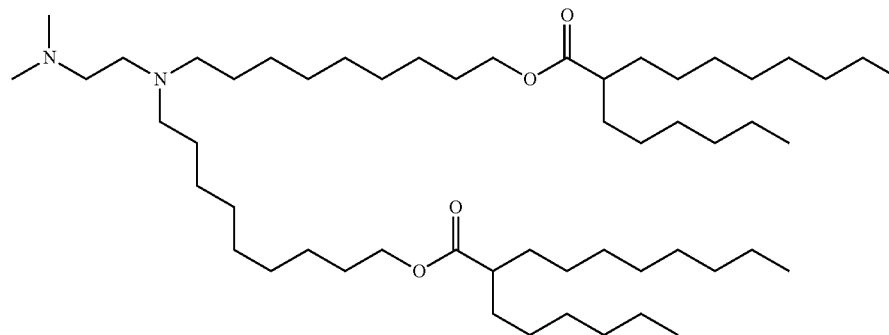


-continued



and salts and isomers thereof.

[0665] In some embodiments, a nanoparticle comprises the following compound:



or salts and isomers thereof.

[0666] In some embodiments, the disclosure features a nanoparticle composition including a lipid component comprising a compound as described herein (e.g., a compound according to Formula (I), (IA), (II), (IIa), (IIb), (IIc), (IId) or (Ile)).

[0667] In some embodiments, the disclosure features a pharmaceutical composition comprising a nanoparticle composition according to the preceding embodiments and a pharmaceutically acceptable carrier. For example, the pharmaceutical composition is refrigerated or frozen for storage and/or shipment (e.g., being stored at a temperature of 4° C. or lower, such as a temperature between about -150° C. and about 0° C. or between about -80° C. and about -20° C. (e.g., about -5° C., -10° C., -15° C., -20° C., -25° C., -30° C., -40° C., -50° C., -60° C., -70° C., -80° C., -90° C., -130° C. or -150° C.)). For example, the pharmaceutical composition is a solution that is refrigerated for storage and/or shipment at, for example, about -20° C., -30° C., -40° C., -50° C., -60° C., -70° C., or -80° C.

[0668] In some embodiments, the disclosure provides a method of delivering a therapeutic and/or prophylactic (e.g., RNA, such as mRNA) to a cell (e.g., a mammalian cell). This method includes the step of administering to a subject (e.g., a mammal, such as a human) a nanoparticle composition including (i) a lipid component including a phospholipid (such as a polyunsaturated lipid), a PEG lipid, a structural lipid, and a compound of Formula (I), (IA), (II), (IIa), (IIb), (IIc), (IId) or (Ile) and (ii) a therapeutic and/or prophylactic, in which administering involves contacting the cell with the nanoparticle composition, whereby the therapeutic and/or prophylactic is delivered to the cell.

[0669] In some embodiments, the disclosure provides a method of producing a polypeptide of interest in a cell (e.g., a mammalian cell). The method includes the step of contacting the cell with a nanoparticle composition including (i) a lipid component including a phospholipid (such as a polyunsaturated lipid), a PEG lipid, a structural lipid, and a compound of Formula (I), (IA), (II), (IIa), (IIb), (IIc), (IId) or (Ile) and (ii) an mRNA encoding the polypeptide of interest, whereby the mRNA is capable of being translated in the cell to produce the polypeptide.

[0670] In some embodiments, the disclosure provides a method of treating a disease or disorder in a mammal (e.g., a human) in need thereof. The method includes the step of

administering to the mammal a therapeutically effective amount of a nanoparticle composition including (i) a lipid component including a phospholipid (such as a polyunsaturated lipid), a PEG lipid, a structural lipid, and a compound of Formula (I), (IA), (II), (IIa), (IIb), (IIc), (IId) or (Ile) and (ii) a therapeutic and/or prophylactic (e.g., an mRNA). In some embodiments, the disease or disorder is characterized by dysfunctional or aberrant protein or polypeptide activity. For example, the disease or disorder is selected from the group consisting of rare diseases, infectious diseases, cancer and proliferative diseases, genetic diseases (e.g., cystic fibrosis), autoimmune diseases, diabetes, neurodegenerative diseases, cardio- and reno-vascular diseases, and metabolic diseases.

[0671] In some embodiments, the disclosure provides a method of delivering (e.g., specifically delivering) a therapeutic and/or prophylactic to a mammalian organ (e.g., a liver, spleen, lung, or femur). This method includes the step of administering to a subject (e.g., a mammal) a nanoparticle composition including (i) a lipid component including a phospholipid, a PEG lipid, a structural lipid, and a compound of Formula (I), (IA), (II), (IIa), (IIb), (IIc), (IId) or (Ile) and (ii) a therapeutic and/or prophylactic (e.g., an mRNA), in which administering involves contacting the cell with the nanoparticle composition, whereby the therapeutic and/or prophylactic is delivered to the target organ (e.g., a liver, spleen, lung, or femur).

[0672] In some embodiments, the disclosure features a method for the enhanced delivery of a therapeutic and/or prophylactic (e.g., an mRNA) to a target tissue (e.g., a liver, spleen, lung, or femur). This method includes administering to a subject (e.g., a mammal) a nanoparticle composition, the composition including (i) a lipid component including a compound of Formula (I), (IA), (II), (IIa), (IIb), (IIc), (IId) or (Ile), a phospholipid, a structural lipid, and a PEG lipid; and (ii) a therapeutic and/or prophylactic, the administering including contacting the target tissue with the nanoparticle composition, whereby the therapeutic and/or prophylactic is delivered to the target tissue.

[0673] In some embodiments, the disclosure features a method of lowering immunogenicity comprising introducing the nanoparticle composition of the disclosure into cells, wherein the nanoparticle composition reduces the induction

of the cellular immune response of the cells to the nanoparticle composition, as compared to the induction of the cellular immune response in cells induced by a reference composition which comprises a reference lipid instead of a compound of Formula (I), (IA), (II), (IIa), (IIb), (IIc), (IId) or (IIE). For example, the cellular immune response is an innate immune response, an adaptive immune response, or both. The disclosure also includes methods of synthesizing a compound of Formula (I), (IA), (II), (IIa), (IIb), (IIc), (IId) or (IIE) and methods of making a nanoparticle composition including a lipid component comprising the compound of Formula (I), (IA), (II), (IIa), (IIb), (IIc), (IId) or (IIE).

Modes of Vaccine Administration

[0674] Respiratory virus RNA (e.g., mRNA) vaccines may be administered by any route which results in a therapeutically effective outcome. These include, but are not limited, to intradermal, intramuscular, and/or subcutaneous administration. The present disclosure provides methods comprising administering RNA (e.g., mRNA) vaccines to a subject in need thereof. The exact amount required will vary from subject to subject, depending on the species, age, and general condition of the subject, the severity of the disease, the particular composition, its mode of administration, its mode of activity, and the like. Respiratory virus RNA (e.g., mRNA) vaccine compositions are typically formulated in dosage unit form for ease of administration and uniformity of dosage. It will be understood, however, that the total daily usage of RNA (e.g., mRNA) vaccine compositions may be decided by the attending physician within the scope of sound medical judgment. The specific therapeutically effective, prophylactically effective, or appropriate imaging dose level for any particular patient will depend upon a variety of factors including the disorder being treated and the severity of the disorder; the activity of the specific compound employed; the specific composition employed; the age, body weight, general health, sex and diet of the patient; the time of administration, route of administration, and rate of excretion of the specific compound employed; the duration of the treatment; drugs used in combination or coincidental with the specific compound employed; and like factors well known in the medical arts. In some embodiments, respiratory virus RNA (e.g., mRNA) vaccine compositions may be administered at dosage levels sufficient to deliver 0.0001 mg/kg to 100 mg/kg, 0.001 mg/kg to 0.05 mg/kg, 0.005 mg/kg to 0.05 mg/kg, 0.001 mg/kg to 0.005 mg/kg, 0.05 mg/kg to 0.5 mg/kg, 0.01 mg/kg to 50 mg/kg, 0.1 mg/kg to 40 mg/kg, 0.5 mg/kg to 30 mg/kg, 0.01 mg/kg to 10 mg/kg, 0.1 mg/kg to 10 mg/kg, or 1 mg/kg to 25 mg/kg, of subject body weight per day, one or more times a day, per week, per month, etc. to obtain the desired therapeutic, diagnostic, prophylactic, or imaging effect (see, e.g., the range of unit doses described in International Publication No WO2013078199, the contents of which are herein incorporated by reference in their entirety). The desired dosage may be delivered three times a day, two times a day, once a day, every other day, every third day, every week, every two weeks, every three weeks, every four weeks, every 2 months, every three months, every 6 months, etc. In some embodiments, the desired dosage may be delivered using multiple administrations (e.g., two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, or more administrations). When multiple administrations are employed, split dosing regimens such as those described

herein may be used. In exemplary embodiments, respiratory virus RNA (e.g., mRNA) vaccine compositions may be administered at dosage levels sufficient to deliver 0.0005 mg/kg to 0.01 mg/kg, e.g., about 0.0005 mg/kg to about 0.0075 mg/kg, e.g., about 0.0005 mg/kg, about 0.001 mg/kg, about 0.002 mg/kg, about 0.003 mg/kg, about 0.004 mg/kg or about 0.005 mg/kg.

[0675] In some embodiments, respiratory virus RNA (e.g., mRNA) vaccine compositions may be administered once or twice (or more) at dosage levels sufficient to deliver 0.025 mg/kg to 0.250 mg/kg, 0.025 mg/kg to 0.500 mg/kg, 0.025 mg/kg to 0.750 mg/kg, or 0.025 mg/kg to 1.0 mg/kg.

[0676] In some embodiments, respiratory virus RNA (e.g., mRNA) vaccine compositions may be administered twice (e.g., Day 0 and Day 7, Day 0 and Day 14, Day 0 and Day 21, Day 0 and Day 28, Day 0 and Day 60, Day 0 and Day 90, Day 0 and Day 120, Day 0 and Day 150, Day 0 and Day 180, Day 0 and 3 months later, Day 0 and 6 months later, Day 0 and 9 months later, Day 0 and 12 months later, Day 0 and 18 months later, Day 0 and 2 years later, Day 0 and 5 years later, or Day 0 and 10 years later) at a total dose of or at dosage levels sufficient to deliver a total dose of 0.0100 mg, 0.025 mg, 0.050 mg, 0.075 mg, 0.100 mg, 0.125 mg, 0.150 mg, 0.175 mg, 0.200 mg, 0.225 mg, 0.250 mg, 0.275 mg, 0.300 mg, 0.325 mg, 0.350 mg, 0.375 mg, 0.400 mg, 0.425 mg, 0.450 mg, 0.475 mg, 0.500 mg, 0.525 mg, 0.550 mg, 0.575 mg, 0.600 mg, 0.625 mg, 0.650 mg, 0.675 mg, 0.700 mg, 0.725 mg, 0.750 mg, 0.775 mg, 0.800 mg, 0.825 mg, 0.850 mg, 0.875 mg, 0.900 mg, 0.925 mg, 0.950 mg, 0.975 mg, or 1.0 mg. Higher and lower dosages and frequency of administration are encompassed by the present disclosure. For example, a respiratory virus RNA (e.g., mRNA) vaccine composition may be administered three or four times.

[0677] In some embodiments, respiratory virus RNA (e.g., mRNA) vaccine compositions may be administered twice (e.g., Day 0 and Day 7, Day 0 and Day 14, Day 0 and Day 21, Day 0 and Day 28, Day 0 and Day 60, Day 0 and Day 90, Day 0 and Day 120, Day 0 and Day 150, Day 0 and Day 180, Day 0 and 3 months later, Day 0 and 6 months later, Day 0 and 9 months later, Day 0 and 12 months later, Day 0 and 18 months later, Day 0 and 2 years later, Day 0 and 5 years later, or Day 0 and 10 years later) at a total dose of or at dosage levels sufficient to deliver a total dose of 0.010 mg, 0.025 mg, 0.100 mg or 0.400 mg.

[0678] In some embodiments, the respiratory virus RNA (e.g., mRNA) vaccine for use in a method of vaccinating a subject is administered to the subject as a single dosage of between 10 µg/kg and 400 µg/kg of the nucleic acid vaccine (in an effective amount to vaccinate the subject). In some embodiments the RNA (e.g., mRNA) vaccine for use in a method of vaccinating a subject is administered to the subject as a single dosage of between 10 µg and 400 µg of the nucleic acid vaccine (in an effective amount to vaccinate the subject). In some embodiments, a respiratory virus RNA (e.g., mRNA) vaccine for use in a method of vaccinating a subject is administered to the subject as a single dosage of 25-1000 µg (e.g., a single dosage of mRNA encoding hMPV, PIV3, RSV, MeV and/or BetaCoV antigen). In some embodiments, a respiratory virus RNA (e.g., mRNA) vaccine is administered to the subject as a single dosage of 25, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950 or 1000 µg. For example, a respiratory virus RNA (e.g., mRNA) vaccine may be

administered to a subject as a single dose of 25-100, 25-500, 50-100, 50-500, 50-1000, 100-500, 100-1000, 250-500, 250-1000, or 500-1000 μ g. In some embodiments, a respiratory virus RNA (e.g., mRNA) vaccine for use in a method of vaccinating a subject is administered to the subject as two dosages, the combination of which equals 25-1000 μ g of the respiratory virus RNA (e.g., mRNA) vaccine.

[0679] A respiratory virus RNA (e.g., mRNA) vaccine pharmaceutical composition described herein can be formulated into a dosage form described herein, such as an intranasal, intratracheal, or injectable (e.g., intravenous, intraocular, intravitreal, intramuscular, intradermal, intracardiac, intraperitoneal, and subcutaneous).

Respiratory Virus RNA (e.g., mRNA) Vaccine Formulations and Methods of Use

[0680] Some aspects of the present disclosure provide formulations of the respiratory virus RNA (e.g., mRNA) vaccine, wherein the RNA (e.g., mRNA) vaccine is formulated in an effective amount to produce an antigen specific immune response in a subject (e.g., production of antibodies specific to an hMPV, PIV3, RSV, MeV and/or BetaCoV antigenic polypeptide). "An effective amount" is a dose of an RNA (e.g., mRNA) vaccine effective to produce an antigen-specific immune response. Also provided herein are methods of inducing an antigen-specific immune response in a subject.

[0681] In some embodiments, the antigen-specific immune response is characterized by measuring an anti-hMPV, anti-PIV3, anti-RSV, anti-MeV and/or anti-BetaCoV antigenic polypeptide antibody titer produced in a subject administered a respiratory virus RNA (e.g., mRNA) vaccine as provided herein. An antibody titer is a measurement of the amount of antibodies within a subject, for example, antibodies that are specific to a particular antigen (e.g., an anti-hMPV, anti-PIV3, anti-RSV, anti-MeV and/or anti-BetaCoV antigenic polypeptide) or epitope of an antigen. Antibody titer is typically expressed as the inverse of the greatest dilution that provides a positive result. Enzyme-linked immunosorbent assay (ELISA) is a common assay for determining antibody titers, for example.

[0682] In some embodiments, an antibody titer is used to assess whether a subject has had an infection or to determine whether immunizations are required. In some embodiments, an antibody titer is used to determine the strength of an autoimmune response, to determine whether a booster immunization is needed, to determine whether a previous vaccine was effective, and to identify any recent or prior infections. In accordance with the present disclosure, an antibody titer may be used to determine the strength of an immune response induced in a subject by the respiratory virus RNA (e.g., mRNA) vaccine.

[0683] In some embodiments, an anti-antigenic polypeptide (e.g., an anti-hMPV, anti-PIV3, anti-RSV, anti-MeV and/or anti-BetaCoV antigenic polypeptide) antibody titer produced in a subject is increased by at least 1 log relative to a control. For example, anti-antigenic polypeptide antibody titer produced in a subject may be increased by at least 1.5, at least 2, at least 2.5, or at least 3 log relative to a control. In some embodiments, the anti-antigenic polypeptide antibody titer produced in the subject is increased by 1, 1.5, 2, 2.5 or 3 log relative to a control. In some embodiments, the anti-antigenic polypeptide antibody titer produced in the subject is increased by 1-3 log relative to a control. For example, the anti-antigenic polypeptide anti-

body titer produced in a subject may be increased by 1-1.5, 1-2, 1-2.5, 1-3, 1.5-2, 1.5-2.5, 1.5-3, 2-2.5, 2-3, or 2.5-3 log relative to a control. In some embodiments, the anti-antigenic polypeptide (e.g., an anti-hMPV, anti-PIV3, anti-RSV, anti-MeV and/or anti-BetaCoV antigenic polypeptide) antibody titer produced in a subject is increased at least 2 times relative to a control. For example, the anti-antigenic polypeptide antibody titer produced in a subject may be increased at least 3 times, at least 4 times, at least 5 times, at least 6 times, at least 7 times, at least 8 times, at least 9 times, or at least 10 times relative to a control. In some embodiments, the anti-antigenic polypeptide antibody titer produced in the subject is increased 2, 3, 4, 5, 6, 7, 8, 9, or 10 times relative to a control. In some embodiments, the anti-antigenic polypeptide antibody titer produced in a subject is increased 2-10 times relative to a control. For example, the anti-antigenic polypeptide antibody titer produced in a subject may be increased 2-10, 2-9, 2-8, 2-7, 2-6, 2-5, 2-4, 2-3, 3-10, 3-9, 3-8, 3-7, 3-6, 3-5, 3-4, 4-10, 4-9, 4-8, 4-7, 4-6, 4-5, 5-10, 5-9, 5-8, 5-7, 5-6, 6-10, 6-9, 6-8, 6-7, 7-10, 7-9, 7-8, 8-10, 8-9, or 9-10 times relative to a control.

[0684] A control, in some embodiments, is the anti-antigenic polypeptide (e.g., an anti-hMPV, anti-PIV3, anti-RSV, anti-MeV and/or anti-BetaCoV antigenic polypeptide) antibody titer produced in a subject who has not been administered a respiratory virus RNA (e.g., mRNA) vaccine of the present disclosure. In some embodiments, a control is an anti-antigenic polypeptide (e.g., an anti-hMPV, anti-PIV3, anti-RSV, anti-MeV and/or anti-BetaCoV antigenic polypeptide) antibody titer produced in a subject who has been administered a live attenuated hMPV, PIV3, RSV, MeV and/or BetaCoV vaccine. An attenuated vaccine is a vaccine produced by reducing the virulence of a viable (live). An attenuated virus is altered in a manner that renders it harmless or less virulent relative to live, unmodified virus. In some embodiments, a control is an anti-antigenic polypeptide (e.g., an anti-hMPV, anti-PIV3, anti-RSV, anti-MeV and/or anti-BetaCoV antigenic polypeptide) antibody titer produced in a subject administered inactivated hMPV, PIV3, RSV, MeV and/or BetaCoV vaccine. In some embodiments, a control is an anti-antigenic polypeptide (e.g., an anti-hMPV, anti-PIV3, anti-RSV, anti-MeV and/or anti-BetaCoV antigenic polypeptide) antibody titer produced in a subject administered a recombinant or purified hMPV, PIV3, RSV, MeV and/or BetaCoV protein vaccine. Recombinant protein vaccines typically include protein antigens that either have been produced in a heterologous expression system (e.g., bacteria or yeast) or purified from large amounts of the pathogenic organism. In some embodiments, a control is an anti-antigenic polypeptide (e.g., an anti-hMPV, anti-PIV3, anti-RSV, anti-MeV and/or anti-BetaCoV antigenic polypeptide) antibody titer produced in a subject who has been administered an hMPV, PIV3, RSV, MeV and/or BetaCoV virus-like particle (VLP) vaccine. For example, an hMPV VLP vaccine used as a control may be a hMPV VLPs, comprising (or consisting of) viral matrix (M) and fusion (F) proteins, generated by expressing viral proteins in suspension-adapted human embryonic kidney epithelial (293-F) cells (see, e.g., Cox R G et al., *J Virol.* 2014 June; 88(11): 6368-6379, the contents of which are herein incorporated by reference).

[0685] In some embodiments, an effective amount of a respiratory virus RNA (e.g., mRNA) vaccine is a dose that is reduced compared to the standard of care dose of a

recombinant hMPV, PIV3, RSV, MeV and/or BetaCoV protein vaccine. A “standard of care,” as provided herein, refers to a medical or psychological treatment guideline and can be general or specific. “Standard of care” specifies appropriate treatment based on scientific evidence and collaboration between medical professionals involved in the treatment of a given condition. It is the diagnostic and treatment process that a physician/clinician should follow for a certain type of patient, illness or clinical circumstance. A “standard of care dose,” as provided herein, refers to the dose of a recombinant or purified hMPV, PIV3, RSV, MeV and/or BetaCoV protein vaccine, or a live attenuated or inactivated hMPV, PIV3, RSV, MeV and/or BetaCoV vaccine, that a physician/clinician or other medical professional would administer to a subject to treat or prevent hMPV, PIV3, RSV, MeV and/or BetaCoV, or a hMPV-, PIV3-, RSV-, MeV- and/or BetaCoV-related condition, while following the standard of care guideline for treating or preventing hMPV, PIV3, RSV, MeV and/or BetaCoV, or a hMPV-, PIV3-, RSV-, MeV- and/or BetaCoV-related condition.

[0686] In some embodiments, the anti-antigenic polypeptide (e.g., an anti-hMPV, anti-PIV3, anti-RSV, anti-MeV and/or anti-BetaCoV antigenic polypeptide) antibody titer produced in a subject administered an effective amount of a respiratory virus RNA (e.g., mRNA) vaccine is equivalent to an anti-antigenic polypeptide (e.g., an anti-hMPV, anti-PIV3, anti-RSV, anti-MeV and/or anti-BetaCoV antigenic polypeptide) antibody titer produced in a control subject administered a standard of care dose of a recombinant or purified hMPV, PIV3, RSV, MeV and/or BetaCoV protein vaccine or a live attenuated or inactivated hMPV, PIV3, RSV, MeV and/or BetaCoV vaccine.

[0687] In some embodiments, an effective amount of a respiratory virus RNA (e.g., mRNA) vaccine is a dose equivalent to an at least 2-fold reduction in a standard of care dose of a recombinant or purified hMPV, PIV3, RSV, MeV and/or BetaCoV protein vaccine. For example, an effective amount of a respiratory virus RNA (e.g., mRNA) vaccine may be a dose equivalent to an at least 3-fold, at least 4-fold, at least 5-fold, at least 6-fold, at least 7-fold, at least 8-fold, at least 9-fold, or at least 10-fold reduction in a standard of care dose of a recombinant or purified hMPV, PIV3, RSV, MeV and/or BetaCoV protein vaccine. In some embodiments, an effective amount of a respiratory virus RNA (e.g., mRNA) vaccine is a dose equivalent to an at least 100-fold, at least 500-fold, or at least 1000-fold reduction in a standard of care dose of a recombinant or purified hMPV, PIV3, RSV, MeV and/or BetaCoV protein vaccine. In some embodiments, an effective amount of a respiratory virus RNA (e.g., mRNA) vaccine is a dose equivalent to a 2-, 3-, 4-, 5-, 6-, 7-, 8-, 9-, 10-, 20-, 50-, 100-, 250-, 500-, or 1000-fold reduction in a standard of care dose of a recombinant or purified hMPV, PIV3, RSV, MeV and/or BetaCoV protein vaccine. In some embodiments, the anti-antigenic polypeptide antibody titer produced in a subject administered an effective amount of a respiratory virus RNA (e.g., mRNA) vaccine is equivalent to an anti-antigenic polypeptide antibody titer produced in a control subject administered the standard of care dose of a recombinant or protein hMPV, PIV3, RSV, MeV and/or BetaCoV protein vaccine or a live attenuated or inactivated hMPV, PIV3, RSV, MeV and/or BetaCoV vaccine. In some embodiments, an effective amount of a respiratory virus RNA (e.g., mRNA) vaccine is

a dose equivalent to a 2-fold to 1000-fold (e.g., 2-fold to 100-fold, 10-fold to 1000-fold) reduction in the standard of care dose of a recombinant or purified hMPV, PIV3, RSV, MeV and/or BetaCoV protein vaccine, wherein the anti-antigenic polypeptide antibody titer produced in the subject is equivalent to an anti-antigenic polypeptide antibody titer produced in a control subject administered the standard of care dose of a recombinant or purified hMPV, PIV3, RSV, MeV and/or BetaCoV protein vaccine or a live attenuated or inactivated hMPV, PIV3, RSV, MeV and/or BetaCoV vaccine.

[0688] In some embodiments, the effective amount of a respiratory virus RNA (e.g., mRNA) vaccine is a dose equivalent to a 2 to 1000-, 2 to 900-, 2 to 800-, 2 to 700-, 2 to 600-, 2 to 500-, 2 to 400-, 2 to 300-, 2 to 200-, 2 to 100-, 2 to 90-, 2 to 80-, 2 to 70-, 2 to 60-, 2 to 50-, 2 to 40-, 2 to 30-, 2 to 20-, 2 to 10-, 2 to 9-, 2 to 8-, 2 to 7-, 2 to 6-, 2 to 5-, 2 to 4-, 2 to 3-, 3 to 1000-, 3 to 900-, 3 to 800-, 3 to 700-, 3 to 600-, 3 to 500-, 3 to 400-, 3 to 300-, 3 to 200-, 3 to 100-, 3 to 90-, 3 to 80-, 3 to 70-, 3 to 60-, 3 to 50-, 3 to 40-, 3 to 30-, 3 to 20-, 3 to 10-, 3 to 9-, 3 to 8-, 3 to 7-, 3 to 6-, 3 to 5-, 3 to 4-, 4 to 1000-, 4 to 900-, 4 to 800-, 4 to 700-, 4 to 600-, 4 to 500-, 4 to 400-, 4 to 300-, 4 to 200-, 4 to 100-, 4 to 90-, 4 to 80-, 4 to 70-, 4 to 60-, 4 to 50-, 4 to 40-, 4 to 30-, 4 to 20-, 4 to 10-, 4 to 9-, 4 to 8-, 4 to 7-, 4 to 6-, 4 to 5-, 4 to 4-, 5 to 1000-, 5 to 900-, 5 to 800-, 5 to 700-, 5 to 600-, 5 to 500-, 5 to 400-, 5 to 300-, 5 to 200-, 5 to 100-, 5 to 90-, 5 to 80-, 5 to 70-, 5 to 60-, 5 to 50-, 5 to 40-, 5 to 30-, 5 to 20-, 5 to 10-, 5 to 9-, 5 to 8-, 5 to 7-, 5 to 6-, 6 to 1000-, 6 to 900-, 6 to 800-, 6 to 700-, 6 to 600-, 6 to 500-, 6 to 400-, 6 to 300-, 6 to 200-, 6 to 100-, 6 to 90-, 6 to 80-, 6 to 70-, 6 to 60-, 6 to 50-, 6 to 40-, 6 to 30-, 6 to 20-, 6 to 10-, 6 to 9-, 6 to 8-, 6 to 7-, 7 to 1000-, 7 to 900-, 7 to 800-, 7 to 700-, 7 to 600-, 7 to 500-, 7 to 400-, 7 to 300-, 7 to 200-, 7 to 100-, 7 to 90-, 7 to 80-, 7 to 70-, 7 to 60-, 7 to 50-, 7 to 40-, 7 to 30-, 7 to 20-, 7 to 10-, 7 to 9-, 7 to 8-, 8 to 1000-, 8 to 900-, 8 to 800-, 8 to 700-, 8 to 600-, 8 to 500-, 8 to 400-, 8 to 300-, 8 to 200-, 8 to 100-, 8 to 90-, 8 to 80-, 8 to 70-, 8 to 60-, 8 to 50-, 8 to 40-, 8 to 30-, 8 to 20-, 8 to 10-, 8 to 9-, 9 to 1000-, 9 to 900-, 9 to 800-, 9 to 700-, 9 to 600-, 9 to 500-, 9 to 400-, 9 to 300-, 9 to 200-, 9 to 100-, 9 to 90-, 9 to 80-, 9 to 70-, 9 to 60-, 9 to 50-, 9 to 40-, 9 to 30-, 9 to 20-, 9 to 10-, 10 to 1000-, 10 to 900-, 10 to 800-, 10 to 700-, 10 to 600-, 10 to 500-, 10 to 400-, 10 to 300-, 10 to 200-, 10 to 100-, 10 to 90-, 10 to 80-, 10 to 70-, 10 to 60-, 10 to 50-, 10 to 40-, 10 to 30-, 10 to 20-, 20 to 1000-, 20 to 900-, 20 to 800-, 20 to 700-, 20 to 600-, 20 to 500-, 20 to 400-, 20 to 300-, 20 to 200-, 20 to 100-, 20 to 90-, 20 to 80-, 20 to 70-, 20 to 60-, 20 to 50-, 20 to 40-, 20 to 30-, 30 to 1000-, 30 to 900-, 30 to 800-, 30 to 700-, 30 to 600-, 30 to 500-, 30 to 400-, 30 to 300-, 30 to 200-, 30 to 100-, 30 to 90-, 30 to 80-, 30 to 70-, 30 to 60-, 30 to 50-, 30 to 40-, 40 to 1000-, 40 to 900-, 40 to 800-, 40 to 700-, 40 to 600-, 40 to 500-, 40 to 400-, 40 to 300-, 40 to 200-, 40 to 100-, 40 to 90-, 40 to 80-, 40 to 70-, 40 to 60-, 40 to 50-, 50 to 1000-, 50 to 900-, 50 to 800-, 50 to 700-, 50 to 600-, 50 to 500-, 50 to 400-, 50 to 300-, 50 to 200-, 50 to 100-, 50 to 90-, 50 to 80-, 50 to 70-, 50 to 60-, 60 to 1000-, 60 to 900-, 60 to 800-, 60 to 700-, 60 to 600-, 60 to 500-, 60 to 400-, 60 to 300-, 60 to 200-, 60 to 100-, 60 to 90-, 60 to 80-, 60 to 70-, 60 to 60-, 70 to 1000-, 70 to 900-, 70 to 800-, 70 to 700-, 70 to 600-, 70 to 500-, 70 to 400-, 70 to 300-, 70 to 200-, 70 to 100-, 70 to 90-, 70 to 80-, 80 to 1000-, 80 to 900-, 80 to 800-, 80 to 700-, 80 to 600-, 80 to 500-, 80 to 400-, 80 to 300-, 80 to 200-, 80 to 100-, 80 to 90-,

90 to 1000-, 90 to 900-, 90 to 800-, 90 to 700-, 90 to 600-, 90 to 500-, 90 to 400-, 90 to 300-, 90 to 200-, 90 to 100-, 100 to 1000-, 100 to 900-, 100 to 800-, 100 to 700-, 100 to 600-, 100 to 500-, 100 to 400-, 100 to 300-, 100 to 200-, 200 to 1000-, 200 to 900-, 200 to 800-, 200 to 700-, 200 to 600-, 200 to 500-, 200 to 400-, 200 to 300-, 300 to 1000-, 300 to 900-, 300 to 800-, 300 to 700-, 300 to 600-, 300 to 500-, 300 to 400-, 400 to 1000-, 400 to 900-, 400 to 800-, 400 to 700-, 400 to 600-, 400 to 500-, 500 to 1000-, 500 to 900-, 500 to 800-, 500 to 700-, 500 to 600-, 600 to 1000-, 600 to 900-, 600 to 800-, 600 to 700-, 700 to 1000-, 700 to 900-, 700 to 800-, 800 to 1000-, 800 to 900-, or 900 to 1000-fold reduction in the standard of care dose of a recombinant hMPV, PIV3, RSV, MeV and/or BetaCoV protein vaccine. In some embodiments, the anti-antigenic polypeptide antibody titer produced in the subject is equivalent to an anti-antigenic polypeptide antibody titer produced in a control subject administered the standard of care dose of a recombinant or purified hMPV, PIV3, RSV, MeV and/or BetaCoV protein vaccine or a live attenuated or inactivated hMPV, PIV3, RSV, MeV and/or BetaCoV vaccine. In some embodiments, the effective amount is a dose equivalent to (or equivalent to an at least) 2-, 3-, 4-, 5-, 6-, 7-, 8-, 9-, 10-, 20-, 30-, 40-, 50-, 60-, 70-, 80-, 90-, 100-, 110-, 120-, 130-, 140-, 150-, 160-, 170-, 180-, 190-, 200-, 210-, 220-, 230-, 240-, 250-, 260-, 270-, 280-, 290-, 300-, 310-, 320-, 330-, 340-, 350-, 360-, 370-, 380-, 390-, 400-, 410-, 420-, 430-, 440-, 450-, 460-, 470-, 480-, 490-, 500-, 510-, 520-, 530-, 540-, 550-, 560-, 570-, 580-, 590-, 600-, 610-, 620-, 630-, 640-, 650-, 660-, 670-, 680-, 690-, 700-, 710-, 720-, 730-, 740-, 750-, 760-, 770-, 780-, 790-, 800-, 810-, 820-, 830-, 840-, 850-, 860-, 870-, 880-, 890-, 900-, 910-, 920-, 930-, 940-, 950-, 960-, 970-, 980-, 990-, or 1000-fold reduction in the standard of care dose of a recombinant hMPV, PIV3, RSV, MeV and/or BetaCoV protein vaccine. In some embodiments, an anti-antigenic polypeptide antibody titer produced in the subject is equivalent to an anti-antigenic polypeptide antibody titer produced in a control subject administered the standard of care dose of a recombinant or purified hMPV, PIV3, RSV, MeV and/or BetaCoV protein vaccine or a live attenuated or inactivated hMPV, PIV3, RSV, MeV and/or BetaCoV vaccine.

[0689] In some embodiments, the effective amount of a respiratory virus RNA (e.g., mRNA) vaccine is a total dose of 50-1000 [lg. In some embodiments, the effective amount of a respiratory virus RNA (e.g., mRNA) vaccine is a total dose of 50-1000, 50-900, 50-800, 50-700, 50-600, 50-500, 50-400, 50-300, 50-200, 50-100, 50-90, 50-80, 50-70, 50-60, 60-1000, 60-900, 60-800, 60-700, 60-600, 60-500, 60-400, 60-300, 60-200, 60-100, 60-90, 60-80, 60-70, 70-1000, 70-900, 70-800, 70-700, 70-600, 70-500, 70-400, 70-300, 70-200, 70-100, 70-90, 70-80, 80-1000, 80-900, 80-800, 80-700, 80-600, 80-500, 80-400, 80-300, 80-200, 80-100, 80-90, 90-1000, 90-900, 90-800, 90-700, 90-600, 90-500, 90-400, 90-300, 90-200, 90-100, 100-1000, 100-900, 100-800, 100-700, 100-600, 100-500, 100-400, 100-300, 100-200, 200-1000, 200-900, 200-800, 200-700, 200-600, 200-500, 200-400, 200-300, 300-1000, 300-900, 300-800, 300-700, 300-600, 300-500, 300-400, 400-1000, 400-900, 400-800, 400-700, 400-600, 400-500, 500-1000, 500-900, 500-800, 500-700, 500-600, 600-1000, 600-900, 600-800, 600-700, 700-1000, 700-900, 700-800, 800-1000, 800-900, or 900-1000 µg. In some embodiments, the effective amount of a respiratory virus RNA (e.g., mRNA) vaccine is

a total dose of 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950 or 1000 µg. In some embodiments, the effective amount is a dose of 25-500 µg administered to the subject a total of two times. In some embodiments, the effective amount of a respiratory virus RNA (e.g., mRNA) vaccine is a dose of 25-500, 25-400, 25-300, 25-200, 25-100, 25-50, 50-500, 50-400, 50-300, 50-200, 50-100, 100-500, 100-400, 100-300, 100-200, 150-500, 150-400, 150-300, 150-200, 200-500, 200-400, 200-300, 250-500, 250-400, 250-300, 300-500, 300-400, 350-500, 350-400, 400-500 or 450-500 µg administered to the subject a total of two times. In some embodiments, the effective amount of a respiratory virus RNA (e.g., mRNA) vaccine is a total dose of 25, 50, 100, 150, 200, 250, 300, 350, 400, 450, or 500 µg administered to the subject a total of two times.

[0690] Examples of Additional Embodiments of the Disclosure

[0691] Additional embodiments of the present disclosure are encompassed by the following numbered paragraphs:

[0692] 1. A respiratory virus vaccine, comprising: at least one ribonucleic acid (RNA) polynucleotide having an open reading frame encoding at least one, at least two, at least three, at least four or at least five antigenic polypeptides selected from human metapneumovirus (hMPV) antigenic polypeptides or immunogenic fragments thereof, human parainfluenza virus type 3 (PIV3) antigenic polypeptides or immunogenic fragments thereof, respiratory syncytial virus (RSV) antigenic polypeptides or immunogenic fragments thereof, measles virus (MeV) antigenic polypeptides or immunogenic fragments thereof, and betacoronavirus (BetaCoV) antigenic polypeptides or immunogenic fragments thereof.

[0693] 2. The respiratory virus vaccine of paragraph 1, comprising:

[0694] at least one RNA polynucleotide having an open reading frame encoding a hMPV antigenic polypeptide or an immunogenic fragment thereof and a PIV3 antigenic polypeptide or an immunogenic fragment thereof; or

[0695] at least two RNA polynucleotides, one having an open reading frame encoding a hMPV antigenic polypeptide or an immunogenic fragment thereof and one having an open reading frame encoding a PIV3 antigenic polypeptide or an immunogenic fragment thereof.

[0696] 3. The respiratory virus vaccine of paragraph 2, wherein the hMPV antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 5-8 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 5-8, and/or wherein the PIV3 antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 12-13 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 12-13.

[0697] 4. The respiratory virus vaccine of paragraph 1, comprising:

[0698] at least one RNA polynucleotide having an open reading frame encoding a hMPV antigenic polypeptide or an immunogenic fragment thereof and a RSV antigenic polypeptide or an immunogenic fragment thereof; or

[0699] at least two RNA polynucleotides, one having an open reading frame encoding a hMPV antigenic polypeptide or an immunogenic fragment thereof and one having an

[0701] 6. The respiratory virus vaccine of paragraph 1, comprising:

[0703] at least two RNA polynucleotides, one having an open reading frame encoding a hMPV antigenic polypeptide or an immunogenic fragment thereof and one having an open reading frame encoding a MeV antigenic polypeptide or an immunogenic fragment thereof.

[0705] 8. The respiratory virus vaccine of paragraph 1, comprising:

[0707] at least two RNA polynucleotides, one having an open reading frame encoding a hMPV antigenic polypeptide or an immunogenic fragment thereof and one having an open reading frame encoding a BetaCoV antigenic polypeptide or an immunogenic fragment thereof.

[0709] 10. The respiratory virus vaccine of paragraph 1, comprising:

[0711] at least two RNA polynucleotides, one having an open reading frame encoding a PIV3 antigenic polypeptide or an immunogenic fragment thereof and one having an open reading frame encoding a RSV antigenic polypeptide or an immunogenic fragment thereof.

[0713] 12. The respiratory virus vaccine of paragraph 1, comprising:

[0715] at least two RNA polynucleotides, one having an open reading frame encoding a PIV3 antigenic polypeptide or an immunogenic fragment thereof and one having an open reading frame encoding a MeV antigenic polypeptide or an immunogenic fragment thereof.

[0717] 14. The respiratory virus vaccine of paragraph 1,
comprising:

[0719] at least two RNA polynucleotides, one having an open reading frame encoding a PIV3 antigenic polypeptide or an immunogenic fragment thereof and one having an open reading frame encoding a BetaCoV antigenic polypeptide or an immunogenic fragment thereof.

[0721] 16. The respiratory virus vaccine of paragraph 1, comprising:

[0723] at least two RNA polynucleotides, one having an open reading frame encoding a RSV antigenic polypeptide or an immunogenic fragment thereof and one having an open reading frame encoding a MeV antigenic polypeptide or an immunogenic fragment thereof.

[0724] 17. The respiratory virus vaccine of paragraph 16, wherein the MeV antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO:

by any one of SEQ ID NO: 12-13 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 12-13.

[0737] 24. The respiratory virus vaccine of paragraph 1, comprising:

[0738] at least one RNA polynucleotide having an open reading frame encoding a hMPV antigenic polypeptide or an immunogenic fragment thereof, a PIV3 antigenic polypeptide or an immunogenic fragment thereof, and a MeV antigenic polypeptide or an immunogenic fragment thereof; or

[0739] at least two or three RNA polynucleotides, one having an open reading frame encoding a hMPV antigenic polypeptide or an immunogenic fragment thereof, one having an open reading frame encoding a PIV3 antigenic polypeptide or an immunogenic fragment thereof, and one having an open reading frame encoding a MeV antigenic polypeptide or an immunogenic fragment thereof.

[0740] 25. The respiratory virus vaccine of paragraph 24, wherein the hMPV antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 5-8 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 5-8, wherein the PIV3 antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 12-13 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 12-13, and/or wherein the MeV antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 47-50 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 47-50.

[0741] 26. The respiratory virus vaccine of paragraph 1, comprising:

[0742] at least one RNA polynucleotide having an open reading frame encoding a hMPV antigenic polypeptide or an immunogenic fragment thereof, a PIV3 antigenic polypeptide or an immunogenic fragment thereof, and a BetaCoV antigenic polypeptide or an immunogenic fragment thereof; or

[0743] at least two or three RNA polynucleotides, one having an open reading frame encoding a hMPV antigenic polypeptide or an immunogenic fragment thereof, one having an open reading frame encoding a PIV3 antigenic polypeptide or an immunogenic fragment thereof, and one having an open reading frame encoding a BetaCoV antigenic polypeptide or an immunogenic fragment thereof.

[0744] 27. The respiratory virus vaccine of paragraph 26, wherein the hMPV antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 5-8 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 5-8, wherein the PIV3 antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 12-13 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 12-13 and/or wherein the BetaCoV antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 23-34 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 23-34.

[0747] at least two or three RNA polynucleotides, one having an open reading frame encoding a hMPV antigenic polypeptide or an immunogenic fragment thereof, one having an open reading frame encoding a RSV antigenic polypeptide or an immunogenic fragment thereof, and one having an open reading frame encoding a MeV antigenic polypeptide or an immunogenic fragment thereof.

[0749] 30. The respiratory virus vaccine of paragraph 1, comprising:

[0751] at least two or three RNA polynucleotides, one having an open reading frame encoding a hMPV antigenic polypeptide or an immunogenic fragment thereof, one having an open reading frame encoding a RSV antigenic polypeptide or an immunogenic fragment thereof, and one having an open reading frame encoding a BetaCoV antigenic polypeptide or an immunogenic fragment thereof.

[0753] 32. The respiratory virus vaccine of paragraph 1, comprising:

[0755] at least two or three RNA polynucleotides, one having an open reading frame encoding a hMPV antigenic polypeptide or an immunogenic fragment thereof, one having an open reading frame encoding a MeV antigenic

[0756] 33. The respiratory virus vaccine of paragraph 32, wherein the hMPV antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 5-8 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 5-8, wherein the MeV antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 47-50 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 47-50, and/or wherein the BetaCoV antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 23-34 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 23-34.

[0759] at least two or three RNA polynucleotides, one having an open reading frame encoding a PIV3 antigenic polypeptide or an immunogenic fragment thereof, one having an open reading frame encoding a RSV antigenic polypeptide or an immunogenic fragment thereof, and one having an open reading frame encoding a MeV antigenic polypeptide or an immunogenic fragment thereof.

[0761] 36. The respiratory virus vaccine of paragraph 1, comprising:

[0763] at least two or three RNA polynucleotides, one having an open reading frame encoding a PIV3 antigenic polypeptide or an immunogenic fragment thereof, one having an open reading frame encoding a RSV antigenic polypeptide or an immunogenic fragment thereof, and one having an open reading frame encoding a BetaCoV antigenic polypeptide or an immunogenic fragment thereof.

[0764] 37. The respiratory virus vaccine of paragraph 36, wherein the PIV3 antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 12-13 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any

[0780] 45. The respiratory virus vaccine of paragraph 44, wherein the hMPV antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 5-8 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 5-8, wherein the PIV3 antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 12-13 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 12-13, and/or wherein the BetaCoV antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 24-34 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 24-34.

[0783] at least two, three or four RNA polynucleotides, one having an open reading frame encoding a hMPV antigenic polypeptide or an immunogenic fragment thereof, one having an open reading frame encoding a PIV3 antigenic polypeptide or an immunogenic fragment thereof, one having an open reading frame encoding a MeV antigenic polypeptide or an immunogenic fragment thereof, and one having an open reading frame encoding a BetaCoV antigenic polypeptide or an immunogenic fragment thereof.

[0785] 48. The respiratory virus vaccine of paragraph 1, comprising:

[0787] at least two, three or four RNA polynucleotides, one having an open reading frame encoding a hMPV antigenic polypeptide or an immunogenic fragment thereof, one having an open reading frame encoding a RSV antigenic polypeptide or an immunogenic fragment thereof, one having an open reading frame encoding a MeV antigenic polypeptide or an immunogenic fragment thereof, and one having an open reading frame encoding a BetaCoV antigenic polypeptide or an immunogenic fragment thereof.

having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 47-50, and/or wherein the BetaCoV antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 24-34 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 24-34.

[0790] at least one RNA polynucleotide having an open reading frame encoding a PIV3 antigenic polypeptide or an immunogenic fragment thereof, a RSV antigenic polypeptide or an immunogenic fragment thereof, a MeV antigenic polypeptide or an immunogenic fragment thereof, and a BetaCoV antigenic polypeptide or an immunogenic fragment thereof; or

[0791] at least two, three or four RNA polynucleotides, one having an open reading frame encoding a PIV3 antigenic polypeptide or an immunogenic fragment thereof, one having an open reading frame encoding a RSV antigenic polypeptide or an immunogenic fragment thereof, one having an open reading frame encoding a MeV antigenic polypeptide or an immunogenic fragment thereof, and one having an open reading frame encoding a BetaCoV antigenic polypeptide or an immunogenic fragment thereof.

[0792] 51. The respiratory virus vaccine of paragraph 50, wherein the PIV3 antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 12-13 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 12-13, wherein the MeV antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 47-50 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 47-50, and/or wherein the BetaCoV antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 24-34 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 24-34.

[0793] 52. The respiratory virus vaccine of paragraph 1, comprising:

[0794] at least one RNA polynucleotide having an open reading frame encoding a hMPV antigenic polypeptide or an immunogenic fragment thereof, a PIV3 antigenic polypeptide or an immunogenic fragment thereof, a RSV antigenic polypeptide or an immunogenic fragment thereof, a MeV antigenic polypeptide or an immunogenic fragment thereof, and a BetaCoV antigenic polypeptide or an immunogenic fragment thereof; or

[0795] at least two, three, four or five RNA polynucleotides, one having an open reading frame encoding a hMPV antigenic polypeptide or an immunogenic fragment thereof, one having an open reading frame encoding a PIV3 antigenic polypeptide or an immunogenic fragment thereof, one having an open reading frame encoding a RSV antigenic polypeptide or an immunogenic fragment thereof, one having an open reading frame encoding a MeV antigenic polypeptide or an immunogenic fragment thereof, and one having an open reading frame encoding a BetaCoV antigenic polypeptide or an immunogenic fragment thereof.

[0796] 53. The respiratory virus vaccine of paragraph 52, wherein the hMPV antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO:

- 5-8 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 5-8, wherein the PIV3 antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 12-13 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 12-13, wherein the MeV antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 47-50 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 47-50, and/or wherein the BetaCoV antigenic polypeptide comprises an amino acid sequence identified by any one of SEQ ID NO: 24-34 or an amino acid sequence having at least 90% or 95% identity to an amino acid sequence identified by any one of SEQ ID NO: 24-34.
- [0797] 54. The vaccine of any one of paragraphs 1-53, wherein at least one RNA polynucleotide has less than 80% identity to wild-type mRNA sequence.
- [0798] 55. The vaccine of any one of paragraphs 1-53, wherein at least one RNA polynucleotide has at least 80% identity to wild-type mRNA sequence, but does not include wild-type mRNA sequence.
- [0799] 56. The vaccine of any one of paragraphs 1-55, wherein at least one antigenic polypeptide has membrane fusion activity, attaches to cell receptors, causes fusion of viral and cellular membranes, and/or is responsible for binding of the virus to a cell being infected.
- [0800] 57. The vaccine of any one of paragraphs 1-56, wherein at least one RNA polynucleotide comprises at least one chemical modification.
- [0801] 58. The vaccine of paragraph 57, wherein the chemical modification is selected from pseudouridine, N1-methylpseudouridine, N1-ethylpseudouridine, 2-thiouridine, 4'-thiouridine, 5-methylcytosine, 5-methyluridine, 2-thio-1-methyl-1-deaza-pseudouridine, 2-thio-1-methyl-pseudouridine, 2-thio-5-aza-uridine, 2-thio-dihydropseudouridine, 2-thio-dihydrouridine, 2-thio-pseudouridine, 4-methoxy-2-thio-pseudouridine, 4-methoxy-pseudouridine, 4-thio-1-methyl-pseudouridine, 4-thio-pseudouridine, 5-aza-uridine, dihydropseudouridine, 5-methoxyuridine and 2'-O-methyl uridine.
- [0802] 59. The vaccine of paragraph 57 or 58, wherein the chemical modification is in the 5-position of the uracil.
- [0803] 60. The vaccine of any one of paragraphs 57-59, wherein the chemical modification is a N1-methylpseudouridine or N1-ethylpseudouridine.
- [0804] 61. The vaccine of any one of paragraphs 57-60, wherein at least 80%, at least 90% or 100% of the uracil in the open reading frame have a chemical modification.
- [0805] 62. The vaccine of any one of paragraphs 1-61, wherein at least one RNA polynucleotide further encodes at least one 5' terminal cap, optionally wherein the 5' terminal cap is 7mG(5')ppp(5')NlmpNp.
- [0806] 63. The vaccine of any one of paragraphs 1-62, wherein at least one antigenic polypeptide or immunogenic fragment thereof is fused to a signal peptide selected from: a HulgGk signal peptide (METPAQLL-FLLLLWLPDTTG; SEQ ID NO: 15); IgE heavy chain epsilon-1 signal peptide (MDWTWILFLVAAATRVHS; SEQ ID NO: 16); Japanese encephalitis PRM signal sequence (MLGSNSGQRVVFITILLLVAPAYS; SEQ ID NO: 17); VSVg protein signal sequence (MKCLLY-LAFLFIGVNCA; SEQ ID NO: 18) and Japanese encephalitis JEV signal sequence (MWLVSLAIVTACAGA; SEQ ID NO: 19).
- [0807] 64. The vaccine of paragraph 63, wherein the signal peptide is fused to the N-terminus or the C-terminus of at least one antigenic polypeptide.
- [0808] 65. The vaccine of any one of paragraphs 1-64, wherein the antigenic polypeptide or immunogenic fragment thereof comprises a mutated N-linked glycosylation site.
- [0809] 66. The vaccine of any one of paragraphs 1-65 formulated in a nanoparticle, optionally a lipid nanoparticle.
- [0810] 67. The vaccine of paragraph 66, wherein the lipid nanoparticle comprises a cationic lipid, a PEG-modified lipid, a sterol and a non-cationic lipid; optionally wherein the lipid nanoparticle carrier comprises a molar ratio of about 20-60% cationic lipid, 0.5-15% PEG-modified lipid, 25-55% sterol, and 25% non-cationic lipid; optionally wherein the cationic lipid is an ionizable cationic lipid and the non-cationic lipid is a neutral lipid, and the sterol is a cholesterol; and optionally wherein the cationic lipid is selected from 2,2-dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoleylmethyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate (L319). Formula (II)
- [0811] 68. The vaccine of paragraph 66 or 67, wherein the nanoparticle (e.g., lipid nanoparticle) comprises a compound of Formula (I) and/or Formula (II), optionally Compound 3, 18, 20, 25, 26, 29, 30, 60, 108-112, or 122.
- [0812] 69. The vaccine of any one of paragraphs 1-68 further comprising an adjuvant, optionally a flagellin protein or peptide that optionally comprises an amino acid sequence identified by any one of SEQ ID NO: 54-56.
- [0813] 70. The vaccine of any one of paragraphs 1-69, wherein the open reading frame is codon-optimized.
- [0814] 71. The vaccine of any one of paragraphs 1-70 formulated in an effective amount to produce an antigen-specific immune response.
- [0815] 72. A method of inducing an immune response in a subject, the method comprising administering to the subject the vaccine of any one of paragraphs 1-71 in an amount effective to produce an antigen-specific immune response in the subject.
- [0816] 73. The method of paragraph 72, wherein the subject is administered a single dose of the vaccine, or wherein the subject is administered a first dose and then a booster dose of the vaccine.
- [0817] 74. The method of paragraph 72 or 73, wherein the vaccine is administered to the subject by intradermal injection or intramuscular injection.
- [0818] 75. The method of any one of paragraphs 72-74, wherein an anti-antigenic polypeptide antibody titer produced in the subject is increased by at least 1 log relative to a control, and/or wherein the anti-antigenic polypeptide antibody titer produced in the subject is increased at least 2 times relative to a control.
- [0819] 76. The method of any one of paragraphs 72-75, wherein the control is an anti-antigenic polypeptide antibody titer produced in a subject who has not been administered a vaccine against the virus, and/or wherein the control is an anti-antigenic polypeptide antibody titer

produced in a subject who has been administered a live attenuated vaccine or an inactivated vaccine against the virus, and/or, wherein the control is an anti-antigenic polypeptide antibody titer produced in a subject who has been administered a recombinant protein vaccine or purified protein vaccine against the virus, and/or wherein the control is an anti-antigenic polypeptide antibody titer produced in a subject who has been administered a VLP vaccine against the virus.

[0820] 77. The method of any one of paragraphs 72-76, wherein the effective amount is a dose equivalent to an at least 2-fold reduction in the standard of care dose of a recombinant protein vaccine or a purified protein vaccine against the virus, and wherein an anti-antigenic polypeptide antibody titer produced in the subject is equivalent to an anti-antigenic polypeptide antibody titer produced in a control subject administered the standard of care dose of a recombinant protein vaccine or a purified protein vaccine against the virus, respectively; and/or wherein the effective amount is a dose equivalent to an at least 2-fold reduction in the standard of care dose of a live attenuated vaccine or an inactivated vaccine against the virus, and wherein an anti-antigenic polypeptide antibody titer produced in the subject is equivalent to an anti-antigenic polypeptide antibody titer produced in a control subject administered the standard of care dose of a live attenuated vaccine or an inactivated vaccine against the virus, respectively; and/or wherein the effective amount is a dose equivalent to an at least 2-fold reduction in the standard of care dose of a VLP vaccine against the virus, and wherein an anti-antigenic polypeptide antibody titer produced in the subject is equivalent to an anti-antigenic polypeptide antibody titer produced in a control subject administered the standard of care dose of a VLP vaccine against the virus.

[0821] 78. The method of any one of paragraphs 72-77, wherein the effective amount is a total dose of 50 µg-1000 µg, optionally wherein the effective amount is a dose of 25 µg, 100 µg, 400 µg, or 500 µg administered to the subject a total of two times.

[0822] 79. The method of any one of paragraphs 72-78, wherein the efficacy of the vaccine against the virus is greater than 65%; and/or wherein the vaccine immunizes the subject against the virus for up to 2 years or wherein the vaccine immunizes the subject against the virus for more than 2 years.

[0823] 80. The method of any one of paragraphs 72-79, wherein the subject has an age of about 5 years old or younger or wherein the subject has an age of about 60 years old or older; and/or wherein the subject has a chronic pulmonary disease; and/or the subject has been exposed to the virus, wherein the subject is infected with the virus, or wherein the subject is at risk of infection by the virus; and/or wherein the subject is immunocompromised.

[0824] 81. The respiratory virus vaccine of any one of paragraphs 1-71, comprising at least one (e.g., at least two, at least three, at least four, or at least five) RNA polynucleotide having an open reading frame encoding at least one (e.g., at least two, at least three, at least four, or at least five) antigenic polypeptide selected from hMPV antigenic polypeptides (SEQ ID NO: 5-8), PIV3 antigenic polypeptides (SEQ ID NO: 12-13), RSV antigenic polypeptides, MeV antigenic polypeptides (SEQ ID NO:

47-50) and BetaCoV antigenic polypeptides (e.g., MERS-CoV, SARS-CoV, HCoV—OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH or HCoV-HKU1; (SEQ ID NO: 24-34)), formulated in a cationic lipid nanoparticle

[0825] (a) having a molar ratio of about 20-60% cationic lipid, about 5-25% non-cationic lipid, about 25-55% sterol, and about 0.5-15% PEG-modified lipid, and/or

[0826] (b) comprising a compound of Formula (I) and/or Formula (II),

[0827] wherein the at least one (e.g., at least two, at least three, at least four, or at least five) RNA polynucleotide comprises at least one chemical modification.

[0828] 82. The respiratory virus vaccine of any one of paragraphs 1-71, comprising at least one (e.g., at least two, at least three, at least four, or at least five) RNA polynucleotide having an open reading frame encoding at least one (e.g., at least two, at least three, at least four, or at least five) antigenic polypeptide selected from hMPV antigenic polypeptides (SEQ ID NO: 5-8), PIV3 antigenic polypeptides (SEQ ID NO: 12-13), RSV antigenic polypeptides, MeV antigenic polypeptides (SEQ ID NO: 47-50) and BetaCoV antigenic polypeptides (e.g., MERS-CoV, SARS-CoV, HCoV—OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH or HCoV-HKU1; (SEQ ID NO: 24-34)), formulated in a cationic lipid nanoparticle

[0829] (a) having a molar ratio of about 20-60% cationic lipid, about 5-25% non-cationic lipid, about 25-55% sterol, and about 0.5-15% PEG-modified lipid, and/or

[0830] (b) comprising at least one (e.g., at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, or 14) Compound selected from Compounds 3, 18, 20, 25, 26, 29, 30, 60, 108-112 and 122.

[0831] 83. The respiratory virus vaccine of paragraphs 81 or 82, wherein the at least one antigenic polypeptide is selected from hMPV antigenic polypeptides (e.g., SEQ ID NO: 5-8).

[0832] 84. The respiratory virus vaccine of any one of paragraphs 81-83, wherein the at least one antigenic polypeptide is selected from PIV3 antigenic polypeptides (e.g., SEQ ID NO: 12-13).

[0833] 85. The respiratory virus vaccine of any one of paragraphs 81-84, wherein the at least one antigenic polypeptide is selected from RSV antigenic polypeptides.

[0834] 86. The respiratory virus vaccine of any one of paragraphs 81-85, wherein the at least one antigenic polypeptide is selected from MeV antigenic polypeptides (e.g., SEQ ID NO: 47-50).

[0835] 87. The respiratory virus vaccine of any one of paragraphs 81-86, wherein the at least one antigenic polypeptide is selected from BetaCoV antigenic polypeptides (e.g., SEQ ID NO: 24-34).

[0836] 88. The respiratory virus vaccine of paragraph 87, wherein the BetaCoV antigenic polypeptides are MERS antigenic polypeptides.

[0837] 89. The respiratory virus vaccine of paragraph 87, wherein the BetaCoV antigenic polypeptides are SARS antigenic polypeptides.

[0838] 90. The respiratory virus vaccine of any one of paragraphs 81-89, wherein the at least one (e.g., at least two, at least three, at least four, or at least five) RNA polynucleotide comprises at least one chemical modification (e.g., selected from pseudouridine, N1-methylpseudouridine, N1-ethylpseudouridine, 2-thiouridine, 4-thiouridine, 5-methylcytosine, 5-methyluridine, 2-thio-1-methyl-1-deaza-pseudouridine, 2-thio-1-methyl-

pseudouridine, 2-thio-5-aza-uridine, 2-thio-dihydropseudouridine, 2-thio-dihydrouridine, 2-thio-pseudouridine, 4-methoxy-2-thio-pseudouridine, 4-methoxy-pseudouridine, 4-thio-1-methyl-pseudouridine, 4-thio-pseudouridine, 5-aza-uridine, dihydropseudouridine, 5-methoxyuridine and 2'-O-methyl uridine).

[0839] 91. A respiratory virus vaccine, comprising:

[0840] at least one messenger ribonucleic acid (mRNA) polynucleotide having a 5' terminal cap, an open reading frame encoding at least one respiratory virus antigenic polypeptide, and a 3' polyA tail.

[0841] 92. The vaccine of paragraph 91, wherein the at least one mRNA polynucleotide comprises a sequence identified by any one of SEQ ID NO: 57-80.

[0842] 93. The vaccine of paragraph 91 or 92, wherein the 5' terminal cap is or comprises 7mG(5')ppp(5')NlmpNp.

[0843] 94. The vaccine of any one of paragraphs 91-93, wherein 100% of the uracil in the open reading frame is modified to include N1-methyl pseudouridine at the 5-position of the uracil.

[0844] 95. The vaccine of any one of paragraphs 91-94, wherein the vaccine is formulated in a lipid nanoparticle comprising: Dlin-MC3-DMA; cholesterol; 1,2-Distearoyl-sn-glycero-3-phosphocholine (DSPC); and polyethylene glycol (PEG)2000-DMG.

[0845] 96. The vaccine of paragraph 95, wherein the lipid nanoparticle further comprises trisodium citrate buffer, sucrose and water.

[0846] 97. A respiratory syncytial virus (RSV) vaccine, comprising:

[0847] at least one messenger ribonucleic acid (mRNA) polynucleotide having a 5' terminal cap 7mG(5')ppp(5')NlmpNp, a sequence identified by any one of SEQ ID NO: 57-80 and a 3' polyA tail, formulated in a lipid nanoparticle comprising Dlin-MC3-DMA, cholesterol, 1,2-Distearoyl-sn-glycero-3-phosphocholine (DSPC), and polyethylene glycol (PEG)2000-DMG, wherein the uracil nucleotides of the sequence identified by any one of SEQ ID NO: 57-80 are modified to include N1-methyl pseudouridine at the 5-position of the uracil nucleotide.

[0848] This disclosure is not limited in its application to the details of construction and the arrangement of components set forth in the following description or illustrated in the drawings. The disclosure is capable of other embodiments and of being practiced or of being carried out in various ways. Also, the phraseology and terminology used herein is for the purpose of description and should not be regarded as limiting. The use of "including," "comprising," or "having," "containing," "involving," and variations thereof herein, is meant to encompass the items listed thereafter and equivalents thereof as well as additional items.

EXAMPLES

Example 1

Manufacture of Polynucleotides

[0849] According to the present disclosure, the manufacture of polynucleotides and/or parts or regions thereof may be accomplished utilizing the methods taught in International Publication WO2014/152027, entitled "Manufactur-

ing Methods for Production of RNA Transcripts," the contents of which is incorporated herein by reference in its entirety.

[0850] Purification methods may include those taught in International Publication WO2014/152030 and International Publication WO2014/152031, each of which is incorporated herein by reference in its entirety.

[0851] Detection and characterization methods of the polynucleotides may be performed as taught in International Publication WO2014/144039, which is incorporated herein by reference in its entirety.

[0852] Characterization of the polynucleotides of the disclosure may be accomplished using polynucleotide mapping, reverse transcriptase sequencing, charge distribution analysis, detection of RNA impurities, or any combination of two or more of the foregoing. "Characterizing" comprises determining the RNA transcript sequence, determining the purity of the RNA transcript, or determining the charge heterogeneity of the RNA transcript, for example. Such methods are taught in, for example, International Publication WO2014/144711 and International Publication WO2014/144767, the content of each of which is incorporated herein by reference in its entirety.

Example 2

Chimeric Polynucleotide Synthesis

[0853] According to the present disclosure, two regions or parts of a chimeric polynucleotide may be joined or ligated using triphosphate chemistry. A first region or part of 100 nucleotides or less is chemically synthesized with a 5' monophosphate and terminal 3'desOH or blocked OH, for example. If the region is longer than 80 nucleotides, it may be synthesized as two strands for ligation.

[0854] If the first region or part is synthesized as a non-positionally modified region or part using in vitro transcription (IVT), conversion the 5'monophosphate with subsequent capping of the 3' terminus may follow.

[0855] Monophosphate protecting groups may be selected from any of those known in the art.

[0856] The second region or part of the chimeric polynucleotide may be synthesized using either chemical synthesis or IVT methods. IVT methods may include an RNA polymerase that can utilize a primer with a modified cap. Alternatively, a cap of up to 130 nucleotides may be chemically synthesized and coupled to the IVT region or part.

[0857] For ligation methods, ligation with DNA T4 ligase, followed by treatment with DNase should readily avoid concatenation.

[0858] The entire chimeric polynucleotide need not be manufactured with a phosphate-sugar backbone. If one of the regions or parts encodes a polypeptide, then such region or part may comprise a phosphate-sugar backbone. Ligation is then performed using any known click chemistry, ortho-click chemistry, solulink, or other bioconjugate chemistries known to those in the art.

[0859] Synthetic Route

[0860] The chimeric polynucleotide may be made using a series of starting segments. Such segments include:

[0861] (a) a capped and protected 5' segment comprising a normal 3'OH (SEG. 1)

[0862] (b) a 5' triphosphate segment, which may include the coding region of a polypeptide and a normal 3'OH (SEG. 2)

[0863] (c) a 5' monophosphate segment for the 3' end of the chimeric polynucleotide (e.g., the tail) comprising cordycepin or no 3'OH (SEG. 3)

[0864] After synthesis (chemical or IVT), segment 3 (SEG. 3) may be treated with cordycepin and then with pyrophosphatase to create the 5' monophosphate.

[0865] Segment 2 (SEG. 2) may then be ligated to SEG. 3 using RNA ligase. The ligated polynucleotide is then purified and treated with pyrophosphatase to cleave the diphosphate. The treated SEG.2-SEG. 3 construct may then be purified and SEG. 1 is ligated to the 5' terminus. A further purification step of the chimeric polynucleotide may be performed.

[0866] Where the chimeric polynucleotide encodes a polypeptide, the ligated or joined segments may be represented as: 5'UTR (SEG. 1), open reading frame or ORF (SEG. 2) and 3'UTR+PolyA (SEG. 3).

[0867] The yields of each step may be as much as 90-95%.

Example 3

PCR for cDNA Production

[0868] PCR procedures for the preparation of cDNA may be performed using 2× KAPA HIFI™ HotStart ReadyMix by Kapa Biosystems (Woburn, Mass.). This system includes 2× KAPA ReadyMix 12.5 µl; Forward Primer (10 µM) 0.75 µl; Reverse Primer (10 µM) 0.75 µl; Template cDNA 100 ng; and dH₂O diluted to 25.0 µl. The reaction conditions may be at 95° C. for 5 min. The reaction may be performed for 25 cycles of 98° C. for 20 sec, then 58° C. for 15 sec, then 72° C. for 45 sec, then 72° C. for 5 min, then 4° C. to termination.

[0869] The reaction may be cleaned up using Invitrogen's PURELINK™ PCR Micro Kit (Carlsbad, Calif.) per manufacturer's instructions (up to 5 µg). Larger reactions may require a cleanup using a product with a larger capacity. Following the cleanup, the cDNA may be quantified using the NANODROPT™ and analyzed by agarose gel electrophoresis to confirm that the cDNA is the expected size. The cDNA may then be submitted for sequencing analysis before proceeding to the in vitro transcription reaction.

Example 4

In Vitro Transcription (IVT)

[0870] The in vitro transcription reaction generates RNA polynucleotides. Such polynucleotides may comprise a region or part of the polynucleotides of the disclosure, including chemically modified RNA (e.g., mRNA) polynucleotides. The chemically modified RNA polynucleotides can be uniformly modified polynucleotides. The in vitro transcription reaction utilizes a custom mix of nucleotide triphosphates (NTPs). The NTPs may comprise chemically modified NTPs, or a mix of natural and chemically modified NTPs, or natural NTPs.

[0871] A typical in vitro transcription reaction includes the following:

1)	Template cDNA	1.0 µg
2)	10x transcription buffer (400 mM Tris-HCl pH 8.0, 190 mM MgCl ₂ , 50 mM DTT, 10 mM Spermidine)	2.0 µl
3)	Custom NTPs (25 mM each)	0.2 µl
4)	RNase Inhibitor	20 U
5)	T7 RNA polymerase	3000 U
6)	dH ₂ O	up to 20.0 µl. and
7)	Incubation at 37° C. for 3 hr-5 hrs.	

[0872] The crude IVT mix may be stored at 4° C. overnight for cleanup the next day. 1 U of RNase-free DNase may then be used to digest the original template. After 15 minutes of incubation at 37° C., the mRNA may be purified using Ambion's MEGACLEAR™ Kit (Austin, Tex.) following the manufacturer's instructions. This kit can purify up to 500 µg of RNA. Following the cleanup, the RNA polynucleotide may be quantified using the NanoDrop and analyzed by agarose gel electrophoresis to confirm the RNA polynucleotide is the proper size and that no degradation of the RNA has occurred.

Example 5

Enzymatic Capping

[0873] Capping of a RNA polynucleotide is performed as follows where the mixture includes: IVT RNA 60 µg-180 µg and dH₂O up to 72 µl. The mixture is incubated at 65° C. for 5 minutes to denature RNA, and then is transferred immediately to ice.

[0874] The protocol then involves the mixing of 10× Capping Buffer (0.5 M Tris-HCl (pH 8.0), 60 mM KCl, 12.5 mM MgCl₂) (10.0 µl); 20 mM GTP (5.0 µl); 20 mM S-Adenosyl Methionine (2.5 µl); RNase Inhibitor (100 U); 2'-O-Methyltransferase (400 U); Vaccinia capping enzyme (Guanylyl transferase) (40 U); dH₂O (Up to 28 µl); and incubation at 37° C. for 30 minutes for 60 µg RNA or up to 2 hours for 180 µg of RNA.

[0875] The RNA polynucleotide may then be purified using Ambion's MEGACLEAR™ Kit (Austin, Tex.) following the manufacturer's instructions. Following the cleanup, the RNA may be quantified using the NANO-DROPT™ (ThermoFisher, Waltham, Mass.) and analyzed by agarose gel electrophoresis to confirm the RNA polynucleotide is the proper size and that no degradation of the RNA has occurred. The RNA polynucleotide product may also be sequenced by running a reverse-transcription-PCR to generate the cDNA for sequencing.

Example 6

PolyA Tailing Reaction

[0876] Without a poly-T in the cDNA, a poly-A tailing reaction must be performed before cleaning the final product. This is done by mixing capped IVT RNA (100 µl); RNase Inhibitor (20 U); 10× Tailing Buffer (0.5 M Tris-HCl (pH 8.0), 2.5 M NaCl, 1100 mM MgCl₂) (12.0 µl); 20 mM ATP (6.0 µl); Poly-A Polymerase (20 U); dH₂O up to 123.5 µl and incubation at 37° C. for 30 min. If the poly-A tail is already in the transcript, then the tailing reaction may be skipped and proceed directly to cleanup with Ambion's MEGACLEAR™ kit (Austin, Tex.) (up to 500 µg). Poly-A Polymerase may be a recombinant enzyme expressed in yeast.

[0877] It should be understood that the processivity or integrity of the polyA tailing reaction may not always result in an exact size polyA tail. Hence, polyA tails of approximately between 40-200 nucleotides, e.g., about 40, 50, 60, 70, 80, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 150-165, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164 or 165 are within the scope of the present disclosure.

Example 7

Natural 5' Caps and 5' Cap Analogues

[0878] 5'-capping of polynucleotides may be completed concomitantly during the in vitro-transcription reaction using the following chemical RNA cap analogs to generate the 5'-guanosine cap structure according to manufacturer protocols: 3'—O-Me-m7G(5')ppp(5') G [the ARCA cap]; G(5')ppp(5')A; G(5')ppp(5')G; m7G(5')ppp(5')A; m7G(5')ppp(5')G (New England BioLabs, Ipswich, Mass.). 5'-capping of modified RNA may be completed post-transcriptionally using a Vaccinia Virus Capping Enzyme to generate the "Cap 0" structure: m7G(5')ppp(5')G (New England BioLabs, Ipswich, Mass.). Cap 1 structure may be generated using both Vaccinia Virus Capping Enzyme and a 2'-O methyl-transferase to generate: m7G(5')ppp(5')G-2'-O-methyl. Cap 2 structure may be generated from the Cap 1 structure followed by the 2'-O-methylation of the 5'-ante-penultimate nucleotide using a 2'-O methyl-transferase. Cap 3 structure may be generated from the Cap 2 structure followed by the 2'-O-methylation of the 5'-preantepenultimate nucleotide using a 2'-O methyl-transferase. Enzymes are preferably derived from a recombinant source.

[0879] When transfected into mammalian cells, the modified mRNAs have a stability of between 12-18 hours or more than 18 hours, e.g., 24, 36, 48, 60, 72 or greater than 72 hours.

Example 8

Capping Assays

Protein Expression Assay

[0880] Polynucleotides (e.g., mRNA) encoding a polypeptide, containing any of the caps taught herein, can be transfected into cells at equal concentrations. The amount of protein secreted into the culture medium can be assayed by ELISA at 6, 12, 24 and/or 36 hours post-transfection. Synthetic polynucleotides that secrete higher levels of protein into the medium correspond to a synthetic polynucleotide with a higher translationally-competent cap structure.

Purity Analysis Synthesis

[0881] RNA (e.g., mRNA) polynucleotides encoding a polypeptide, containing any of the caps taught herein can be compared for purity using denaturing Agarose-Urea gel electrophoresis or HPLC analysis. RNA polynucleotides with a single, consolidated band by electrophoresis correspond to the higher purity product compared to polynucleotides with multiple bands or streaking bands. Chemically modified RNA polynucleotides with a single HPLC peak also correspond to a higher purity product. The capping reaction with a higher efficiency provides a more pure polynucleotide population.

Cytokine Analysis

[0882] RNA (e.g., mRNA) polynucleotides encoding a polypeptide, containing any of the caps taught herein can be transfected into cells at multiple concentrations. The amount of pro-inflammatory cytokines, such as TNF-alpha and IFN-beta, secreted into the culture medium can be assayed by ELISA at 6, 12, 24 and/or 36 hours post-transfection. RNA polynucleotides resulting in the secretion of higher levels of pro-inflammatory cytokines into the medium correspond to a polynucleotides containing an immune-activating cap structure.

Capping Reaction Efficiency

[0883] RNA (e.g., mRNA) polynucleotides encoding a polypeptide, containing any of the caps taught herein can be analyzed for capping reaction efficiency by LC-MS after nuclease treatment. Nuclease treatment of capped polynucleotides yield a mixture of free nucleotides and the capped 5'-5-triphosphate cap structure detectable by LC-MS. The amount of capped product on the LC-MS spectra can be expressed as a percent of total polynucleotide from the reaction and correspond to capping reaction efficiency. The cap structure with a higher capping reaction efficiency has a higher amount of capped product by LC-MS.

Example 9

Agarose Gel Electrophoresis of Modified RNA or RT PCR Products

[0884] Individual RNA polynucleotides (200-400 ng in a 20 µl volume) or reverse transcribed PCR products (200-400 ng) may be loaded into a well on a non-denaturing 1.2% Agarose E-Gel (Invitrogen, Carlsbad, Calif.) and run for 12-15 minutes, according to the manufacturer protocol.

Example 10

Nanodrop Modified RNA Quantification and UV Spectral Data

[0885] Chemically modified RNA polynucleotides in TE buffer (1 µl) are used for Nanodrop UV absorbance readings to quantitate the yield of each polynucleotide from an chemical synthesis or in vitro transcription reaction.

Example 11

Formulation of Modified mRNA Using Lipidoids

[0886] RNA (e.g., mRNA) polynucleotides may be formulated for in vitro experiments by mixing the polynucleotides with the lipidoid at a set ratio prior to addition to cells. In vivo formulation may require the addition of extra ingredients to facilitate circulation throughout the body. To test the ability of these lipidoids to form particles suitable for in vivo work, a standard formulation process used for siRNA-lipidoid formulations may be used as a starting point. After formation of the particle, polynucleotide is added and allowed to integrate with the complex. The encapsulation efficiency is determined using a standard dye exclusion assays.

Example 12

Immunogenicity Study

[0887] The instant study is designed to test the immunogenicity in mice of candidate hMPV vaccines comprising a mRNA polynucleotide encoding Fusion (F) glycoprotein, major surface glycoprotein G, or a combination thereof, obtained from hMPV.

[0888] Mice are immunized intravenously (IV), intramuscularly (IM), or intradermally (ID) with candidate vaccines. Candidate vaccines are chemically modified or unmodified. A total of four immunizations are given at 3-week intervals (i.e., at weeks 0, 3, 6, and 9), and sera are collected after each immunization until weeks 33-51. Serum antibody titers against Fusion (F) glycoprotein or major surface glycoprotein (G) protein are determined by ELISA. Sera collected from each mouse during weeks 10-16 are pooled, and total IgG purified. Purified antibodies are used for immunoelectron microscopy, antibody-affinity testing, and in vitro protection assays.

Example 13

hMPV Rodent Challenge

[0889] The instant study is designed to test the efficacy in cotton rats of candidate hMPV vaccines against a lethal challenge using an hMPV vaccine comprising mRNA encoding Fusion (F) glycoprotein, major surface glycoprotein G, or a combination of both antigens obtained from hMPV. Cotton rats are challenged with a lethal dose of the hMPV.

[0890] Animals are immunized intravenously (IV), intramuscularly (IM), or intradermally (ID) at week 0 and week 3 with candidate hMPV vaccines with and without adjuvant. Candidate vaccines are chemically modified or unmodified. The animals are then challenged with a lethal dose of hMPV on week 7 via IV, IM or ID. Endpoint is day 13 post infection, death or euthanasia. Animals displaying severe illness as determined by >30% weight loss, extreme lethargy or paralysis are euthanized. Body temperature and weight are assessed and recorded daily.

[0891] In experiments where a lipid nanoparticle (LNP) formulation is used, the formulation may include a cationic lipid, non-cationic lipid, PEG lipid and structural lipid in the ratios 50:10:1.5:38.5. The cationic lipid is DLin-KC2-DMA (50 mol %) or DLin-MC3-DMA (50 mol %), the non-cationic lipid is DSPC (10 mol %), the PEG lipid is PEG-DOMG (1.5 mol %) and the structural lipid is cholesterol (38.5 mol %), for example.

Example 14

Immunogenicity of hMPV mRNA Vaccine in BALB/c Mice

[0892] The instant study was designed to test the immunogenicity in BALB/c mice of hMPV vaccines comprising an mRNA polynucleotide encoding the hMPV Fusion (F) glycoprotein. The mRNA polynucleotide encodes the full-length fusion protein and comprises the wild-type nucleotide sequence obtained from the hMPV A2a strain. Mice were divided into 3 groups (n=8 for each group) and immunized intramuscularly (IM) with PBS, a 10 µg dose of mRNA vaccines encoding hMPV fusion protein, or a 2 µg dose of

mRNA vaccines encoding hMPV fusion protein. A total of two immunizations were given at 3-week intervals (i.e., at weeks 0, and 3 weeks), and sera were collected after each immunization according to the schedule described in Table 1. Serum antibody titers against hMPV fusion glycoprotein were determined by ELISA and antibodies were detected in the sera collected on day 14 onward. Both vaccine doses tested induced comparable levels of immune response in mice (FIGS. 2A-2C).

[0893] Additionally, mice sera were used for IgG isotyping (FIGS. 3A-3C). Both hMPV fusion protein-specific IgG1 and IgG2a were detected in mice sera. hMPV fusion protein mRNA vaccine also induced Th1 and Th2 cytokine responses, with a Th1 bias.

[0894] Sera from mice immunized with either 10 µg or 2 µg doses of the hMPV fusion protein mRNA vaccine contain neutralizing antibodies. The ability of these antibodies to neutralize hMPV B2 strain was also tested. The antibody-containing sera successfully neutralized the hMPV B2 virus (FIG. 4).

Example 15

T-Cell Stimulation

[0895] The instant study was designed to test T-cell stimulation in the splenocytes of mice immunized with mRNA vaccines encoding hMPV fusion protein, as described herein. Immunization of BALB/c mice was performed as described in Example 14. The splenocytes for each group were pooled and split into two parts. One part of splenocytes from each group of mice was stimulated with hMPV-free media, Concanavalin A or a hMPV fusion protein peptide pool comprising 15-mers (15 amino acids long); while the other part of splenocytes from each group of mice was stimulated with hMPV-free media, Concanavalin A or inactivated hMPV virus. Secreted mouse cytokines were measured using the Meso Scale Discovery (MSD) assay.

[0896] Cytokines specific to Th1 or Th2 responses were measured. For Th1 response, IFN-γ, IL2 and IL12 were detected from splenocytes stimulated with the hMPV fusion protein peptide pool at a level comparable to that of Concanavalin A (FIGS. 5A-5C). For a Th2 response, the hMPV fusion protein peptide pool induced the secretion of detectable IL10, TNF-α, IL4 and IL, but not IL5, while Concanavalin A stimulated the secretion of all the above-mentioned Th2 cytokines (FIGS. 6A-6E) at a much higher level.

[0897] In contrast, inactivated hMPV virus only induced the secretion of IL2 in the Th1 response comparable to that of Concanavalin A (FIGS. 7A-7C). For the Th2 response, the inactivated hMPV virus induced the secretion of detectable IL10, TNF-α, IL4 and IL6, but not IL5, while Concanavalin A stimulated the secretion of all the above-mentioned Th2 cytokines (FIGS. 8A-8E) at a much higher level.

Example 16

hMPV Rodent Challenge in Cotton Rats
Immunized with mRNA Vaccine Encoding hMPV
Fusion Protein

[0898] The instant study was designed to test the efficacy in cotton rats of hMPV vaccines against a lethal challenge. mRNA vaccines encoding hMPV fusion protein were used. The mRNA polynucleotide encodes a full-length fusion

protein and comprises the wild-type nucleotide sequence obtained from the hMPV A2a strain.

[0899] Cotton rats were immunized intramuscularly (IM) at week 0 and week 3 with the mRNA vaccines encoding hMPV fusion protein with either 2 µg or 10 µg doses for each immunization. The animals were then challenged with a lethal dose of hMPV in week 7 post initial immunization via IV, IM or ID. The endpoint was day 13 post infection, death or euthanasia. Viral titers in the noses and lungs of the cotton rats were measured. The results (FIGS. 9A and 9B) show that a 10 µg dose of mRNA vaccine protected the cotton mice 100% in the lung and drastically reduced the viral titer in the nose after challenge (~2 log reduction). Moreover, a 2 µg dose of mRNA vaccine showed a 1 log reduction in lung viral titer in the cotton mice challenged.

[0900] Further, the histopathology of the lungs of the cotton mice immunized and challenged showed no pathology associated with vaccine-enhanced disease (FIG. 10).

Example 17

Immunogenicity Study

[0901] The instant study is designed to test the immunogenicity in mice of candidate PIV3 vaccines comprising a mRNA polynucleotide encoding hemagglutinin-neuraminidase or fusion protein (F or F0) obtained from PIV3.

[0902] Mice are immunized intravenously (IV), intramuscularly (IM), or intradermally (ID) with candidate vaccines. Candidate vaccines are chemically modified or unmodified. A total of four immunizations are given at 3-week intervals (i.e., at weeks 0, 3, 6, and 9), and sera are collected after each immunization until weeks 33-51. Serum antibody titers against hemagglutinin-neuraminidase or fusion protein (F or F0) are determined by ELISA. Sera collected from each mouse during weeks 10-16 are, optionally, pooled, and total IgGs are purified. Purified antibodies are used for immunoelectron microscopy, antibody-affinity testing, and in vitro protection assays.

Example 18

PIV3 Rodent Challenge

[0903] The instant study is designed to test the efficacy in cotton rats of candidate PIV3 vaccines against a lethal challenge using a PIV3 vaccine comprising mRNA encoding hemagglutinin-neuraminidase or fusion protein (F or F0) obtained from PIV3. Cotton rats are challenged with a lethal dose of the PIV3.

[0904] Animals are immunized intravenously (IV), intramuscularly (IM), or intradermally (ID) at week 0 and week 3 with candidate PIV3 vaccines with and without adjuvant. Candidate vaccines are chemically modified or unmodified. The animals are then challenged with a lethal dose of PIV3 on week 7 via IV, IM or ID. Endpoint is day 13 post infection, death or euthanasia. Animals displaying severe illness as determined by >30% weight loss, extreme lethargy or paralysis are euthanized. Body temperature and weight are assessed and recorded daily.

[0905] In experiments where a lipid nanoparticle (LNP) formulation is used, the formulation may include a cationic lipid, non-cationic lipid, PEG lipid and structural lipid in the ratios 50:10:1.5:38.5. The cationic lipid is DLin-KC2-DMA (50 mol %) or DLin-MC3-DMA (50 mol %), the non-cationic lipid is DSPC (10 mol %), the PEG lipid is

PEG-DOMG (1.5 mol %) and the structural lipid is cholesterol (38.5 mol %), for example.

Example 19

hMPV/PIV Cotton Rat Challenge

[0906] The instant study was designed to test the efficacy in cotton rats of candidate hMPV mRNA vaccines, PIV3 mRNA vaccines, or hMPV/PIV combination mRNA vaccines against a lethal challenge using PIV3 strain or hMPV/A2 strain. The study design is shown in Table 9.

[0907] Cotton rats of 10-12 weeks old were divided into 12 groups (n=5), and each group was vaccinated with mRNA vaccines indicated in Table 9. The PIV3 vaccine comprises mRNA encoding hemagglutinin-neuraminidase or fusion protein (F or F0) obtained from PIV3. The hMPV mRNA vaccine encodes the full-length hMPV fusion protein. The hMPV/PIV combination mRNA vaccine is a mixture of the PIV3 vaccine and hMPV vaccine at a 1:1 ratio.

[0908] Cotton rats were immunized intramuscularly (IM) at week 0 and week 3 with candidate vaccines with the doses indicated in Table 9. Cotton rats immunized with hMPV mRNA vaccines or hMPV/PIV combination mRNA vaccines were challenged with a lethal dose of hMPV/A2 strain on week 7 via IM. Cotton rats immunized with PIV mRNA vaccines or hMPV/PIV combination mRNA vaccines were challenged with a lethal dose of PIV3 strain on week 7 via IM.

[0909] The endpoint was day 13 post infection, death or euthanasia. Animals displaying severe illness as determined by >30% weight loss, extreme lethargy or paralysis were euthanized. Body temperature and weight were assessed and recorded daily.

[0910] Lung and nose hMPV/A2 (FIG. 12) or PIV3 (FIG. 13) viral titers were assessed. Lung histopathology of the immunized and challenged cotton rat immunized and challenged were assessed to determine pathology associated with vaccine enhance disease. Neutralization antibody titers in the serum of immunized cotton rats on day 0 and 42 post immunization were assessed (FIG. 11).

[0911] hMPV/A2 (FIG. 14) or PIV3 (FIG. 15) neutralizing antibody titers in the serum samples of the immunized cotton rat 42 days post immunization were measured. All mRNA vaccines tested induced strong neutralizing antibodies cotton rats. Lung histopathology of the immunized cotton rats were also evaluated (FIG. 16). Low occurrence of alevolitis and interstitial pneumonia was observed, indicating no antibody-dependent enhancement (ADE) of hMPV or PIV associated diseases.

Example 20

Betacoronavirus Immunogenicity Study

[0912] The instant study is designed to test the immunogenicity in rabbits of candidate betacoronavirus (e.g., MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH or HCoV-HKU1 or a combination thereof) vaccines comprising a mRNA polynucleotide encoding the spike (S) protein, the S1 subunit (S1) of the spike protein, or the S2 subunit (S2) of the spike protein obtained from a betacoronavirus (e.g., MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH or HCoV-HKU1).

[0913] Rabbits are vaccinated on week 0 and 3 via intravenous (IV), intramuscular (IM), or intradermal (ID) routes. One group remains unvaccinated and one is administered inactivated betacoronavirus. Serum is collected from each rabbit on weeks 1, 3 (pre-dose) and 5. Individual bleeds are tested for anti-S, anti-S1 or anti-S2 activity via a virus neutralization assay from all three time points, and pooled samples from week 5 only are tested by Western blot using inactivated betacoronavirus (e.g., inactivated MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH or HCoV-HKU1).

[0914] In experiments where a lipid nanoparticle (LNP) formulation is used, the formulation may include a cationic lipid, non-cationic lipid, PEG lipid and structural lipid in the ratios 50:10:1.5:38.5. The cationic lipid is DLin-KC2-DMA (50 mol %) or DLin-MC3-DMA (50 mol %), the non-cationic lipid is DSPC (10 mol %), the PEG lipid is PEG-DOMG (1.5 mol %) and the structural lipid is cholesterol (38.5 mol %), for example.

Example 21

Betacoronavirus Challenge

[0915] The instant study is designed to test the efficacy in rabbits of candidate betacoronavirus (e.g., MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-HKU1 or a combination thereof) vaccines against a lethal challenge using a betacoronavirus (e.g., MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-HKU1 or a combination thereof) vaccine comprising mRNA encoding the spike (S) protein, the S1 subunit (S1) of the spike protein, or the S2 subunit (S2) of the spike protein obtained from betacoronavirus (e.g., MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH or HCoV-HKU1). Rabbits are challenged with a lethal dose (10xLD90; ~100 plaque-forming units; PFU) of betacoronavirus (e.g., MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH or HCoV-HKU1).

[0916] The animals used are 6-8 week old female rabbits in groups of 10. Rabbits are vaccinated on weeks 0 and 3 via an IM, ID or IV route of administration. Candidate vaccines are chemically modified or unmodified. Rabbit serum is tested for microneutralization (see Example 14). Rabbits are then challenged with ~1 LD90 of betacoronavirus (e.g., MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH or HCoV-HKU1) on week 7 via an IN, IM, ID or IV route of administration. Endpoint is day 13 post infection, death or euthanasia. Animals displaying severe illness as determined by >30% weight loss, extreme lethargy or paralysis are euthanized. Body temperature and weight are assessed and recorded daily.

Example 22

Microneutralization Assay

[0917] Nine serial 2-fold dilutions (1:50-1:12,800) of rabbit serum are made in 50 μ l virus growth medium (VGM) with trypsin in 96 well microtiter plates. Fifty microliters of virus containing ~50 pfu of betacoronavirus (e.g., MERS-CoV, SARS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63, HCoV-NL, HCoV-NH or HCoV-HKU1) is added to the serum dilutions and allowed to incubate for 60 minutes at room temperature (RT). Positive control wells of virus

without sera and negative control wells without virus or sera are included in triplicate on each plate. While the serum-virus mixtures incubate, a single cell suspension of Madin-Darby Canine-Kidney cells are prepared by trypsinizing (Gibco 0.5% bovine pancrease trypsin in EDTA) a confluent monolayer and suspended cells are transferred to a 50 ml centrifuge tube, topped with sterile PBS and gently mixed. The cells are then pelleted at 200 g for 5 minutes, supernatant aspirated and cells resuspended in PBS. This procedure is repeated once and the cells are resuspended at a concentration of 3×10^5 /ml in VGM with porcine trypsin. Then, 100 μ l cells are added to the serum-virus mixtures and the plates incubated at 35° C. in CO₂ for 5 days. The plates are fixed with 80% acetone in phosphate buffered saline (PBS) for 15 minutes at RT, air dried and then blocked for 30 minutes containing PBS with 0.5% gelatin and 2% FCS. An antibody to the S proteins, S1 protein or S2 protein is diluted in PBS with 0.5% gelatin/2% FCS/0.5% Tween 20 and incubated at RT for 2 hours. Wells are washed and horseradish peroxidase-conjugated goat anti-mouse IgG added, followed by another 2 hour incubation. After washing, O-phenylenediamine dihydrochloride is added and the neutralization titer is defined as the titer of serum that reduced color development by 50% compared to the positive control wells.

Example 23

MERS CoV Vaccine Immunogenicity Study in Mice

[0918] The instant study was designed to test the immunogenicity in mice of candidate MERS-CoV vaccines comprising a mRNA polynucleotide encoding the full-length Spike (S) protein, or the S2 subunit (S2) of the Spike protein obtained from MERS-CoV.

[0919] Mice were vaccinated with a 10 μ g dose of MERS-CoV mRNA vaccine encoding either the full-length MERS-CoV Spike (S) protein, or the S2 subunit (S2) of the Spike protein on days 0 and 21. Sera were collected from each mice on days 0, 21, 42, and 56. Individual bleeds were tested for anti-S, anti-S2 activity via a virus neutralization assay from all four time points.

[0920] As shown in FIG. 17, the MERS-CoV vaccine encoding the full-length S protein induced strong immune response after the boost dose on day 21. Further, full-length S protein vaccine generated much higher neutralizing antibody titers as compared to S2 alone (FIG. 18).

Example 24

MERS CoV Vaccine Immunogenicity Study in New Zealand White Rabbits

[0921] The instant study was designed to test the immunogenicity of candidate MERS-CoV mRNA vaccines encoding the full-length Spike (S) protein. The New Zealand white rabbits used in this study weighed about 4-5 kg. The rabbits were divided into three groups (Group 1a, Group 1b, and Group 2, n=8). Rabbits in Group 1a were immunized intramuscularly (IM) with one 20 μ g dose of the MERS-CoV mRNA vaccine encoding the full-length Spike protein on day 0. Rabbits in Group 1b were immunized intramuscularly (IM) with one 20 μ g dose of the MERS-CoV mRNA vaccine encoding the full-length Spike protein on day 0, and again on day 21 (booster dose). Group 2 received placebo (PBS). The immunized rabbits were then challenged and

samples were collected 4 days after challenge. The viral loads in the lungs, bronchoalveolar lavage (Bal), nose, and throat of the rabbits were determined, e.g., via quantitative PCR. Replicating virus in the lung tissues of the rabbits were also detected. Lung histopathology were evaluated and the neutralizing antibody titers in serum samples of the rabbits were determined.

[0922] Two 20 µg doses of MERS-CoV mRNA vaccine resulted in a 3 log reduction of viral load in the nose and led to complete protection in the throat of the New Zealand white rabbits (FIG. 19A). Two 20 µg doses of MERS-CoV mRNA vaccine also resulted in a 4 log reduction of viral load in the BAL of the New Zealand white rabbits (FIG. 19B). One 20 µg dose of MERS-CoV mRNA vaccine resulted in a 2 log reduction of viral load, while two 20 µg doses of MERS-CoV mRNA vaccine resulted in an over 4 log reduction of viral load in the lungs of the New Zealand white rabbits (FIG. 19C).

[0923] Quantitative PCR results show that two 20 µg doses of MERS-CoV mRNA vaccine reduced over 99% (2 log) of viruses in the lungs of New Zealand white rabbits (FIG. 20A). No replicating virus were detected in the lungs (FIG. 20B).

[0924] Further, as shown in FIG. 21, two 20 µg doses of MERS-CoV mRNA vaccine induced significant amount of neutralizing antibodies against MERS-CoV (EC₅₀ between 500-1000). The MERS-CoV mRNA vaccine induced antibody titer is 3-5 fold better than any other vaccines tested in the same model.

Example 25

Immunogenicity Study

[0925] The instant study is designed to test the immunogenicity in mice of candidate MeV vaccines comprising a mRNA polynucleotide encoding MeV hemagglutinin (HA) protein, MeV Fusion (F) protein or a combination of both. [0926] Mice are immunized intravenously (IV), intramuscularly (IM), or intradermally (ID) with candidate vaccines. Up to three immunizations are given at 3-week intervals (i.e., at weeks 0, 3, 6, and 9), and sera are collected after each

immunization until weeks 33-51. Serum antibody titers against MeV HA protein or MeV F protein are determined by ELISA.

Example 26

MeV Rodent Challenge

[0927] The instant study is designed to test the efficacy in transgenic mice of candidate MeV vaccines against a lethal challenge using a MeV vaccine comprising mRNA encoding MeV HA protein or MeV F protein. The transgenic mice express human receptor CD46 or signaling lymphocyte activation molecule (SLAM) (also referred to as CD150). Humans are the only natural host for MeV infection, thus transgenic lines are required for this study. CD46 is a complement regulatory protein that protects host tissue from complement deposition by binding to complement components C3b and C4b. Its expression on murine fibroblast and lymphoid cell lines renders these otherwise refractory cells permissive for MeV infection, and the expression of CD46 on primate cells parallels the clinical tropism of MeV infection in humans and nonhuman primates (Rall GF et al. PNAS USA 1997;94(9):4659-63). SLAM is a type 1 membrane glycoprotein belonging to the immunoglobulin superfamily. It is expressed on the surface of activated lymphocytes, macrophages, and dendritic cells and is thought to play an important role in lymphocyte signaling. SLAM is a receptor for both wild-type and vaccine MeV strains (Sellin CI et al. J Virol. 2006;80(13):6420-29).

[0928] CD46 or SLAM/CD150 transgenic mice are challenged with a lethal dose of the MeV. Animals are immunized intravenously (IV), intramuscularly (IM), or intradermally (ID) at week 0 and week 3 with candidate MeV vaccines with and without adjuvant. The animals are then challenged with a lethal dose of MeV on week 7 via IV, IM or ID. Endpoint is day 13 post infection, death or euthanasia. Animals displaying severe illness as determined by >30% weight loss, extreme lethargy or paralysis are euthanized. Body temperature and weight are assessed and recorded daily.

[0929] In experiments where a lipid nanoparticle (LNP) formulation is used, the formulation may include a cationic lipid, non-cationic lipid, PEG lipid and structural lipid in the ratios 50:10:1.5:38.5. The cationic lipid is DLin-KC2-DMA (50 mol %), the non-cationic lipid is DSPC (10 mol %), the PEG lipid is PEG-DOMG (1.5 mol %) and the structural lipid is cholesterol (38.5 mol %), for example.

TABLE 1

hMPV Immunogenicity studies bleeding schedule										
Animal groups		Day								
(n = 8)	vaccine	-2	0	7	14	21	28	35	56	
Placebo	Group 1 (n = 8)	PBS (IM)	Pre-Bleed	Prime	Bleeds	Bleeds	Bleeds/Boost	Bleeds	Bleeds	Harvest Spleens/Terminal Bleeds
10 µg Dose	Group 2 (n = 8)	10 µg (IM)								
2 µg Dose	Group 3 (n = 8)	2 µg (IM)								

Total n = 24

[0930] Each of the sequences described herein encompasses a chemically modified sequence or an unmodified sequence which includes no nucleotide modifications.

TABLE 2

hMPV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO:
gi 122891979 gb EF051124.1 Human metapneumovirus isolate TN/92-4 fusion protein gene, complete genome	ATGAGCTGGAAGGTGGTGATTATCTTCAGCCTGCTGATTA CACCTCAACACGGCCTGAAGGAGAGCTACCTGGAAGAGA GCTGCTCCACCATCACCGAGGGCTACCTGAGCGTGCTGC GGACCGGCTGGTACACCAACGTGTTCACCTGGAGGTGG GCGACGTGGAGAACCTGACCTGCAGCGACGGCCCTAGCC TGATCAAGACCGAGCTGGACCTGACCAAGAGCGCTCTGA GAGAGCTGAAGACCGTGTCCGCCGACCAGCTGGCCAGAG AGGAACAGATCGAGAACCCTCGGCAGAGCAGATTCTGTC TGGGCGCCATCGCTCTGGGAGTCCGCCGCTGCCGCTGCAG TGACAGCTGGAGTGGCCATTGCTAAGACCATCAGACTGG AAAGCGAGGTGACAGCCATCAACAATGCCCTGAAGAAG ACCAACGAGGGCGTGAGCACCTGGGCAATGGAGTGAGA GTGCTGGCCACAGCGGTGCGGGAGCTGAAGGACTTCGTG AGCAAGAACCCTGACCAGAGCCATCAACAAGAACAAGTG CGACATCGATGACCTGAAGTGGCCGTGAGCTTCTCCCA GTTCAACAGACGGTTCCTGAACGTGGTGAGACAGTTCTC CGACAACGCTGGAATCACACCTGCCATTAGCCTGGACCT GATGACCGACGCCGAGCTGGCTAGAGCCGTGCCCAACAT GCCACCAAGCGCTGGCCAGATCAAGCTGATGCTGGAGAA CAGAGCCATGGTGGGAGAAAGGGCTTCGGCATCCTGAT TGGGGTGTATGGAAGCTCCGTGATCTACATGGTGAGCT GCCCATCTTCGGCGTGATCGACACACCTGCTGGATCGTG AAGGCCGCTCTAGCTGCTCCGAGAAGAAAGGAACTAT GCCTGTCTGTGAGAGAGGACAGGGCTGGTACTGCCAG AACGCCGGAAGCACAGTGTACTATCCCAACGAGAAGGAC TGCGAGACCAGAGGCGACACGTGTTCTGCGACACCGCT GCCGGAATCAACGTGGCCGAGCAGAGCAAGGAGTGCAA CATCAACATCAGCACAAACCACTACCCCTGCAAGGTGAG CACCGGACGGCACCCCATCAGCATGGTGGCTCTGAGCCC TCTGGGCGCTCTGGTGGCTGCTATAAGGGCGTGTCTGT AGCATCGGCAGCAATCGGGTGGGCATCATCAAGCAGCTG AACAAGGGATGCTCCTACATCACCAACCAGGACGCCGAC ACCGTGACCATCGACAACACCGTGATCCAGCTGAGCAAG GTGGAGGGCGAGCAGCAGTGTCAAGGGCAGACCCGT GAGCTCCAGCTTCGACCCCATCAAGTTCCCTGAGGACCA GTTCAACGTGGCCCTGGACAGGTGTTGAGAATCATCGA GAACAGCCAGGCCCTGGTGACCAGAGCAACAGAATCCT GTCCAGCGCTGAGAAGGGCAACACCGGCTTCATCATTGT GATCATTTGATCGCCGTGCTGGGCAGCTCCATGATCCTG GTGAGCATCTTCATCATTATCAAGAAGACCAAGAAACCC ACCGGAGCCCCCTCTGAGCTGAGCGCGTGACCAACAAT GGCTTCATTCCCCACAACCTGA	1
gb AY525843.1 : 3065-4684 Human metapneumovirus isolate NL/1/99, complete genome	ATGTCTTGAAAGTGATGATCATCATTTCTGTTACTCATAA CACCCAGCACGGGCTAAAGGAGAGTTATTTGGAAGAAT CATGTAGTACTATAACTGAGGGATACCTCAGTGTTTAAAG AACAGGCTGGTACACTAATGTCTTCACATTAGAAGTTGGT GATGTTGAAAATCTTACATGTACTGATGGACCTAGCTTAA TCAAAACAGAACTTGATCTAACAATAAGTGCTTTAAGGG AACTCAAAACAGTCTCTGCTGATCAGTTGGCGAGAGAGG AGCAAAATTGAAAATCCAGACAATCAAGATTGTCTTAG GTGCGATAGCTCTCGGAGTTGCTACAGCAGCAGCAGTCA CAGCAGGCATTGCAATAGCCAAAACCATAAGGCTTGAGA GTGAGGTGAATGCAATTAAAGGTGCTCTCAAAACAACTA ATGAAGCAGTATCCACATTAGGGAATGGTGTGCGGGTCC TAGCCACTGCAGTGAGAGAGCTAAAAGAATTTGTGAGCA AAAACCTGACTAGTGCAATCAACAGGAACAAATGTGACA TTGCTGATCTGAAGATGGCTGTGAGCTTCAGTCAATTCAA CAGAAGATTTCTAAATGTTGCGGCAGTTTTCAGACAAT GCAGGGATAACACCAGCAATATCATTGGACCTGATGACT GATGCTGAGTTGGCCAGAGCTGTATCATACATGCCAACA TCTGCAGGGCAGATAAACTGATGTTGGAGAACCAGCGCA ATGGTAAGGAGAAAAGGATTTGGAATCCTGATAGGGGTC TACGGAAGCTCTGTGATTTACATGGTTCAATTGCCGATCT TTGGTGTATAGATACACCTTGTGGATCATCAAGGCAGC TCCCTCTTGCTCAGAAAAAACCAGGAATTATGCTTGCTC CTAAGAGAGGATCAAGGTGGTATTGTAAAAATGACGGA	2

TABLE 2-continued

hMPV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO:
	TCTACTGTTTACTACCCAAATGAAAAAGACTGCGAAACA AGAGGTGATCATGTTTTTTGTGACACAGCAGCAGGGATC AATGTTGCTGAGCAATCAAGAGAATGCAACATCAACATA TCTACTACCAACTACCCATGCAAAGTCAGCACAGGAAGA CACCCCTATAAGCATGGTTGCACTATCACCTCTCGGTGCTT TGGTGGCTTGCTATAAAGGGTAAGCTGCTCGATTGGCA GCAATTGGGT TGGAATCATCAAACAATTACCCAAAGGCTGCTCATACAT AACCAACCAGGATGCAGACACTGTAACAATTGACAATAC CGTGTATCAACTAAGCAAAGTTGAAGGTGAACAGCATGT AATAAAAGGGAGACCAGTTTCAAGCAGTTTGTATCCAAT CAAGTTTCCTGAGGATCAGTTCAATGTTGCGCTTGATCAA GTCTTCGAAAGCATTGAGAACAGTCAGGCACATAGTGGAC CAGTCAAACAAAATTCTAAACAGTGCAGAAAAAGGAAA CACTGGTTTCATTATCGTAGTAATTTGGTTGCTGTTCTTG GTCTAACCATGATTTTCAGTGAGCATCATCATATAATCAA GAAAACAAGGAAGCCACAGGAGCACCTCCAGAGCTGA ATGGTGTCAACACGGCGGTTTCATACCACATAGTTA	
gb KJ627414.1 : 3015-4634 Human metapneumovirus strain hMPV/ <i>Homo sapiens</i> /PER/CFI0497/ 2010/B, complete genome	ATGTCTTGAAAGTGATGATTATCATTTCTGTTACTCATAA CACCTCAGCATGGACTAAAAGAAAGTTATTTAGAAGAAT CATGTAGTACTATAACTGAAGGATATCTCAGTGTTTTAAG AACAGGTTGGTACACCAATGTCTTTACATTAGAAGTTGGT GATGTTGAAAATCTTACATGTACTGATGGACCTAGCTTAA TCAAAACAGAAGTTGACCTAACCAAAAGTGCTTTAAGAG AACTCAAACAGTTTCTGCTGATCAGTTAGCGAGAGAAG AACAAATTGAAAATCCAGACAATCAAGGTTTGTCTTAG GTGCAATAGCTCTTGGAGTTGCCACAGCAGCAGCAGTCA CAGCAGGCATTGCAATAGCCAAAATATAAGGCTTGAGA GTGAAGTGAATGCAATCAAGGTGCTCTCAAAACAACCA ATGAGGCAGTATCAACACTAGGAAATGGAGTGCGGGTCC TAGCCACTGCAGTAAGAGAGCTGAAAGAATTGTGAGCA AAAACCTGACTAGTGCGATCAACAAGAACAAAGTGTGACA TTGCTGATTTGAAGATGGCTGTGAGCTTCAGTCAGTTCAA CAGAAGATTCTAAATGTTGTGCGGCAGTTTTCAGACAAT GCAGGGATAACACCAGCAATATCATTGGACCTGATGAAT GATGCTGAGCTGGCCAGAGCTGTATCATACATGCCAACA TCTGCAGGACAGATAAACTAATGTTAGAGAACCGTGCA ATGGTGAGGAGAAAAGGATTTGGAATCTTGATAGGGGTC TACGGAAGCTCTGTGATTTACATGGTCCAGCTGCCGATCT TTGGTGTCTATAAATACACCTTGTGGATAATCAAGGCAGC TCCCTCTTGTTTCAAAAAGATGGAATTTATGCTTGCCTC CTAAGAGAGGATCAAGGGTGGTATTGTAATAATGCAGGA TCCACTGTTTACTACCCAAATGAAAAAGACTGCGAAACA AGAGGTGATCATGTTTTTTGTGACACAGCAGCAGGGATC AATGTTGCTGAGCAATCAAGAGAATGCAACATCAACATA TCTACCACTAATACCCATGCAAAGTCAGCACAGGAAGA CACCTATCAGCATGGTTGCACTATCACCTCTCGGTGCTT TGGTAGCTTGCTACAAAGGGGTTAGCTGCTCGACTGGCA GTAATCAGGTTGGAATAATCAAACAATACCTAAAGGCT GCTCATACATAACTAACAGGACGCAGACACTGTAACAA TTGACAACACTGTGTATCAACTAAGCAAAGTTGAGGGTG AACAGCATGTAATAAAAGGGAGACCAGTTTCAAGCAGTT TTGATCCAATCAGGTTTCCTGAGGATCAGTTCAATGTTGC GCTTGATCAAGTCTTTGAAAGCATTGAAAACAGTCAAGC ACTAGTGGACAGTCAACAAAATTTGAACAGTGCAGA AAAAGGAACACTGGT TTCATTATTGTAATAATTTTGATTGCTGTTCTTGGGTTAAC CATGATTTTCAGTGAGCATCATCATATAATCAAAAAAC AAGGAAGCCACAGGGGCACCTCCGGAGCTGAATGGTGT TACCAACGGCGGTTTCATACCGCATAGTTAG	3
gb KJ723483.1 : 5586-7310 Human respiratory syncytial virus strain RSVA/ <i>Homo sapiens</i> /USA/84I- 215A-01/1984, complete genome	ATGGAGTTGCCAATCCTCAAACAAATGCAATTACCACA ATCCTTGCTGCAGTCACACTCTGTTTCGCTTCCAGTCAAA ACATCACTGAAGAATTTTATCAATCAACATGCAGTGCA TTAGCAAAGGCTATCTTAGTGCTCTAAGAACTGGTTGGTA TACTAGTGTATAACTATAGAATTAAGTAATATCAAGGA AAATAAGTGAATGGAACAGATGCTAAGGTAATAATGAT AAAACAAGAATTAGATAAATATAAAATGCTGTAACAGA ATTGCAGTTGCTCATGCAAAGCACACCAGCAGCCAACAA TCGAGCCAGAAGAGAATACCAAGGTTTATGAATTATAC ACTCAATAATACCAAAAATACCAATGTAACATTAGCAA	4

TABLE 2-continued

hMPV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO:
	GAAAAGGAAAAGAAGATTTCTTGGCTTTTGTAGGTGTT GGATCTGCAATCGCCAGTGGCATTGCTGTATCTAAGGTCC TGCACCTAGAAGGGGAGTGAACAAATCAAAGTGCTC TACTATCCACAAACAAGGCTGTAGTCAGCTTATCAAATG GAGTTAGTGTCTTAACCAGCAAAGTGTAGACCTCAAAA ACTATATAGATAAACAGTTGTACCTATTGTGAACAAGC AAAGCTGCAGCATATCAAACATTGAACTGTGATAGAGT TCCAACAAAAGAACACAGACTACTAGAGATTACCAGGG AATTTAGTGTAAATGCAAGGTGAACACCTGTAAGCAC TTATATGTTAACTAATAGTGAATTATTATCATTAAATCAAT GATATGCCCTATAACAAATGATCAGAAAAAGTTAATGTCC AACATGTTCAAATAGTTAGACAGCAAAGTTACTCTATC ATGTCCATAATAAAGGAGGAAGTCTTAGCATATGTAGTA CAATTACCACTATATGGTGTAAATAGATACCCCTGTTGGA AACTGCACACATCCCCTCTATGTACAACCAACAAAGG AAGGGTCCAACATCTGCTTAACAAGAACCGACAGAGGAT GGTATTGTGACAATGCAGGATCAGTATCTTTCTTCCACA AGCTGAAACATGTAAAGTTCATCGAATCGGGTATTTGT GACACAATGAACAGTTTAAACATTACCAAGTGAAGTAAAT CTCTGCAACATTGACATATTCAACCCCAAATATGATTGCA AAATTATGACTTCAAAACAGATGTAAGCAGCTCCGTTA TCACATCTCTAGGAGCCATTGTGTATGCTATGGCAAAAC TAAATGTACAGCATCCAATAAAAAATCGTGGGATCATAAA GACATTTTCTAACGGGTGTGATTATGTATCAATAAGGG GGTGGATACTGTGTCTGTAGGTAATACATTATATTATGTA AATAAGCAAGAAGGCAAAAGTCTCTATGTAAAAGGTGAA CCAATAATAAATTTCTATGACCCATTAGTGTCCCTCTG ATGAATTTGATGCATCAATATCTCAAGTCAATGAGAAGA TTAACCAAGAGCTAGCATTTATTCTGTAATCCGATGAATT ATTACATAATGTAAATGCTGGTAAATCCACCACAAATAT CATGATAACTACTATAATTATAGTGATTATAGTAATATTG TTATCATTAATTGCAAGTTGGACTGCTCCTATACTGCAAGG CCAGAAGCACACCAGTCACACTAAGTAAGGATCAACTGA GTGGTATAAATAATATTGCATTTAGTAACTGA	
hMPV mRNA Sequences		
gi 122891979 gb EF051124.1 Human metapneumo virus isolate TN/92-4 fusion protein gene, complete genome	AUGAGCUGGAAGGUGGUGAUUAUCUUCAGCCUGCUGAU UACACCUCAACACCGCCUGAAGGAGAGCUACCUUGGAAG AGAGCUGCUCCACCAUCACCGAGGGCUACCUAGAGCGUG CUGCGGACCGGCUGGUACCAACGUGUUCACCCUGGA GGUGGGCGACGUGGAGAACCUAGCCUGCAGCGACGGCC CUAGCCUGAUCAAGACCGAGCUGGACCUAGCCAAGAGC GCUCUGAGAGAGCUGAAGACCGUGUCCGCCGACGAGCU GGCCAGAGAGGAACAGAUCCGAGAACCUCGGCAGAGCA GAUUCGUGCUGGGCGCCAUCCGUCUGGGAGUCGCCGCU GCCGCUAGUGACAGCUGGAGUGGCCAUUGCUAAGAC CAUCAGACUGGAAAGCGAGGUGACAGCCAUCAACAAUG CCCUGAAGAAGACCAACGAGGCCUGAGCACCUCUGGGC AAUGGAGUGAGAGUGCUUGGCCACAGCCGUGCGGGAGCU GAAGGACUUCGUGAGCAAGAACCUGACCAGAGCCAUCA ACAAGAACAAGUGCGACAUCGAUGACCUGAAGAUGGCC GUGAGCUUCUCCAGUUCACAGACGGUUCUGAACGU GGUGAGACAGUUCUCCGACAACGCUUGGAUACACACCU CCAUUAAGCCUGGACCUGAUGACCGACGCCGAGCUGGCU AGAGCCGUGCCCAACAUCCACAGCGCUGGCCAGAU CAAGCUGAUGCUGGAGAACAGAGCCAUGGUGCGGAGAA AGGGCUUCGGCAUCCUGAUUGGGGUGUAUGGAAGCUCC GUGAUCUACAUGGUGCAGCUGCCCAUCUUCGGCGUGAU CGACACACCCUGCUGGAUCUGUAAGGCCGCUCCUAGCU GCUCCGAGAAGAAAGGAAACUAUGCCUGUCUGCUGAGA GAGGACCAGGGCUGGUACUGCCAGAACGCCGGAAGCAC AGUGUACUAUCCCAACGAGAAGGACUGCGAGACCAAG GCGACCACGUGUUCUGCGACACCGCUGCCGGAUCAAAC GUGGCCGAGCAGAGCAAGGAGUGCAACAUCAACAUAG CACAACCAACUACCCUGCAAGGUGAGCACCGGACGGC ACCCAUCAGCAUGGUGGCUUGAGGCCUUCUGGGCGCU CUGGUGGCCUGCUAUAAGGGCGUGUCCUGUAGCAUCGG CAGCAAUCCGGUGGGCAUCAUACAGCAGCUGAACAAAG GAUGCUCUACAUCACCAACCAAGGACGCCGACACCGUG ACCAUCGACAACACCGUUAACAGCUGAGCAAGGUGGA GGGCGAGCAGCACGUGAUCAAGGGCAGACCGUGAGCU	57

TABLE 2-continued

hMPV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO:
	CCAGCUUCGACCCCAUCAAGUCCUGAGGACCAGUUC AACGUGGCCUGGACCAGGUGUUUGAGAACAUCGAGAA CAGCCAGGCCUGGUGGACCAGAGCAACAGAAUCCUGU CCAGCGCUGAGAAGGGCAACACCGGCUUCAUCAUUGUG AUCAUUCUGAUCGCCUGGUGGAGCUCUUGAUCCU GGUGAGCAUCUUCAUCAUUAUCAAGAGACCAAGAAAC CCACCGGAGCCCCUUCUGAGCUGAGCGGCGUGACCAAC AAUGGCUUCAUUCGCCACAACUGA	
gb AY525843.1 : 3065-4684 Human metapneumovirus isolate NL/1/99, complete genome	AUGUCUUGGAAAGUGAUGAUCAUUUUCGUUACUCAU AACACCCAGCAGCGGCUAAAAGGAGAGUUAUUUGGAAG AAUCAUGUAGUACUAUAACUGAGGGAUACCCUCAGUGUU UUAAGAACAGGCUGGUACACUAAUGUCUUCACAUUAGA AGUUGGUGAUGUUGAAAAUCUUAACAUAGUACUGAUGGA CCUAGCUUAUAACAAACAGAACUUGAUCUAACAAAAAG UGCUUUUAGGGAAUCUAAAAAGUCUCUGCUGAUCAGU UGGCGAGAGAGGAGCAAAUUGAAAAUCCAGACAAUCA AGAUUUGUCUUGAGGUGCGAUAGCUCUGGAGUUGCUAC AGCAGCAGCAGUCACAGCAGGCAUUGCAUAGCCAAAA CCAUAAGGCUUGAGAGUGAGGUGAAUGCAUUAAGG UGCUCUCAACAAACUAUGAAGCAGUAUCCACAUAUAG GGAAUGGUGUGCGGGUCCUAGCCACUGCAGUGAGAGAG CUAAAAGAAUUUGAGAGCAAAACCUAGCUAGUGCAAU CAACAGGAACAAUUGUGACAUUGCUGAUCUGAAGAUGG CUGUCAGCUUCAGUCAAUUCAACAGAAAGAUUUCUAAAU GUUGUGCGGCAGUUUUCAGACAAUGCAGGGAUAAACAC AGCAAUAUCAUUGGACCUAGUAGCUGAUGCUGAGUUGG CCAGAGCUGUAUCAUAUGCCAACAUCUGCAGGGCAG AUAAAAUCUGAUGUUGGAGAACCGCGCAUUGUAAGGAG AAAAGGAUUUGGAUCCUGAUAGGGGUCUACGGAAGCU CUGUGAUUUACAUGGUUCAUUGCCGAUCUUUGGUGUC AUAGAUACACCUUGUUGGAUCAUCAAGGCAGCUCUUC UUGCUCAGAAAAAAACGGGAAUUAUGCUUGCCUCCUAA GAGAGGAUCAAGGGUGGUUAUUGUAAAAAUGCAGGAUC UACUGUUUACUACCCAAUAGAAAAGACUGCGAAACAA GAGGUGAUCUUGUUUUUGACACAGCAGCAGGGAUC AAUGUUGCUGAGCAAUCAAGAGAAUGCAACAUCAACAU AUCUACUACCAACUACCAUGCAAAGUCAGCACAGGAA GACACCUUAUAAGCAUGGUUGCACAUAUCACCUUCGGU GCUUUGGUGGCUUGCUAUAAGGGGUAAGCUGCUCGAU UGGCAGCAAUUGGGU UGGAAUCAUCAACAAUUAACCAAAGGCUGCUCAUACA UAACCAACCAGGAUGCAGACACUGUAACAAUUGACAAU ACCGUGUAUCAACUAAGCAAAGUUGAAGGUAAACAGCA UGUAAUAAAAGGGAGACCAGUUUCAAGCAGUUUUGAUC CAUACAAGUUUCCUGAGGAUCAGUUAUUGUUGCGCUU GAUCAAGUCUUCGAAAGCAUUGAGAAAGUAGGCAUCU AGUGGACCAGUCAACAAAAUUCUAAACAGUGCAGAAA AAGGAAACACUGGUUUCAUUAUCGUAGUAAUUUGGU UGCUGUUCUUGGUCUAACCAUGAUUUUAGUGAGCAUCA UCAUCAUAUCAAAGAAACAAAGGAAGCCACAGGAGCA CCUCCAGAGCUGAAUGGUGUACCAACCGGCGGUUCAU ACCAUAAGUUAG	58
gb KJ627414.1 : 3015-4634 Human metapneumovirus strain hMPV/Homo sapiens/PER/CFI0497/ 2010/B, complete genome	AUGUCUUGGAAAGUGAUGAUUAUCAUUUCGUUACUCAU AACACCUAGCAUGGACUAAAAGAAAGUUAUUUAGAG AAUCAUGUAGUACUAUAACUGAAGGAUUAUCUAGUGUU UUAAGAACAGGUUGGUACACCAUUGUCUUUACAUUAGA AGUUGGUGAUGUUGAAAAUCUUAACAUAGUACUGAUGGA CCUAGCUUAUAACAAACAGAACUUGACCUAACCAAAAG UGCUUUUAGAGAAUCUAAAAAGUUUCUGCUGAUCAGU UAGCGAGAGAAAGCAAAUUGAAAAUCCAGACAAUCA AGGUUUGUCCUAGGUGCAUAGCUCUUGGAGUUGCCAC AGCAGCAGCAGUCACAGCAGGCAUUGCAUAGCCAAAA CUAUAAGGCUUGAGAGUGAAGUGAAUGCAUCAAAGG UGCUCUCAAAACAACCAUAGGCGAGUAUACAACUAG GAAUUGGAGUGCGGGUCCUAGCCACUGCAGUAAGAGAG CUGAAAGAAUUUGAGAGCAAAACCUAGCUAGUGCGAU CAACAAGAACAGUGUGACAUUGCUGAUUUUGAAGAUGG CUGUCAGCUUCAGUCAGUUAACAGAAAGAUUCCUAAAU GUUGUGCGGCAGUUUUCAGACAAUGCAGGGAUAAACAC AGCAAUAUCAUUGGACCUAGAAUGAUGCUGAGCUGG	59

TABLE 2-continued

hMPV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO:
gb KJ723483.1 : 5586-7310 Human respiratory syncytial virus strain RSVA/ <i>Homo sapiens</i> /USA/84I-215A-01/1984, complete genome	CCAGAGCUGUAUCAUACAUGCCAACAUUCUGCAGGACAG AUAAAACUAAUGUUAAGAGAACCUGCAUUGGUGAGGA GAAAAGGAUUUGGAAUCUUGAUAGGGGUUACGGAAG CUCUGUGAUUUACAUGGUCCAGCUGCCGAUCUUUGGUG UCAUAAAUAACCCUUGUUGGAUUAUCAAGGCAGCUCCT UCUUGUUCAGAAAAAGAUUGGAAUUAUGCUUGCCUCCU AAGAGAGGAUCAAGGGUGGUUUAUGUAAAAUUGCAGGA UCCACUGUUUAUCUCCAAAUGAAAAAGACUGCGAAAC AAGAGGUGAUCAUGUUUUUGUGACACAGCAGCAGGGA UCAUGUUGCUGAGCAUCAAAGAAUGCAACAUCAAC AUUUCUACCAACCAUACCAUGCAAAGUCAGCACAGG AAGACACCCUUAUCAGCAUGGUUGCACUAUACCCUCUG GUGCUUUGGUAGCUUGCUACAAGGGGUUAGCUGCUCG ACUGGCAGUAAUACAGGUUGGAAUUAUCAAACAACUACC UAAAGGCUGCUCAUACAUAACUAAACAGGACGCAGACA CUGUAACAUAUGACAACACUGUGUAUCAAUAAGCAAA GUUGAGGGUGAACAGCAUGUAAUAAAAGGGAGACCAG UUUCAAGCAGUUUGAUCCAUCAGGUUUCUGAGGAU CAGUUCAAUGUUGCGCUUGAUCAAGUCUUUGAAAGCAU UGAAAACAGUCAAGCACUAGUGGACCAGUCAACAAAA UUUGAACAGUGCAGAAAAAGGAAACACUGGU UUCAUUAUUGUAAUAAUUUUGAUUGCUGUUCUUGGGU UAACCAUGAUUUCAGUGAGCAUCAUCAUAAUCAA AAAACAAGGAAGCCACAGGGGCACCCGAGCUGAA UGGUGUUAACCAACGGCGGUUCAUACCGCAUAGUUAG	60
	AUGGAGUUGCCAAUCCUCAAACAAUAGCAUUAACCAC AAUCCUUGCUGCAGUCAACUCUGUUUUGCUUCCAGUC AAAACAUCACUGAAGAAUUUAUCAUCAAACAUAGCAGU GCAGUUAGCAAAGGCUAUCUUAGUGCUCUAGAACUGG UUGGUUAUCUAGUGUUUAUACAUAUAGAAUUAAGUAAU AUCAAAGGAAAAUAGUGUAAUGGAACAGAUUCUAAGG UAAAAUUGAUAAAACAAGAAUUAAGAUAAUUAUAAAA UGCUGUAACAGAAUUGCAGUUGCUCAUGCAAAGCACAC CAGCAGCCAACAUCGAGCCAGAAGAGAACUACCAAGG UUUAUGAAUUAUACACUCAAUAAUACCAAAAUUACCAA UGUAACAUAUAGCAAGAAAAGGAAAAGAAGAUUUCUU GGCUUUUUGUAGGUGUUGGAUCUGCAAUCGCCAGUGG CAUUGCUGUAUCUAAAGGUCUGCACCUAGAAGGGGAAG UGAACAAAUCAAAAGUGCUUCUACUACCAAAACAAG GCUGUAGUCAGCUUAUCAAAUGGAGUAGUGUCUUAAC CAGCAAAGUGUUAGACCUCAAAACUAUUAUAGAUAAAC AGUUGUUAACCUAUUGUGAACAAAGCAGCAGCAUA UCAAACAUUGAAACUGUGAUAGAGUUCCAACAAAAGAA CAACAGACUACUAGAGAUUACAGGGAAUUAUGUGUUA AUGCAGGUGUAACUACCCUGUAAGCACUUAUUGUUA ACUAAUAGUGAAUUAUUAUUAUUAUUAUUAUUAUGCC UAUAACAAUAGAUCAAAAAAGUUAUUGUCCAAACAAG UUCAAAUAGUUAGACAGCAAAGUUAUCUUAUCUAGUCC AUAAUAAAGGAGGAAGUCUUAAGCAUUAUGUAGUACA UAACCAUUAUUGGUGUAAUAGAUACACCCUGUUGGAAA CUGCACACAUCUCCUUAUGUACAAACCAACAAAGGA AGGGUCCAAACUUCUGCUUAACAAGAACCGACAGAGGAU GGUAUUGUGACAAUGCAGGAUCAGUUAUCUUUCUCCCA CAAGCUGAAACAUUGAAAGUUAUUAUGAAUCGGGUAAU UUGUGACACAAGUAAACAGUUUAACAUAUACCAAGUGAAG UAAAUCUCUGCAACAUAUGACAUAUUAACCCCAAUAU GAUUGCAAAUUAUAGACUUCAAAAACAGAUUAAGCAG CUCCGUUAUCACUUCUAGGAGCCAUGUGUUAUGCU AUGGCAAAACUAAUUGUACAGCAUCCAAUAAAAUUCGU GGGAUCAUAAAGACAUUUUAACGGGUGUGAUUAUG UAUCAAAUAAAGGGGUGGAUACUGUGUCUGUAGGUAA UACAUAUUAUUAUGUAAUUAAGCAAGAAAGGCAAAAGU CUCUAUGUAAAAGGUGAACCAUAAUAAUUAUUAUGA CCCAUUAUGUUCUCCUUGAUGAAUUAUGAUGCAUCAA UAUCUCAAGUCAUAGAGAAGAUUAACAGAGCCUAGCA UUUAUUCGUAAUCCGAUGAAUUAUUAUUAUUAUUA AUGCUGGUAAUCCACCACAAUUAUCAUGAUAAUUAU	

TABLE 2-continued

hMPV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO:
	AUAUUUAUAGUGAUUAUAGUAAUUAUUGUUAUCAUUA UUGCAGUUGGACUGCUCUUAUACUGCAAGGCCAGAAGC ACACCAGUCACACUAAGUAAGGAUCAACUGAGUGUAU AAAUAAUUAUGCAUUUAGUAAACUGA	

TABLE 3

hMPV Amino Acid Sequences		
Description	Sequence	SEQ ID NO:
gi 122891979 gb EF051124.1 Human metapneumovirus isolate TN/92-4 fusion protein gene, complete cds	MSWKVVIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGW YTNVFTLEVGDVENLTCSGDSLKTLELDLTKSALRELKTVS ADQLAREEQIENPRQSRFVLGAIALGVAAAAVTAAGVAIAK TIRLESEVTAIINNALKKTNEAVSTLGNVRLATAVRELKD FVSKNLTRAINKNKCDIDDLKMAVSFSQFNRRFLNVVRQFS DNAGITPAISLDLMTDAELARAVPNMPTSAGQIKLMLENRA MVRKGFGLIGVYGSSVIYMQLPFIGVIDTPCWIVKAAPS CSEKKGNYACLLREDQGWYCKNAGSTVYYPNEKDCETR DHVFCDTAAGINVAEQSKECNINISTTNYPCVKSTGRHPISM VALSPLGALVACYKGVSCSIGSNRVGIIKQLNKGCSYITNQD ADTVTIDNTVYQLSKVEGEQHVIKGRPVSSSFDPIKFPEDQF NVALDQVFENIENSQALVDQSNRILSSAEKNGTGFIIVILIAV LGSSMILVSIFIIKKTKKPTGAPPELNGVTNNGFIPHN	5
gb AY525843.1 : 3065-4684 Human metapneumovirus isolate NL/1/99, complete cds	MSWKVMIIISLLITPQHGLKESYLEESCSTITEGYLSVLRTGW YTNVFTLEVGDVENLTCTDGPDLKTLELDLTKSALRELKTVS ADQLAREEQIENPRQSRFVLGAIALGVATAAAVTAAGIAIAKT IRLESEVNAIKGALKQTNEAVSTLGNVRLATAVRELKEF VSKNLTSAINRNKCDIADLKMAVSFSQFNRRFLNVVRQFSD NAGITPAISLDLMTDAELARAVSYMPTSAGQIKLMLENRAM VRRKGFGLIGVYGSSVIYMQLPFIGVIDTPCWIIKAAPSCS EKNKGNYACLLREDQGWYCKNAGSTVYYPNEKDCETR VFCDTAAGINVAEQSRECNINISTTNYPCVKSTGRHPISMVA LSPLGALVACYKGVSCSIGSNWVGIIKQLPKGCSYITNQDAD TVTIDNTVYQLSKVEGEQHVIKGRPVSSSFDPIKFPEDQFNV ALDQVFESIENSQALVDQSNKILNSAEKNGTGFIIVVILVAVL GLTMISVSIIIIKKTKKPTGAPPELNGVTNNGFIPHS	6
gb KJ627414.1 : 3015-4634 Human metapneumovirus strain hMPV/ <i>Homo sapiens</i> /PER/CFI0497/ 2010/B, complete cds	MSWKVMIIISLLITPQHGLKESYLEESCSTITEGYLSVLRTGW YTNVFTLEVGDVENLTCTDGPDLKTLELDLTKSALRELKTVS ADQLAREEQIENPRQSRFVLGAIALGVATAAAVTAAGIAIAKT IRLESEVNAIKGALKQTNEAVSTLGNVRLATAVRELKEF VSKNLTSAINKNKCDIADLKMAVSFSQFNRRFLNVVRQFSD NAGITPAISLDLMTDAELARAVSYMPTSAGQIKLMLENRAM VRRKGFGLIGVYGSSVIYMQLPFIGVINTPCWIIKAAPSCS EKDGNVYACLLREDQGWYCKNAGSTVYYPNEKDCETR VFCDTAAGINVAEQSRECNINISTTNYPCVKSTGRHPISMVA LSPLGALVACYKGVSCSIGSNQVGIIKQLPKGCSYITNQDAD TVTIDNTVYQLSKVEGEQHVIKGRPVSSSFDPIRFPEDQFNV ALDQVFESIENSQALVDQSNKILNSAEKNGTGFIIVVILVAVL LTMISVSIIIIKKTKKPTGAPPELNGVTNNGFIPHS	7
gb KJ723483.1 : 5586-7310 Human respiratory syncytial virus strain RSVA/ <i>Homo sapiens</i> /USA/84I- 215A-01/1984, complete cds	MELPILKTNAITTILAAVTLCFASSQNI TEEFYQSTCSAVSKG YLSALRTGWYTSVITIELSNIKENKCNKGTDAKVLKIQELDK YKNAVTELQLLMQSTPAANNRARELPRFMNYTLNNTKNT NVTLSKKRRRFLGFLGVSAGIAVSKVLHLEGEVNKI KSALLSTNKAVVSLNGVSVLTSKVLDLKNYIDKQLPIVN KQSCSISNIETVIEFQQKNRLLITREFSVNAGVTPVSTYM LTNSELLSLINDMPI TNDQKKLMSNNVQIVRQSYSIMSIIKE EVLAYVVQLPLYGVIDTPCWKLHTSPLCTNTKEGSLICLTR TDRGWYCDNAGSVSFFPQAECKVQSNRVFCDTMNSLTLP SEVNLNIDIFNPKYDCKIMTSKTDVSSSVITSLGAIVSCYK TKCTASNKNRGIIKTFSGNCDYVSNKGVDTVSVGNTLYYN KQEGKSLYVKGEPIINFYDPLVFPSEDFASISQVNEKINQSL AFIRKSDLLHNVNAGKSTTNIMITIIIVIIIVLLSLIAVGLL YCKARSTPVTLSKDLQSGINNIASFN	8

TABLE 4

hMPV NCBI Accession Numbers (Amino Acid Sequences)	
Virus	GenBank Accession
F [Human metapneumovirus] [Human metapneumovirus]	AEK26895.1
fusion glycoprotein [Human metapneumovirus]	ACJ53565.1
fusion glycoprotein [Human metapneumovirus]	ACJ53566.1
fusion glycoprotein [Human metapneumovirus]	ACJ53569.1
fusion protein [Human metapneumovirus]	AEZ52347.1
fusion glycoprotein [Human metapneumovirus]	ACJ53574.1
fusion glycoprotein [Human metapneumovirus]	AHV79473.1
fusion glycoprotein [Human metapneumovirus]	ACJ53570.1
fusion glycoprotein [Human metapneumovirus]	ACJ53567.1
fusion protein [Human metapneumovirus]	AAS22125.1
fusion glycoprotein [Human metapneumovirus]	AHV79795.1
fusion glycoprotein [Human metapneumovirus]	AHV79455.1
fusion glycoprotein [Human metapneumovirus]	ACJ53568.1
fusion protein [Human metapneumovirus]	AAS22109.1
fusion glycoprotein [Human metapneumovirus]	AGU68417.1
fusion glycoprotein [Human metapneumovirus]	AGJ74228.1
fusion glycoprotein [Human metapneumovirus]	ACJ53575.1
fusion protein [Human metapneumovirus]	AAU25820.1
fusion glycoprotein [Human metapneumovirus]	AGU68377.1
fusion glycoprotein [Human metapneumovirus]	AGU68371.1
fusion glycoprotein [Human metapneumovirus]	AGJ74087.1
fusion glycoprotein [Human metapneumovirus]	ACJ53560.1
fusion glycoprotein [Human metapneumovirus]	AHV79858.1
fusion glycoprotein [Human metapneumovirus]	ACJ53577.1
fusion protein [Human metapneumovirus]	AAS22085.1
fusion protein [Human metapneumovirus]	AEZ52348.1
fusion glycoprotein [Human metapneumovirus]	AGJ74044.1
fusion glycoprotein [Human metapneumovirus]	ACJ53563.1
fusion glycoprotein precursor [Human metapneumovirus]	YP_012608.1
fusion glycoprotein [Human metapneumovirus]	AGJ74053.1
fusion protein [Human metapneumovirus]	BAM37562.1
fusion glycoprotein [Human metapneumovirus]	ACJ53561.1
fusion glycoprotein [Human metapneumovirus]	AGU68387.1
fusion [Human metapneumovirus]	AGL74060.1
fusion glycoprotein precursor [Human metapneumovirus]	AAV88364.1
fusion protein [Human metapneumovirus]	AAN52910.1
fusion protein [Human metapneumovirus]	AAN52915.1
fusion protein [Human metapneumovirus]	BAM37564.1
fusion glycoprotein precursor [Human metapneumovirus]	BAH59618.1
fusion protein [Human metapneumovirus]	AAQ90144.1
fusion glycoprotein [Human metapneumovirus]	AHV79446.1
fusion protein [Human metapneumovirus]	AEI.87260.1
fusion glycoprotein [Human metapneumovirus]	AHV79867.1
fusion protein [Human metapneumovirus]	ABQ66027.2
fusion glycoprotein [Human metapneumovirus]	ACJ53621.1
fusion protein [Human metapneumovirus]	AAN52911.1
fusion glycoprotein [Human metapneumovirus]	AHV79536.1
fusion glycoprotein [Human metapneumovirus]	AGU68411.1
fusion protein [Human metapneumovirus]	AEZ52346.1
fusion protein [Human metapneumovirus]	AAN52913.1
fusion protein [Human metapneumovirus]	AAN52908.1
fusion glycoprotein [Human metapneumovirus]	ACJ53553.1
fusion glycoprotein [Human metapneumovirus]	AIY25727.1
fusion protein [Human metapneumovirus]	ABM67072.1
fusion protein [Human metapneumovirus]	AEZ52361.1
fusion protein [Human metapneumovirus]	AAS22093.1
fusion glycoprotein [Human metapneumovirus]	AGH27049.1
fusion protein [Human metapneumovirus]	AAK62968.2
fusion glycoprotein [Human metapneumovirus]	ACJ53556.1
fusion glycoprotein [Human metapneumovirus]	ACJ53620.1
fusion protein [Human metapneumovirus]	ABQ58820.1
F [Human metapneumovirus] [Human metapneumovirus]	AEK26886.1
fusion glycoprotein [Human metapneumovirus]	ACJ53619.1
fusion glycoprotein [Human metapneumovirus]	ACJ53555.1
fusion [Human metapneumovirus]	AGL74057.1
fusion protein [Human metapneumovirus]	ABD27850.1
fusion protein [Human metapneumovirus]	AEZ52349.1
fusion protein [Human metapneumovirus]	ABD27848.1
fusion protein [Human metapneumovirus]	ABD27846.1
fusion protein [Human metapneumovirus]	ABQ66021.1
fusion protein [Human metapneumovirus]	AFM57710.1
fusion protein [Human metapneumovirus]	AFM57709.1
fusion protein [Human metapneumovirus]	ABH05968.1

TABLE 4-continued

hMPV NCBI Accession Numbers (Amino Acid Sequences)	
Virus	GenBank Accession
fusion protein [Human metapneumovirus]	AEZ52350.1
fusion protein [Human metapneumovirus]	AFM57712.1
fusion protein [Human metapneumovirus]	AEZ52364.1
fusion protein [Human metapneumovirus]	AAN52912.1
fusion protein [Human metapneumovirus]	AEZ52363.1
fusion [Human metapneumovirus]	AGL74059.1
fusion glycoprotein [Human metapneumovirus]	ACJ53583.1
fusion protein [Human metapneumovirus]	AEZ52356.1
fusion protein [Human metapneumovirus]	AEZ52353.1
fusion glycoprotein [Human metapneumovirus]	ACJ53581.1
fusion glycoprotein [Human metapneumovirus]	ACJ53578.1
fusion protein [Human metapneumovirus]	AAS22117.1
fusion protein [Human metapneumovirus]	BAN75965.1
fusion protein [Human metapneumovirus]	AGF92105.1
fusion protein [Human metapneumovirus]	AAS22077.1
fusion protein [Human metapneumovirus]	AAN52909.1
fusion glycoprotein [Human metapneumovirus]	ACJ53586.1
fusion protein [Human metapneumovirus]	AAQ90145.1
fusion glycoprotein [Human metapneumovirus]	AGT75042.1
fusion [Human metapneumovirus]	AGL74058.1
fusion protein [Human metapneumovirus]	AEL87263.1
fusion glycoprotein [Human metapneumovirus]	AGH27057.1
fusion glycoprotein [Human metapneumovirus]	AHV79491.1
F [Human metapneumovirus] [Human metapneumovirus]	AEK26906.1
fusion glycoprotein [Human metapneumovirus]	ACJ53580.1
fusion protein [Human metapneumovirus]	AEZ52354.1
fusion protein [Human metapneumovirus]	AAN52914.1
G [Human metapneumovirus] [Human metapneumovirus]	AEK26901.1
glycoprotein [Human metapneumovirus]	AFI56738.1
glycoprotein [Human metapneumovirus]	AFI56739.1
glycoprotein [Human metapneumovirus]	AFI56745.1
G protein [Human metapneumovirus]	AAQ62718.1
G protein [Human metapneumovirus]	AAQ62719.1
attachment glycoprotein G [Human metapneumovirus]	AGH27104.1
G protein [Human metapneumovirus]	AAQ62729.1
G protein [Human metapneumovirus]	AAQ62728.1
glycoprotein [Human metapneumovirus]	AFI56753.1
glycoprotein [Human metapneumovirus]	AFI56746.1
glycoprotein [Human metapneumovirus]	AFI56750.1
glycoprotein [Human metapneumovirus]	AFI56747.1
G protein [Human metapneumovirus]	AAQ62721.1
glycoprotein [Human metapneumovirus]	AAT46573.1
glycoprotein [Human metapneumovirus]	AFI56748.1
glycoprotein [Human metapneumovirus]	AFI56736.1
glycoprotein [Human metapneumovirus]	AFI56749.1
attachment glycoprotein G [Human metapneumovirus]	AGH27131.1
attachment glycoprotein G [Human metapneumovirus]	AHV79558.1
glycoprotein [Human metapneumovirus]	AFI56740.1
glycoprotein [Human metapneumovirus]	AFI56741.1
glycoprotein [Human metapneumovirus]	AFI56744.1
attachment glycoprotein G [Human metapneumovirus]	AHV79790.1
attachment glycoprotein G [Human metapneumovirus]	AGH27122.1
attachment glycoprotein G [Human metapneumovirus]	AHV79763.1
attachment glycoprotein G [Human metapneumovirus]	AGZ48849.1
glycoprotein [Human metapneumovirus]	AFI56743.1
attachment glycoprotein G [Human metapneumovirus]	AHV79450.1
glycoprotein [Human metapneumovirus]	AFI56751.1
attachment glycoprotein [Human metapneumovirus]	AAS48482.1
attachment glycoprotein G [Human metapneumovirus]	AHV79889.1
attachment surface glycoprotein [Human metapneumovirus]	AGW43050.1
glycoprotein [Human metapneumovirus]	AFI56754.1
attachment glycoprotein G [Human metapneumovirus]	AHV79601.1
glycoprotein [Human metapneumovirus]	AFI56752.1
attachment glycoprotein G [Human metapneumovirus]	AHV79871.1
G protein [Human metapneumovirus]	AEZ68099.1
attachment glycoprotein G [Human metapneumovirus]	AHV79817.1
attachment glycoprotein G [Human metapneumovirus]	AHV79943.1
attachment glycoprotein G [Human metapneumovirus]	BAN75968.1
attachment surface glycoprotein [Human metapneumovirus]	AGW43045.1
attachment glycoprotein G [Human metapneumovirus]	AHV79628.1
attachment glycoprotein [Human metapneumovirus]	AFK49783.1

TABLE 4-continued

hMPV NCBI Accession Numbers (Amino Acid Sequences)	
Virus	GenBank Accession
G protein [Human metapneumovirus]	AAQ62723.1
attachment glycoprotein [Human metapneumovirus]	ABD27839.1
attachment surface glycoprotein [Human metapneumovirus]	AGW43046.1
G protein [Human metapneumovirus]	AAQ62717.1
glycoprotein [Human metapneumovirus]	AFI56742.1
attachment protein [Human metapneumovirus]	ABQ44522.1
glycoprotein [Human metapneumovirus]	AFI56735.1
attachment surface glycoprotein [Human metapneumovirus]	AGW43065.1
G protein [Human metapneumovirus]	AAQ62724.1
attachment surface glycoprotein [Human metapneumovirus]	AGW43075.1
attachment surface glycoprotein [Human metapneumovirus]	AGW43062.1
glycoprotein [Human metapneumovirus]	AAT46579.1
attachment surface glycoprotein [Human metapneumovirus]	AGW43064.1
attachment surface glycoprotein [Human metapneumovirus]	AGW43054.1
attachment surface glycoprotein [Human metapneumovirus]	AGW43042.1
attachment surface glycoprotein [Human metapneumovirus]	AGW43078.1
attachment surface glycoprotein [Human metapneumovirus]	AGW43067.1
G protein [Human metapneumovirus]	AAQ62722.1
attachment surface glycoprotein [Human metapneumovirus]	AGW43063.1
glycoprotein [Human metapneumovirus]	AAT46571.1
glycoprotein [Human metapneumovirus]	AAT46578.1
attachment glycoprotein G [Human metapneumovirus]	AGJ74232.1
glycoprotein [Human metapneumovirus]	AAT46580.1
glycoprotein [Human metapneumovirus]	AAT46574.1
attachment surface glycoprotein [Human metapneumovirus]	AGW43061.1
attachment glycoprotein [Human metapneumovirus]	AFK49791.1
attachment surface glycoprotein [Human metapneumovirus]	AGW43047.1
glycoprotein [Human metapneumovirus]	ABC26386.1
attachment glycoprotein [Human metapneumovirus]	AAS48466.1
attachment surface glycoprotein [Human metapneumovirus]	AGW43048.1
attachment glycoprotein G [Human metapneumovirus]	AGH27140.1
attachment surface glycoprotein [Human metapneumovirus]	AGW43049.1
attachment glycoprotein G [Human metapneumovirus]	AGJ74082.1
attachment glycoprotein G [Human metapneumovirus]	AHV79442.1
attachment glycoprotein G [Human metapneumovirus]	AGJ74091.1
attachment glycoprotein G [Human metapneumovirus]	AHV79477.1
attachment surface glycoprotein [Human metapneumovirus]	AGW43056.1
attachment protein [Human metapneumovirus]	ABQ44523.1
attachment glycoprotein G [Human metapneumovirus]	BAH59622.1
attachment surface glycoprotein [Human metapneumovirus]	AGW43070.1
glycoprotein [Human metapneumovirus]	AAT46585.1
attachment glycoprotein G [Human metapneumovirus]	AGU68409.1
attachment glycoprotein G [Human metapneumovirus]	AGJ74223.1
attachment glycoprotein [Human metapneumovirus]	AAS22129.1
attachment glycoprotein G [Human metapneumovirus]	AGJ74048.1
G protein [Human metapneumovirus]	AAQ62725.1
glycoprotein [Human metapneumovirus]	ABC26384.1
attachment protein [Human metapneumovirus]	ABQ44525.1
attachment glycoprotein G [Human metapneumovirus]	YP_012612.1
attachment surface glycoprotein [Human metapneumovirus]	AGW43071.1
attachment glycoprotein G [Human metapneumovirus]	AGJ74162.1
attachment glycoprotein G [Human metapneumovirus]	AGH27095.1
attachment glycoprotein G [Human metapneumovirus]	AHV79531.1
G protein [Human metapneumovirus]	AAQ62726.1
attachment glycoprotein [Human metapneumovirus]	AAS48465.1
attachment surface glycoprotein [Human metapneumovirus]	AGW43058.1
P [Human metapneumovirus] [Human metapneumovirus]	AEK26894.1
phosphoprotein [Human metapneumovirus]	AHV79631.1
phosphoprotein [Human metapneumovirus]	AHV79901.1
phosphoprotein [Human metapneumovirus]	AHV79570.1
phosphoprotein [Human metapneumovirus]	AGJ74076.1
phosphoprotein [Human metapneumovirus]	AAS22123.1
phosphoprotein [Human metapneumovirus]	ABB16895.1
phosphoprotein [Human metapneumovirus]	AHV79579.1
phosphoprotein [Human metapneumovirus]	AGJ74244.1
phosphoprotein [Human metapneumovirus]	AHV79856.1
phosphoprotein [Human metapneumovirus]	ACJ70113.1
phosphoprotein [Human metapneumovirus]	AGZ48843.1
phosphoprotein [Human metapneumovirus]	AHV79498.1
phosphoprotein [Human metapneumovirus]	AHV79480.1
phosphoprotein [Human metapneumovirus]	ABQ43382.1
phosphoprotein [Human metapneumovirus]	AAS22107.1
phosphoprotein [Human metapneumovirus]	ABB16898.1

TABLE 4-continued

hMPV NCBI Accession Numbers (Amino Acid Sequences)		
Virus		GenBank Accession
phosphoprotein [Human metapneumovirus]		AGH27134.1
phosphoprotein [Human metapneumovirus]		ABB16899.1
phosphoprotein [Human metapneumovirus]		AGH27098.1
phosphoprotein [Human metapneumovirus]		AAN52866.1
phosphoprotein [Human metapneumovirus]		AAS22083.1
phosphoprotein [Human metapneumovirus]		YP_012606.1
phosphoprotein [Human metapneumovirus]		AHV79973.1
phosphoprotein [Human metapneumovirus]		AHV79462.1
phosphoprotein [Human metapneumovirus]		AGJ74042.1
phosphoprotein [Human metapneumovirus]		AAV88362.1
P [Human metapneumovirus] [Human metapneumovirus]		AIL23591.1
phosphoprotein [Human metapneumovirus]		AHV79453.1
phosphoprotein [Human metapneumovirus]		AGJ74261.1
phosphoprotein [Human metapneumovirus]		AGH27116.1
phosphoprotein [Human metapneumovirus]		ABB16444.1
phosphoprotein [Human metapneumovirus]		ABB16445.1
phosphoprotein [Human metapneumovirus]		AHV79507.1
phosphoprotein [Human metapneumovirus]		BAH59616.1
phosphoprotein [Human metapneumovirus]		ABB16443.1
phosphoprotein [Human metapneumovirus]		ABQ43388.1
phosphoprotein [Human metapneumovirus]		ABQ43389.1
phosphoprotein [Human metapneumovirus]		ABQ43395.1
phosphoprotein [Human metapneumovirus]		ABQ43385.1
phosphoprotein [Human metapneumovirus]		AAP84042.1
phosphoprotein [Human metapneumovirus]		AAN52868.1
phosphoprotein [Human metapneumovirus]		AAP84041.1
phosphoprotein [Human metapneumovirus]		AGH27080.1
phosphoprotein [Human metapneumovirus]		ABQ43387.1
phosphoprotein [Human metapneumovirus]		AAS22099.1
phosphoprotein [Human metapneumovirus]		ABB16896.1
phosphoprotein [Human metapneumovirus]		AGJ74094.1
phosphoprotein [Human metapneumovirus]		AEZ68089.1
phosphoprotein [Human metapneumovirus]		ABK97002.1
phosphoprotein [Human metapneumovirus]		AAP13486.1
phosphoprotein [Human metapneumovirus]		AHV79444.1
phosphoprotein [Human metapneumovirus]		AHV79865.1
phosphoprotein [Human metapneumovirus]		AGJ74226.1
phosphoprotein [Human metapneumovirus]		ABQ43383.1
phosphoprotein [Human metapneumovirus]		AAN52863.1
phosphoprotein [Human metapneumovirus]		AHV79775.1
phosphoprotein [Human metapneumovirus]		AEZ68094.1
phosphoprotein [Human metapneumovirus]		AHV79883.1
phosphoprotein [Human metapneumovirus]		AEZ68092.1
phosphoprotein [Human metapneumovirus]		ABQ43390.1
phosphoprotein [Human metapneumovirus]		ABQ43386.1
phosphoprotein [Human metapneumovirus]		ABQ43391.1
phosphoprotein [Human metapneumovirus]		ACS16062.1
phosphoprotein [Human metapneumovirus]		AEZ68090.1
phosphoprotein [Human metapneumovirus]		AAK62967.1
phosphoprotein [Human metapneumovirus]		AEZ68093.1
phosphoprotein [Human metapneumovirus]		AEZ68088.1
phosphoprotein [Human metapneumovirus]		ABQ43392.1
phosphoprotein [Human metapneumovirus]		ABQ43393.1
phosphoprotein [Human metapneumovirus]		ABQ43384.1
phosphoprotein [Human metapneumovirus]		ABQ43394.1
phosphoprotein [Human metapneumovirus]		ABK96999.1
phosphoprotein [Human metapneumovirus]		AHV79489.1
phosphoprotein [Human metapneumovirus]		AGJ74235.1
phosphoprotein [Human metapneumovirus]		AAS22075.1
phosphoprotein [Human metapneumovirus]		AAS22115.1
phosphoprotein [Human metapneumovirus]		AII17601.1
phosphoprotein [Human metapneumovirus]		ABK97000.1
phosphoprotein [Human metapneumovirus]		AHV79561.1
phosphoprotein [Human metapneumovirus]		AGT75040.1
phosphoprotein [Human metapneumovirus]		AAN52864.1
phosphoprotein [Human metapneumovirus]		ABK97001.1
phosphoprotein [Human metapneumovirus]		AGT74979.1
phosphoprotein [Human metapneumovirus]		AHV79955.1
phosphoprotein [Human metapneumovirus]		AGH27055.1
phosphoprotein [Human metapneumovirus]		AAV88361.1
phosphoprotein [Human metapneumovirus]		ABQ43397.1
phosphoprotein [Human metapneumovirus]		AGJ74173.1

TABLE 4-continued

hMPV NCBI Accession Numbers (Amino Acid Sequences)	
Virus	GenBank Accession
P [Human metapneumovirus] [Human metapneumovirus]	AEK26904.1
phosphoprotein [Human metapneumovirus]	ACJ70104.1
phosphoprotein [Human metapneumovirus]	ABK97003.1
phosphoprotein [Human metapneumovirus]	AGT74955.1
phosphoprotein [Human metapneumovirus]	AAN52856.1
phosphoprotein [Human metapneumovirus]	AAN52862.1
phosphoprotein [Human metapneumovirus]	AGJ74138.1
phosphoprotein [Human metapneumovirus]	AHV79613.1
phosphoprotein [Human metapneumovirus]	AGJ74060.1
phosphoprotein [Human metapneumovirus]	AAQ67684.1
phosphoprotein [Human metapneumovirus]	AEA02278.1
N [Human metapneumovirus] [Human metapneumovirus]	AEK26899.1
nucleoprotein [Human metapneumovirus]	ACS16061.1
nucleoprotein [Human metapneumovirus]	AAS88425.1
nucleoprotein [Human metapneumovirus]	YP_012605.1
nucleoprotein [Human metapneumovirus]	AHV79882.1
nucleoprotein [Human metapneumovirus]	AHV79774.1
nucleocapsid protein [Human metapneumovirus]	AAN52886.1
nucleoprotein [Human metapneumovirus]	AAS22082.1
nucleoprotein [Human metapneumovirus]	AHV79864.1
nucleoprotein [Human metapneumovirus]	AHV79828.1
nucleoprotein [Human metapneumovirus]	AGJ74084.1
nucleocapsid protein [Human metapneumovirus]	AAN52888.1
N [Human metapneumovirus] [Human metapneumovirus]	AIL23590.1
nucleoprotein [Human metapneumovirus]	AAK62966.1
nucleoprotein [Human metapneumovirus]	AHV79972.1
nucleoprotein [Human metapneumovirus]	AHV79470.1
nucleoprotein [Human metapneumovirus]	AHV79452.1
nucleoprotein [Human metapneumovirus]	AGJ74243.1
nucleoprotein [Human metapneumovirus]	AHV79533.1
nucleoprotein [Human metapneumovirus]	AGJ74181.1
nucleoprotein [Human metapneumovirus]	AHV79497.1
nucleoprotein [Human metapneumovirus]	AHV79702.1
nucleoprotein [Human metapneumovirus]	AHV79648.1
nucleoprotein [Human metapneumovirus]	AHV79435.1
putative nucleoprotein [Human metapneumovirus]	AGJ74260.1
nucleocapsid protein [Human metapneumovirus]	AAN52887.1
nucleoprotein [Human metapneumovirus]	AGU68386.1
nucleocapsid protein [Human metapneumovirus]	AAN52899.1
nucleoprotein [Human metapneumovirus]	AAR17673.1
nucleocapsid protein [Human metapneumovirus]	AAN52898.1
nucleoprotein [Human metapneumovirus]	AEA02277.1
nucleoprotein [Human metapneumovirus]	AHV79612.1
nucleoprotein [Human metapneumovirus]	AGU68416.1
nucleoprotein [Human metapneumovirus]	AGU68408.1
nucleoprotein [Human metapneumovirus]	AGU68370.1
nucleoprotein [Human metapneumovirus]	AAQ67683.1
nucleoprotein [Human metapneumovirus]	AGJ74137.1
nucleoprotein [Human metapneumovirus]	AGU68344.1
nucleocapsid protein [Human metapneumovirus]	ABK96997.1
nucleoprotein [Human metapneumovirus]	AGU68413.1
nucleocapsid protein [Human metapneumovirus]	AAN52891.1
nucleoprotein [Human metapneumovirus]	AGU68360.1
nucleoprotein [Human metapneumovirus]	AGU68353.1
nucleocapsid protein [Human metapneumovirus]	ABK96996.1
nucleoprotein [Human metapneumovirus]	AAR17666.1
N [Human metapneumovirus] [Human metapneumovirus]	AEK26903.1
nucleoprotein [Human metapneumovirus]	AGT75039.1
nucleoprotein [Human metapneumovirus]	AGU68410.1
nucleoprotein [Human metapneumovirus]	AAS22074.1
nucleoprotein [Human metapneumovirus]	AHV79560.1
nucleoprotein [Human metapneumovirus]	AGT74978.1
nucleoprotein [Human metapneumovirus]	AGJ74128.1
nucleoprotein [Human metapneumovirus]	AAR17663.1
nucleoprotein [Human metapneumovirus]	AAR17662.1
nucleoprotein [Human metapneumovirus]	AAR17664.1
nucleoprotein [Human metapneumovirus]	AAR17657.1
nucleoprotein [Human metapneumovirus]	AAR17659.1
nucleoprotein [Human metapneumovirus]	AAR17661.1
nucleoprotein [Human metapneumovirus]	AGU68352.1
nucleoprotein [Human metapneumovirus]	AGU68373.1
nucleoprotein [Human metapneumovirus]	AGU68376.1
nucleoprotein [Human metapneumovirus]	AGU68342.1

TABLE 4-continued

hMPV NCBI Accession Numbers (Amino Acid Sequences)	
Virus	GenBank Accession
nucleoprotein [Human metapneumovirus]	AGU68365.1
nucleoprotein [Human metapneumovirus]	AGU68363.1
nucleoprotein [Human metapneumovirus]	AGU68398.1
nucleoprotein [Human metapneumovirus]	AGU68348.1
nucleoprotein [Human metapneumovirus]	AGU68354.1
nucleoprotein [Human metapneumovirus]	AGU68391.1
nucleoprotein [Human metapneumovirus]	AGU68389.1
nucleoprotein [Human metapneumovirus]	AGU68399.1
nucleoprotein [Human metapneumovirus]	AGU68337.1
nucleoprotein [Human metapneumovirus]	AAR17660.1
nucleoprotein [Human metapneumovirus]	AAR17667.1
nucleoprotein [Human metapneumovirus]	AGU68402.1
nucleoprotein [Avian metapneumovirus type C]	CDN30025.1
nucleoprotein [Avian metapneumovirus]	AGZ87947.1
Nucleoprotein [Avian metapneumovirus type C]	CAL25113.1
nucleocapsid protein [Avian metapneumovirus]	ABO42286.1
nucleocapsid protein [Avian metapneumovirus]	AAK38430.1
nucleocapsid protein [Avian metapneumovirus]	AAK54155.1
nucleocapsid protein [Avian metapneumovirus]	AAK38426.1
nucleocapsid protein [Avian metapneumovirus]	AAK38425.1
nucleocapsid protein [Avian metapneumovirus]	AAK38424.1
nucleocapsid protein [Avian metapneumovirus]	AAF05909.1
nucleocapsid protein [Avian metapneumovirus]	AAK38435.1
nucleocapsid protein [Avian metapneumovirus]	AAK38428.1
nucleoprotein [Human metapneumovirus]	AAR17669.1
nucleocapsid protein [Avian metapneumovirus]	AAK38429.1
nucleocapsid protein [Avian metapneumovirus]	AAK38427.1
nucleocapsid protein [Avian metapneumovirus]	AAK38423.1
nucleocapsid protein [Avian metapneumovirus]	AAK38434.1
nucleoprotein [Human metapneumovirus]	AGU68338.1
nucleoprotein [Avian metapneumovirus]	YP_443837.1
nucleoprotein [Human metapneumovirus]	AGU68384.1
nucleocapsid protein [Avian metapneumovirus]	AAK38431.1
nucleoprotein [Human metapneumovirus]	AGU68405.1
nucleoprotein [Human metapneumovirus]	AGU68382.1
nucleoprotein [Human metapneumovirus]	AGU68395.1
nucleocapsid [Human metapneumovirus]	AAL35389.3
nucleoprotein [Human metapneumovirus]	AEZ68064.1

TABLE 5

PIV3 Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO:
>gb KJ672601.1 : 4990-6609 Human parainfluenza virus 3 strain HPIV3/Homo sapiens/PER/FLA4815/ 2008[fusion glycoprotein F0]	ATGCCAATTTCAACTACTGTTAATTATTACAACCATGATC ATGGCATCACACTGCCAAATAGACATCACAAAACCTACA GCATGTAGGTGTATTGGTCAACAGTCCCAAAGGGATGA AGATATCACAAAACCTCGAAACAAGATATCTAATCCCTGA GTCTCATACCAAAAATAGAAGATTCTAACTCTTGTGGTG ACCAACAGATCAAGCAATACAAGAGGTTATTGGATAGA CTGATCATTCCTTTATATGATGGACTAAGATTACAGAAG GATGTGATAGTGACTAATCAAGAATCCAATGAAAACAC TGATCCAGAAACAGAACGATTCTTTGGAGGGGTAAATTGG AATATTGCTCTAGGAGTAGCAACCTCAGCACAAATTAC AGCAGCAGTTGCTCTGGTTGAAGCCAAGCAGGCAAGAT CAGACATTGAAAACTCAAGGAAGCAATCAGGGACACA AATAAAGCAGTGCAAGTCAGTTCAAGGCTCTGTAGGAAA TTTGATAGTAGCAATTAAATCAGTCCAGGATTATGTCAA CAAAGAAATCGTGCCATCGATTGCGAGACTAGGTTGTG AAGCAGCAGGACTTCAGTTAGGGATTGCATTAACACAG CATTACTCAGAATTAACAAATATATTTGGTGATAACATA GGATCGTTACAGAAAAGGAATAAAATTACAAGGTAT AGCATCATATACCGTACAAATATCACAGAAATATTCAC AACATCAACAGTTGACAAATATGATATTATGATCTATT ATTTACAGAAATCAATAAGGTGAGAGTTATAGATGTTGA TTTGAATGATTACTCAATAACCCCTCCAAGTCAGACTCCC TTTATTGACCAGACTGCTGAACACTCAAATCTACAAAGT AGATTCCATATCATACAATATCCAAATAGAGAAATGGTA	9

TABLE 5-continued

PIV3 Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO:
	TATCCCTCTTCCCAGCCATATCATGACGAAAGGGGCATT TCTAGGTGGAGCAGATGTCAAAGAATGCATAGAAGCAT TCAGCAGTTATATATGCCCTTCTGATCCAGGATTGTACT AAACCATGAAATGGAGAGCTGTCTATCAGGAAACATAT CCCAATGTCCAAGAACCACAGTCACATCAGACATAGTTC CTAGGTATGCATTGTCAATGGAGGAGTGGTTGCGAATT GTATAACAACATACATGTACATGCAATGGTATCGGTAATA GAATCAACCAACCACCTGATCAAGGAGTCAAAATTATA ACACATAAAGAATGTAATACAATAGGTATCAACGGAAT GCTATTCAACACAAACAAAGAAGGAACCTTGTGATTCTA CACACCAGACGACATAACATTAAACAATTCTGTTGCACT TGATCCGATTGACATATCAATCGAGCTCAACAAGGCCAA ATCAGATCTTGAGGAATCAAAGAATGGATAAGAAGGT CAAATCAAAGCTAGATTCTATTGGAAGTTGGCATCAAT CTAGCACTACAATCATAGTTATTTTGATAATGATGATTA TATTGTTTATAATTAATATAACAATAATACAATTGCAA TTAAGTATTACAGAATTCAAAGAGAAATCGAGTGGAT CAAATGATAAGCCGTATGTATTACAACAACAG	
gi 612507167 gb AHX22430.1 hemagglutinin- neuraminidase [Human parainfluenza virus 3]	ATGGAATACTGGAAGCACACCAACCACGGAAGGATGC TGGTAATGAGCTGGAGACATCCACAGCCACTCATGGCA ACAAGCTCACCAACAAGATAACATATATATTGTGGACG ATAACCTGGTGTATTATCAATAGTCTTCATCATAGTG CTAACTAATCCATCAAAGTGAAAGGCCCGCGAATC ATTGCTACAAGACATAAATAATGAGTTTATGGAAGTTAC AGAAAAGATCCAAGTGGCATCGGATAATACTAATGATC TAATACAGTCAGGAGTGAATACAAGGCTTCTTACAATTC AGAGTCATGTCCGAATTATATACCAATATCATTGACAC AACAAATATCGGATCTTAGGAAATTCATTAGTGAAATTA CAATTAGAAATGATAATCAAGAAGTGCCACCACAAAGA ATAACACATGATGTGGGTATAAAACCTTTAAATCCAGAT GATTTCTGGAGATGCACGTCTGGTCTTCCATCTTTGATG AAAACCTCAAATAAAGATTAAATGCCGGGACCAGGATT ATTAGCTATGCCAACGACTGTTGATGGCTGTGTGAGAAC CCCGTCTTAGTGATAAATGATCTGATTTATGCTTACAC CTCAAATCTAATTACTCGAGGTTGCCAGGATATAGGGAA ATCATATCAAGTATTACAGATAGGGATAATAACTGTAAA CTCAGACTTGGTACCTGACTTAAATCCTAGGATCTCTCA TACCTTCAACATAAATGACAATGAAAGTCATGTTCTCT AGCACTCCTAAATACAGATGTATATCAACTGTGTTCAAC CCCAAAGTTGATGAAAGATCAGATTATGCATCATCAG GCATAGAAGATATTGTACTTGATATTGCAATTATGATG GCTCAATCTCGACAACAAGATTAAAGAATAAATAATAA GTTTTGATCAACCATATGCCGCATTATACCCATCTGTTG GACCAGGGATATACTACAAAGGCAAAATAATTTCTC GGGTATGGAGTCTTGAACATCCAATAAATGAGAATGC AATCTGCAACACAACCTGGGTGTCTGGGAAAAACACAGA GAGACTGTAATCAAGCATCTCATAGTCCATGGTTTTCAG ATAGAAGGATGGTCAACTCTATAATTGTTGTTGACAAGG GCTTGAACCTCAGTTCCAAATTTGAAGGTATGGACGATAT CTATGAGACAAAATTACTGGGGTCAAGGAAGATTATTA CTTCTACTAGGTAACAAGATCTACATATACACAAGATCT ACAAGTTGGCACAGCAAGTTACAATTAGGAATAATTGA CATTACTGACTACAGTGATATAAGGATAAAATGGACAT GGCATAATGTGCTATCAAGACCAGGAACAATGAATGT CCATGGGGACATTATGTCCGATGGATGTATAACGGG AGTATATACCGATGCATATCCACTCAATCCACAGGAAG CATTGTATCATCTGTATATTTGGACTCACAAAAATCGAG AGTCAACCCAGTCATAACTTACTCAACAGCAACCGAAA GGGTAAACGAGCTGGCTATCCGAAACAAAACACTCTCA GCTGGGTACACAACAACAGCTGCATTACACACTATAA CAAAGGGTATTGTTTTCATATAGTAGAAATAAATCATAA AAGCTTAAACACATTTCAACCCATGTTGTTCAAACAGA GATTCCAAAAGCTGCAGT	10
HPIV3_HN_Codon Optimized	ATGGAATACTGGAAGCACACCAACCACGGCAAGGACGC CGGCAACGAGCTGGAACACGACAGCCACACACGGCA ACAAGCTGACCAACAAGATCACCTACATCCTGTGGACC ATCACCTGGTGTCTGCTGAGCATCGTGTTCATCATCGTG CTGACCAATAGCATCAAGAGCGAGAAGGCCAGAGAGAG CCTGCTGCAGGACATCAACAACGAGTTCATGGAAGTGA CCGAGAAGATCCAGGTGGCCAGCGACAACCAACGAC	11

TABLE 5-continued

PIV3 Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO:
	CTGATCCAGAGCGGCGTGAACACCCGGCTGCTGACCATC CAGAGCCACGTGCAGAACTACATCCCCATCAGCCTGACC CAGCAGATCAGCGACCTGCGGAAGTTATCAGCGAGAT CACCATCCGGAACGACAACCAGGAAGTGCCCCCCAGA GAATCACCACGACGTGGGCATCAAGCCCCGAAACCC GACGATTCTGGCGGTGTACAAGCGGCTGCCAGCCTG ATGAAGACCCCAAGATCCGGCTGATGCCTGGCCCTGG ACTGCTGGCCATGCCATACCACAGTGGATGGCTGTGTGCG GACCCCGAGCCTCGTGATCAACGATCTGATCTACGCCTA CACCAGCAACCTGATCACCCTGGGCTGCCAGGATATCG GCAAGAGCTACCAGGTGCTGCAGATCGGCATCATCACC GTGAACCTCGACCTGGTGCCCGACCTGAACCTCGGATC AGCCACACCTTCAACATCAACGACAACAGAAAGAGCTG CAGCCTGGCTCTGCTGAACACCGAGTGTACCAGCTGTG CAGCACCCTCAAGGTGGACGAGAGAAGCGATACGCCA GCAGCGCATCGAGGATATCGTGTGGACATCGTGAAAC TACGACGGCAGCATCAGCACCACCGGTTCAAGAACA CAACATCAGCTTCGACAGCCCTACGCCGCCCTGTACCC TTCTGTGGGCCCTGGCATCTACTACAAGGGCAAGATCAT CTTCTGGGCTACGGCGGCTGGAAACCCCATCAACGA GAACGCCATCTGCAACACCACCGCTGCCCTGGCAAGA CCCAGAGAGCTGCAATCAGGCCAGCCACAGCCCTGG TTCAGCGACCGCAGAATGGTCAACTCTATCATCGTGGTG GACAAGGGCTGAACAGCGTGCCCAAGCTGAAAGTGTG GACAATCAGCATGCGCCAGAATACTGGGGCAGCGAGG GCAGACTTCTGCTGCTGGGAAACAAGATCTACATCTACA CCCGGTCCACCAGCTGGCACAGCAAACTGCAGCTGGGA ATCATCGACATCACCGACTACAGCGACATCCGGATCAA GTGGACCTGGCACAACTGCTGAGCAGACCCGGCAACA ATGAGTGCCTTGGGGCCACAGCTGCCCGATGGATGTA TCACCGCGGTGTACACCGACGCCCTACCCCTGAATCCTA CCGGCTCCATCGTGTCCAGCGTGATCCTGGACAGCCAGA AAAGCAGAGTGAACCCCGTGATCACATACAGCACCGCC ACCGAGAGAGTGAACGAACTGGCCATCAGAAACAAGAC CCTGAGCGCCGGCTACACCACCACAAGCTGCATCACAC ACTACAACAAGGGCTACTGCTTCCACATCTGGAAATCA ACCACAAGTCCCTGAACACCTTCCAGCCCATGCTGTTCA AGACCGAGATCCCCAAGAGCTGCTCC	
HPIV3_F_Codon Optimized	ATGCCCCATCAGCATCCTGCTGATCATCACCACAATGATC ATGGCCAGCCACTGCCAGATCGACATCACCAGCTGCA GCACGTGGGCGTGCTCGTGAACAGCCCCAAGGGCATGA AGATCAGCCAGAACTTCGAGACAGCTACCTGATCCTGA GCCTGATCCCCAAGATCGAGGACAGCAACAGCTGCGGC GACCAGCAGATCAAGCAGTACAAGCGGCTGCTGGACAG ACTGATCATCCCCCTGTACGACGGCCTGCGGCTGCAGAA AGACGTGATCGTGACCAACCAGGAAAGCAACGAGAACA CCGACCCCGGACCGAGAGATTCTTCGGCGGCGTGATCG GCACAATCGCCCTGGGAGTGGCCACAAGCGCCAGATT ACAGCCGCTGTGGCCCTGGTGAAGCCAAGCAGGCCAG AAGCGACATCGAGAAGCTGAAAGAGGCCATCCGGGACA CCAACAAGGCCGTGCAGAGCGTGAGTCCAGCGTGGGC AATCTGATCGTGGCCATCAAGTCCGTGCAGGACTACGTG AACAAAGAAATCGTGCCCTCTATCGCCCGGCTGGGCTGT GAAGCTGCCGACTGCAGCTGGGCATGGCCCTGACACA GCACTACAGCGAGCTGACCAACATCTCGGCGACAACA TCGGCAGCCTGCAGGAAAAGGGCATTAAGCTGCAGGGA ATCGCCAGCCTGTACCGCACCAACATCACCAGATCTTC ACCACCAGCACCGTGGATAAGTACGACATCTACGACCT GCTGTTACCCGAGAGCATCAAAGTGCCTGATCGACGT GGACCTGAACGACTACAGCATCACCTGCAAGTGCAGC TGCCCCTGCTGACCAGACTGCTGAACACCCAGATCTACA AGGTGGACAGCATCTCTACAACATCCAGAACCAGCAG TGGTACATCCCTCTGCCCAGCCACATTATGACCAAGGGC GCCTTTCTGGGCGGAGCCGACGTGAAAGAGTGATCGA GGCCCTCAGCAGCTACATCTGCCCCAGCGACCTGGCTT CGTGCTGAACCACGAGATGGAAAGCTGCCTGAGCGGCA ACATCAGCCAGTGCCCCAGAACCCGTGACCTCCGAC ATCGTGCCAGATACGCCTTCGTGAATGGCGGCGTGGTG GCCAACTGCATCACCACCACCTGTACCTGCAACGGCATC GGCAACCGGATCAACCAGCCTCCCGATCAGGGCGTGAA GATTATCACCACAAAGAGTGTAACACCATCGGCATCA	12

TABLE 5-continued

PIV3 Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO:
	ACGGCATGCTGTTCAATACCAACAAGAGGGCACCCTG GCCTTCTACACCCCGACGATATCACCTGAACAACTCC GTGGCTCTGGACCCCATCGACATCTCCATCGAGCTGAAC AAGGCCAAGAGCGACCTGGAAGAGTCCAAAGAGTGGAT CCGGCGGAGCAACCAGAAGCTGGACTCTATCGGCAGCT GGCACCAGAGCAGCACCACCATCATCGTGATCCTGATTA TGATGATTATCCTGTTTCATCATCAACATTACCATCATCAC TATCGCCATTAAGTACTACCGGATCCAGAAACGGAACC GGGTGGACCAGAATGACAAGCCCTACGTGCTGACAAAC AAG	
	PIV3 mRNA Sequences	
>gb KJ672601.1 : 4990-6609 Human parainfluenza virus 3 strain HPIV3/ <i>Homo sapiens</i> /PER/FLA4815/ 2008[fusion glycoprotein F0]	AUGCCAAUUUCAAUACUGUUAAUUUACAACCAUGA UCAUGGCAUCACACUGCCAAAUAGACAUCAAAACU ACAGCAUGUAGGUGUAUUGGUCAACAGUCCCAAAGGG AUGAAGAUUACACAAAACUUCGAAACAGAUAUCUAA UCCUGAGUCUAUACCAAAAUAGAAGAUUCUAACUC UUGUGUGACCAACAGAUCAAGCAUACAAGAGGUUA UUGGAUAGACUGAUCAUUCUUUAUUAUGAUGGACUAA GAUUACAGAAGGAUGUGAUAGUGACUAAUCAGAAUC CAAUGAAAACACUGAUCCAGAACAGAACGAUUCUUU GGAGGGGUAAUUGGAACUAUUGCUCUAGGAGUAGCAA CCUCAGCACAAAUACAGCAGCAGUUGCUCUGGUUGA AGCCAAGCAGGCAAGAUCAGACAUUGAAAACUCUAG GAAGCAUUCAGGGACACAAUAAAGCAGUAGCAGUCAG UUCAGAGCUCUGUAGGAAAUUGAUAGUAGCAAUUAA AUCAGUCCAGGAUUAUGUACAACAAAGAAUUCGUGCCA UCGAUUGCGAGACUAGGUUGUGAAGCAGCAGGACUUC AGUUAAGGAUUGCAUUAACACAGCAUUAUCAGAAUU AACAAAUUAUUUGGUGUAACAUAAGGAUCGUUACAA GAAAAAGGAUAAAAUUAAGGUUAUAGCAUUAUUU ACCGUACAAAUUACAGAAAUUAUUCACCAUCAUAC AGUUGACAAAUUAUGAUUUUAUGAUCUAAUUUUACA GAAUCAUUAAGGUGAGAGUUUAUAGAUUUUAUUUA AUGAUUACUCAAUAAACCCUCCAGUCAGACUCCUUU AUUGACCAGACUGCUGAACACUCAAUUCUACAAAGUA GAUUCCAUUAUACAUAUACCAAAUAGAGAAUGGU AUAUCCCUUCCAGCCAUUAUCAGACGAAAGGGGC AUUUCUAGGUGGAGCAGAUUGCAAAGAAUGCAUAGAA GCAUUCAGCAGUUUAUUAUGCCCUUCUGAUCCAGGAU UUGUACUAAACCAUGAAUUGGAGAGCUGUCUAUCAGG AAACAUAUCCCAUGUCCAGAACACAGUCACAUCA GACAUAGUUCUAGGUUUGCAUUGUCAAUGGAGGAG UGGUUGCGAAUUGUAUAACACUACUAGUACAUGCAA UGGUUUCGGUAAUAGAAUACCAACACCACCUUGAUCAA GGAGUCAAAAUUAUAACACAUAAAGAAUGUAAUACAA UAGGUUAUACCGGAUUGCUAUUACACAAACAAAGA AGGAAACUCUUGCAUUCUACACACCAGACGACAUAA UUAACAAUUCUGUUGCACUUGAUCCGAUUGACAUU CAAUCGAGCUCAAACAGGCCAAUUCAGAUUCUUGAGGA AUCAAAAGAAUGGAUAGAAGGUCAAAUCAAAGCUA GAUUCUAUUGGAAGUUGGCAUCAAUCUAGCACUACAA UCAUAGUUAUUUGAUAAUGAUAUUAUUGUUUAU AAUUAUUAACAAUUAUUAUUAUUGCAUUAAGUAU UACAGAAUUCAAAAGAGAAUUCGAGUGGAUCAAUUG AUAAGCCGUAGUUAUAAACAACAG	61
gi 612507167 gb AHX22430.1 hemagglutinin- neuraminidase [Human parainfluenza virus 3]	AUGGAUACUGGAAGCACCAACCACGGAAGGAUG CUGGUAAUGAGCUGGAGACAUCCACAGCCACUCAUGG CAACAAGCUCACCAACAAGAUACAUAUUAUUGUGG ACGAUAAACCCUGGUGUUAUUAUCAAUAGUUCUUAUCA UAGUGCUAACUAAUUCUACAAAAGUGAAAAGGCCCG CGAAUUAUUGCUACAAGACAUAAUUAUAGUUAUUG GAAGUUAACAGAAAAGAUCCAAGUGGCACGGAUAAUA CUAAUGAUUAUUAACAGUCAGGAGUGAAUACAAGGCU UCUUAACAAUUCAGAGUCUAGUCCAGAAUUAUUAACCA AUUAUUAUGACACACAAAUUAUCGGAUUCUAGGAAAU UCAUUAUGUAAAUAUCAAUUAAGAAUUAUUAUUAAGA AGUGCCACCACAAAGAAUACACAUAGUGGGUUAUA AAACCUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU CUGGUCUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAU	62

TABLE 5-continued

PIV3 Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO:
	AUUAAUGCCGGGACCAGGAUUUUAGCUAUGCCAACG ACUGUUGAUGGCGUGUCAGAACCCGUCUUAGUGA UAAAUGAUCUGAUUUUAGCUUACCCUCAAUCUAU UACUCGAGGUUGCCAGGAUUAUAGGGAUUAUCAA GUUUUACAGAUAGGGAUUAUACUGUAAACUCAGACU UGGUACCGACUUAAAUCUAGGAUCUCUACUACCU CAACAUAAAUGACAAUAGAAAGUCAUGUUCUCUAGCA CUCCUAAAUAACAGAUUAUUAACUGUGUUAACCC CAAAAGUUGAUGAAAGAUCAUUAUGCAUCAUCAGG CAUAGAAGAUUUUAGUUAUUAUUGUCAUUAUAGAU GGCUCAAUCUCGACACAAGAUUUUAGAAUAAUUA UAAGUUUUGAUCACCAUAUGCGGCAUUAUACCCAU UGUUGGACCAGGGAUUAUACUACAAGGCAAAUUAU UUUUCGCGUAUGGAGGUCUUGAACUCCAAUAAUAG AGAUGCAAUUCGACACAAACUGGGUGUCUGGGAA AACACAGAGAGACUGUAUUAAGCAUCUCAUAGUCCA UGGUUUUCAGAUAGAAGGAGGUCACUCUUAUAAUUG UUGUUGACAAGGGCUUGAACUCAGUUCCAAUUGAA GGUUAGGACGAUUCUUAUGAGACAAAUUAUCUGGGG UCAGAAGGAAGAUUACUUCUACUAGGUAAACAGAU ACAUAUACACAAAGAUUCACAGUUGGCAAGCAAGUU ACAAUUAGGAUUAUUGACAUUACUGACUACAGUGAU AUAAGGAUAAAAGGACAUUGGCAUUAUUGUCUUAUCAA GACCAGGAACAAUAGAUUGUCAUGGGGACAUUCAUG UCCGGAUGGAUGUAUUAACGGGAGUAUUAUACCGAUGCA UAUCACUCUAAUCCACAGGAAGCAUUGUAUCAUCUG UCAUAUUGGACUCACAAAACUGAGAGUCAACCCAGU CAUAACUUAUCUACACAGCAACCGAAAGGUAACAGAG CUGGCUAUCCGAAACAAACACUCUCAGCUGGGUACA CAACAACAAAGCUGCAUUAACACUAUAAACAAAGGUA UUGUUUUAUUAUAGUAGAAUAAUUAUAAAGCUUA AACACAUUUCACCCAUUGUUGUCAAACAGAGAUUC CAAAAGCUGCAGU	
HPV3_HN_Codon Optimized	AUGGAUACUGGAAGCACACCAACCACGGCAAGGACG CCGGCAACGAGCUGGAAACACGACAGCCACACACGGC AACAAAGCUGACCAACAAGAUACCUACAUCCUGUGGA CCAUACCCUGGUGCUGCUGAGCAUCGUGUUAUCAUC GUGCUGACCAAUAGCAUCAAGAGCGAGAAAGGCCAGAG AGAGCCUGCUGCAGGACAUCAACAACGAGUUAUGGA AGUGACCGAGAAGAUCCAGGUGGCCAGCGACAACACC AACGACUGAUCCAGAGCGGCGUGAACACCCGGCUGCU GACCAUCCAGAGCCACGUGCAGAAUACAUCCCAUCA GCUGACCCAGCAGAUACGACCCUGCGGAAGUUAUC AGCGAGAUACCAUCCGGAACGACAACAGGAAGUGC CCCCCAGAGAAUACCCACGACGUGGGCAUCAAAGCCC CUGAACCCCGACGAUUCUGGCGGUGUACAAGCGGCC UGCCAGCCUGAUGAAGACCCCAAGAUCCGGCUGAUG CCUGGCCUGGACUGCUGGCCAUCCUACACAGUGGA UGGCUGUGUGCGGACCCACGCCUGUGAUCAACGAUC UGAUCUACGCCUACACAGCAACCGAUACCCGGGGC UGCCAGGAUACGGCAAGAGCUACAGGUGCUGCAGA UCGGCAUACUACCGUGAACUCCGACCGUGUGCCGAC CUGAACCCUGGAUCAGCCACACCUUAACAUCAACGA CAACAGAAAGAGCUGCAGCCUGGCUUGCUGAACACC GACGUGUACAGCUGUGCAGCAGCCCAAGGUGGACG AGAGAAGCGACUACGCCAGCAGCGGCAUCGAGGAUUA CGUGCUGGACAUUGUAACUACGACGGCAGCAUCAGC ACCACCGGUUAAGAACAACAACAUAGCUUCGACCA GCCUACGCCGCCUGUACCCUUCUGGGGCCUGGCA UCUACUACAAGGGCAAGAUCAUUCUGGGCUACGG CGGCCUGGAACACCCAUACAGAGAACGCCAUUCGCA ACACACCCGGCUGCCUGGGCAAGACCAGAGAGACUGC AAUCAGGCCAGCCACAGCCCCUGGUUCAGCGACCGCAG AAUGGUCAACUCUUAUCUUGGUGGACAAAGGCCUG AACAGCGUGCCCAAGCUGAAAGUGUGGACAAUCAGCA UGCGCCAGAACUACUGGGGAGCGAGGGCAGACUUCU GCUGCUGGGAACAAAGAUUAUCAUACACCCGGUCC ACCAGCUGGCAACAGCAACUGCAGCUGGGAUUAUCG ACAUACCGACUACAGCGACAUCCGGAUCAAUGGACC UGGCACACGUGCUGAGCAGACCCGGCAACAAUGAGU GCCUUGGGGCCACAGCUGCCCCGAUGAUGUAUACCC	63

TABLE 5-continued

PIV3 Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO:
	GGCGUGUACACCGACGCCUACCCCGUGAAUCCUACCGG CUCCAUCGUGUCCAGCGUGAUCCUGGACAGCCAGAAA AGCAGAGUGAACCCCGUGAUACAUAACGACCCGCCAC CGAGAGAGUGAACGAACUGGCCAUAGAAAACAGACC CUGAGCGCCGGCUACACCACCACAAGCUGCAUCACACA CUACAACAAGGGCUACUGCUUCCAUCUGGAAAUC AACCACAAGUCCUGAACACCUUCCAGCCCCAUGCUGUU CAAGACCGAGAUCCCCAAGAGCUGCUC	
HPIV3_F_Codon Optimized mRNA sequence	AUGCCCaucagcauccugcugaucaucaccacaaugau cauggccagccacugccagauccgacauccacaaagcugc agcagcugggcugucuguaacagccccaagggcau gaagaucagccagaaucucgagacacgcuaccugauc cugagccugauccccaagaucgaggacagcaaacgcu gCGGCGACcagcagaucAAGCAGUACAAGCGGCUGCU GGACAGACUGAUCAUCCCCUGUACGACGGCCUGCGGC UGCAGAAAGACGUGAUCGUGACCAACCAGGAAGCAA CGAGAACACCGACCCCCGGACCGAGAGAUUCUUCGGCG GCGUGAUCGGCACAAUCGCCUGGGAGUGGCCACAAG CGCCcagaUUAACAGCGCGUGUGGCCUGGUGGAAGCCA AGCAGGCCAGAAAGCGACAUcGAGAAGCUGAAAGAGGC CAUCCGGGACACCAACAAGGCCGUGCAGAGCGUGCAG UCCAGCGUGGGCAAUcGUAUCGUGGCCAUCAAGUCCG UGCAGGACUACGUGAAcAAAGAAUcGUGCCUCUAU CGCCCCGCGUGGGCUGUGAAGCUGCCGACUcGAGCUG GGCAUUGCCcUGACACAGCACUACAGCGAGCUGACCAA CAUCUUCGGCGACAAcAUCGGCAGCCUGCAGGAAAAG GGCAUUAAGCUGCAGGGAAUCGCCAGCCUGUACCGCA CCAACAUCACCGAGAUcUUAACCAACAGCACCGUGGAU AAGUACGACAUcUACGACCGUGCUUACCGAGAGCA UCAAGUGCGCGUGAUCGACGUGGACUGAACGACUA CAGCAUCACCCUGCAAGUGCGGCUGCCCCUGCUGACCA GACUGCUGAACACCCAGAUcUACAAGGUGGACAGCAU CUCCUACAACAUCcAGAACCcGAGUGGUACAUCCCUC UGCCcAGCCACAUAUGACCAAGGGCGCCUUUCUGGGC GGAGCCGACGUGAAAGAGUGCAUCGAGGCCUUCAGCA GCUACAUCUGCCCAGCGACCCUGGCUUCGUGCUGAAC CACGAGAUgGAAAGCUGCCUGAGCGGCAACAUCAGCC AGUGCCCAGAACcACCGUGACCUCcGACAUCGUGCCC AGAUAACGCCUUCGUGAAUGCGCGCGUGGUGGCCAAcU GCAUcACCAcCAcCUGUACUGCAACGGCAUCGGCAAC CGGAUcAACCAGCCUCCGAUCAGGGCGUGAAGAUUA UCACCCACAAGAGUGUAACCAcAUCGGCAUcAACGGC AUGCUGUUAcAAUACCAcAAAGAGGGCACCCUGGCCU UCUACACCCCCGACGAUAUCACCCUGAACAAcUCCGUG GCUCUGGACCCAUcGACAUCUCCAUCGAGCUGAACAA GGCCAAGAGCGACcUGGAAGAGUCCAAGAGUGGAUC CGCGGAGCAACcAGAAGCUGGACUUAUCGGCAGCU GGCAcCAGAGCAGCACCAcUAUCUGGAUCUGAUU AUGAUGAUUAUCUGUUCAUCAUCAcAAUUAACAUCA UCACUAUCGCCAUUAAGUACUACCGGAUcCAGAAACG GAACCGGUGGACcAGAAUGACAAGCCUACGUGCUG ACAAACAAG	64

TABLE 6

PIV3 Amino Acid Sequences		
Description	Sequence	SEQ ID NO:
>gi 612507166 gb AHX22429.1 fusion glycoprotein FO [Human parainfluenza virus 3]	MPISILLIITTMIMASHCQIDITKLQHVGLVNSPKGMKISQ NFETRYLILSLIPKIEDSNSCGDQIKQYKRLDLRIIPLYDG LRLQKDVIVTNQESNENTDPRTERFFGVIGTIALGVATSA QITAAVALVEAKQARSDIEKLKEAIRDTNKAVQSVQSSVG NLIVAIKSVQDYVNKEIVPSIARLGCEAAGLQLGIALTQHYS ELTNIFGDNIGSLQEKIKLQGIASLYRTNITEIFTSTVDKY DIYDLLFTESIKVRVIDVDLNDYSITLQVRLPLLTRLNTQIY KVDSISYNIQNREWIPLPSHIMTKGAPLGADVKECIEAFS	13

TABLE 6-continued

PIV3 Amino Acid Sequences		
Description	Sequence	SEQ ID NO:
	SYICPSDPGPFVLNHEMESCLSGNISQCPRTTTSDIVPRYAF VNGGVVANCITTTCTCNGIGNRINQPPDQGVKII THKECNT I GINGMLFNTNKEGTLPFYTPDDITLNNVALDPIDISIELNK AKSDLEESKEWIRRSNQKLD SIGSWHQSTTII VILIMMILFI INITIIITIAIKYYRIQKRN RVDQNDKPYVLTNK	
gi 612507167 gb AHX22430.1 hemagglutinin- neuraminidase [Human parainfluenza virus 3]	MEYWKHTNHGKDAGNELETSTATHGNKLTNKITYILWTIT LVLLSIVFII VLTNSIKSEKARESLQDINNEFMEVTEKIQVA SDNTNDLIQSGVNRLLTIQSHVQNYIPISLTQQISDLRKFIS EITIRNDNQEVPPQRITHDVGIKPLNPDDFWRCTSGLP SLMK TPKIRLMPGPGLLAMPTTVDCVTRPSLVINDLIYAYTSNLI TRGCQDIGKSYQVLQIGIITVNSDLVDP LNPRI SHTF NINDN RKSCSLALLNTDVYQLCSTPKVDERSDYASSGIEDIVLDIV NYDGSISTTRFKNNNISFDQPYAALYPSVGP GIIYKGI IFL GYGGLEHPINENAI CNTTGCPGKTQRDCNQASHSPWFSDR RMVNSII VVDKGLNSVPKLVWTISMRQNYWGSEGRLLLL GNKIYIYTRSTSWHSLQLGI IDITDYS DIRIKWTHMNL SR PGNNECPWGHSCPDGCITGVYTDAYPLNPTGSIVSSVILDS QKSRVNPVITYSTATERNELAIRNKTLSAGYTTTSCITHY NKGYCFHIVEINHKS LNTFQPM LFKTEIPKSCS	14

TABLE 7

PIV3 NCBI Accession Numbers (Nucleic Acid and Amino Acid Sequences)	
Description	GenBank Accession
Fusion glycoprotein F0 [Human parainfluenza virus 3] HPIV3/ <i>Homo sapiens</i> /PER/FLA4815/2008	KJ672601.1: 4990-6609 AHX22429 (Fusion protein)
hemagglutinin-neuraminidase [Human parainfluenza virus 3] HPIV3/ <i>Homo sapiens</i> /PER/FLA4815/2008	KJ672601.1: 6724-8442 AHX22430 (HN protein)
Recombinant PIV3/PIV1 virus fusion glycoprotein (F) and hemagglutinin (HN) genes, complete cds; and RNA dependent RNA polymerase (L) gene, partial cds.	AF016281 AAC23947 (hemagglutinin)
Recombinant PIV3/PIV1 virus fusion glycoprotein (F) and hemagglutinin (HN) genes, complete cds; and RNA dependent RNA polymerase (L) gene, partial cds.	AF016281 AAC23947 (fusion protein)
hemagglutinin-neuraminidase [Human parainfluenza virus 3]	BAO32044.1
hemagglutinin-neuraminidase [Human parainfluenza virus 3]	BAO32051.1
C protein [Human parainfluenza virus 3]	NP_599251.1
C protein [Human parainfluenza virus 3]	ABZ85670.1
C protein [Human parainfluenza virus 3]	AGT75164.1
C protein [Human parainfluenza virus 3]	AAB48686.1
C protein [Human parainfluenza virus 3]	AHX22115.1
C protein [Human parainfluenza virus 3]	AGW51066.1
C protein [Human parainfluenza virus 3]	AGW51162.1
C protein [Human parainfluenza virus 3]	AGT75252.1
C protein [Human parainfluenza virus 3]	AGT75188.1
C protein [Human parainfluenza virus 3]	AGW51218.1
C protein [Human parainfluenza virus 3]	AGW51074.1
C protein [Human parainfluenza virus 3]	AGT75323.1
C protein [Human parainfluenza virus 3]	AGT75307.1
C protein [Human parainfluenza virus 3]	AHX22131.1
C protein [Human parainfluenza virus 3]	AGW51243.1
C protein [Human parainfluenza virus 3]	AGT75180.1
C protein [Human parainfluenza virus 3]	AGT75212.1
C protein [Human parainfluenza virus 3]	AGW51186.1
C protein [Human parainfluenza virus 3]	AHX22075.1
C protein [Human parainfluenza virus 3]	AHX22163.1
C protein [Human parainfluenza virus 3]	AGT75196.1
C protein [Human parainfluenza virus 3]	AHX22491.1
C protein [Human parainfluenza virus 3]	AHX22139.1
C protein [Human parainfluenza virus 3]	AGW51138.1
C protein [Human parainfluenza virus 3]	AGW51114.1
C protein [Human parainfluenza virus 3]	AGT75220.1

TABLE 7-continued

PIV3 NCBI Accession Numbers (Nucleic Acid and Amino Acid Sequences)	
Description	GenBank Accession
C protein [Human parainfluenza virus 3]	AHX22251.1
RecName: Full = Protein C; AltName: Full = VP18 protein	P06165.1
C protein [Human parainfluenza virus 3]	AHX22187.1
C protein [Human parainfluenza virus 3]	AGT75228.1
C protein [Human parainfluenza virus 3]	AHX22179.1
C protein [Human parainfluenza virus 3]	AHX22427.1
C protein [Human parainfluenza virus 3]	AGW51210.1
nonstructural protein C [Human parainfluenza virus 3]	BAA00922.1
C protein [Human parainfluenza virus 3]	AHX22315.1
C protein [Human parainfluenza virus 3]	AGW51259.1
C protein [Human parainfluenza virus 3]	AHX22435.1
C protein [Human parainfluenza virus 3]	AHX22123.1
C protein [Human parainfluenza virus 3]	AHX22299.1
C protein [Human parainfluenza virus 3]	AGW51267.1
unnamed protein product [Human parainfluenza virus 3]	CAA28430.1
C protein [Human parainfluenza virus 3]	AGW51178.1
C protein [Human parainfluenza virus 3]	AHX22411.1
RecName: Full = Protein C	P06164.1
phosphoprotein [Human parainfluenza virus 3]	NP_067149.1
phosphoprotein [Human parainfluenza virus 3]	AAB48685.1
phosphoprotein [Human parainfluenza virus 3]	AHX22498.1
phosphoprotein [Human parainfluenza virus 3]	AHX22490.1
phosphoprotein [Human parainfluenza virus 3]	AGT75259.1
phosphoprotein [Human parainfluenza virus 3]	AGW51137.1
phosphoprotein [Human parainfluenza virus 3]	AGW51145.1
phosphoprotein [Human parainfluenza virus 3]	AGT75298.1
phosphoprotein [Human parainfluenza virus 3]	AGW51113.1
phosphoprotein [Human parainfluenza virus 3]	AGT75203.1
phosphoprotein [Human parainfluenza virus 3]	AGT75163.1
phosphoprotein [Human parainfluenza virus 3]	AHX22506.1
phosphoprotein [Human parainfluenza virus 3]	AGW51129.1
phosphoprotein [Human parainfluenza virus 3]	AHX22194.1
phosphoprotein [Human parainfluenza virus 3]	AGT75211.1
phosphoprotein [Human parainfluenza virus 3]	AHX22258.1
phosphoprotein [Human parainfluenza virus 3]	AGW51121.1
phosphoprotein [Human parainfluenza virus 3]	AGT75282.1
phosphoprotein [Human parainfluenza virus 3]	AHX22146.1
phosphoprotein [Human parainfluenza virus 3]	AHX22138.1
phosphoprotein [Human parainfluenza virus 3]	AHX22322.1
phosphoprotein [Human parainfluenza virus 3]	AHX22370.1
phosphoprotein [Human parainfluenza virus 3]	AHX22098.1
phosphoprotein [Human parainfluenza virus 3]	AHX22130.1
phosphoprotein [Human parainfluenza virus 3]	AHX22418.1
phosphoprotein [Human parainfluenza virus 3]	AHX22114.1
phosphoprotein [Human parainfluenza virus 3]	AHX22410.1
phosphoprotein [Human parainfluenza virus 3]	AGT75306.1
phosphoprotein [Human parainfluenza virus 3]	AHX22170.1
phosphoprotein [Human parainfluenza virus 3]	AHX22266.1
phosphoprotein [Human parainfluenza virus 3]	AHX22090.1
phosphoprotein [Human parainfluenza virus 3]	AGT75195.1
phosphoprotein [Human parainfluenza virus 3]	AHX22226.1
phosphoprotein [Human parainfluenza virus 3]	AHX22178.1
phosphoprotein [Human parainfluenza virus 3]	AHX22122.1
phosphoprotein [Human parainfluenza virus 3]	AHX22186.1
phosphoprotein [Human parainfluenza virus 3]	AHX22066.1
phosphoprotein [Human parainfluenza virus 3]	AHX22522.1
phosphoprotein [Human parainfluenza virus 3]	AGW51225.1
phosphoprotein [Human parainfluenza virus 3]	BAN29032.1
phosphoprotein [Human parainfluenza virus 3]	ABZ85669.1
phosphoprotein [Human parainfluenza virus 3]	AHX22426.1
phosphoprotein [Human parainfluenza virus 3]	AHX22058.1
phosphoprotein [Simian Agent 10]	ADR00400.1
phosphoprotein [Human parainfluenza virus 3]	AHX22250.1
phosphoprotein [Human parainfluenza virus 3]	AHX22434.1
phosphoprotein [Human parainfluenza virus 3]	AHX22298.1
phosphoprotein [Human parainfluenza virus 3]	AHX22442.1
phosphoprotein [Human parainfluenza virus 3]	AHX22074.1
phosphoprotein [Human parainfluenza virus 3]	AGW51153.1
phosphoprotein [Human parainfluenza virus 3]	AGW51241.1
phosphoprotein [Human parainfluenza virus 3]	AHX22210.1
phosphoprotein [Human parainfluenza virus 3]	AGW51105.1
phosphoprotein [Human parainfluenza virus 3]	AGT75251.1
phosphoprotein [Human parainfluenza virus 3]	AHX22362.1

TABLE 7-continued

PIV3 NCBI Accession Numbers (Nucleic Acid and Amino Acid Sequences)	
Description	GenBank Accession
phosphoprotein [Human parainfluenza virus 3]	AHX22474.1
phosphoprotein [Human parainfluenza virus 3]	AGW51217.1
phosphoprotein [Human parainfluenza virus 3]	AIG60038.1
phosphoprotein [Human parainfluenza virus 3]	AHX22378.1
phosphoprotein [Human parainfluenza virus 3]	AGW51057.1
phosphoprotein [Human parainfluenza virus 3]	AGT75187.1
phosphoprotein [Human parainfluenza virus 3]	AGW51233.1
phosphoprotein [Human parainfluenza virus 3]	AHX22482.1
phosphoprotein [Human parainfluenza virus 3]	AGW51161.1
phosphoprotein [Human parainfluenza virus 3]	AHX22306.1
phosphoprotein [Human parainfluenza virus 3]	AHX22162.1
phosphoprotein [Human parainfluenza virus 3]	ACJ70087.1
phosphoprotein [Human parainfluenza virus 3]	AHX22466.1
phosphoprotein [Human parainfluenza virus 3]	AHX22346.1
phosphoprotein [Human parainfluenza virus 3]	AGW51089.1
phosphoprotein [Human parainfluenza virus 3]	AGW51073.1
phosphoprotein [Human parainfluenza virus 3]	AGW51185.1
phosphoprotein [Human parainfluenza virus 3]	AGW51065.1
phosphoprotein [Human parainfluenza virus 3]	ABY47603.1
phosphoprotein [Human parainfluenza virus 3]	AGW51049.1
phosphoprotein [Human parainfluenza virus 3]	AHX22330.1
phosphoprotein [Human parainfluenza virus 3]	AGW51250.1
phosphoprotein [Human parainfluenza virus 3]	AGT75227.1
phosphoprotein [Human parainfluenza virus 3]	AGW51282.1
phosphoprotein [Human parainfluenza virus 3]	AGW51209.1
phosphoprotein [Human parainfluenza virus 3]	AGW51193.1
phosphoprotein [Human parainfluenza virus 3]	AGT75322.1
phosphoprotein [Human parainfluenza virus 3]	AGT75219.1
phosphoprotein [Human parainfluenza virus 3]	AGW51258.1
phosphoprotein [Human parainfluenza virus 3]	AGW51041.1
phosphoprotein [Human parainfluenza virus 3]	ACD99698.1
phosphoprotein [Human parainfluenza virus 3]	AGW51266.1
phosphoprotein [Human parainfluenza virus 3]	AGT75179.1
phosphoprotein [Human parainfluenza virus 3]	AHX22282.1
phosphoprotein [Human parainfluenza virus 3]	AGW51169.1
phosphoprotein [Human parainfluenza virus 3]	AGW51274.1
phosphoprotein [Human parainfluenza virus 3]	AGW51201.1
phosphoprotein [Human parainfluenza virus 3]	AGW51177.1
RecName: Full = Phosphoprotein; Short = Protein P	P06162.1
P protein [Human parainfluenza virus 3]	AAA66818.1
phosphoprotein [Human parainfluenza virus 3]	AAA46866.1
phosphoprotein [Human parainfluenza virus 3]	BAA00031.1
polymerase-associated nucleocapsid phosphoprotein (version 2) - parainfluenza virus type 3	RRNZP5
[Human parainfluenza virus 3]	
phosphoprotein [Human parainfluenza virus 3]	AGT75171.1
phosphoprotein [Human parainfluenza virus 3]	BAA00921.1
D protein [Human parainfluenza virus 3]	NP_599250.1
D protein [Human parainfluenza virus 3]	AHX22377.1
D protein [Human parainfluenza virus 3]	AHX22121.1
D protein [Human parainfluenza virus 3]	AGT75297.1
D protein [Human parainfluenza virus 3]	AGW51136.1
D protein [Human parainfluenza virus 3]	AGW51242.1
D protein [Human parainfluenza virus 3]	AGW51112.1
D protein [Human parainfluenza virus 3]	AHX22497.1
D protein [Human parainfluenza virus 3]	AHX22145.1
D protein [Human parainfluenza virus 3]	AGT75202.1
D protein [Human parainfluenza virus 3]	AHX22385.1
D protein [Human parainfluenza virus 3]	AGW51216.1
D protein [Human parainfluenza virus 3]	AGT75281.1
D protein [Human parainfluenza virus 3]	AGT75194.1
D protein [Human parainfluenza virus 3]	AHX22521.1
D protein [Human parainfluenza virus 3]	AGW51120.1
D protein [Human parainfluenza virus 3]	AGT75313.1
D protein [Human parainfluenza virus 3]	AHX22249.1
D protein [Human parainfluenza virus 3]	AHX22097.1
D protein [Human parainfluenza virus 3]	AGW51144.1
D protein [Human parainfluenza virus 3]	AHX22089.1
D protein [Human parainfluenza virus 3]	AHX22225.1
D protein [Human parainfluenza virus 3]	AHX22137.1
D protein [Human parainfluenza virus 3]	AHX22065.1
D protein [Human parainfluenza virus 3]	AGW51224.1
D protein [Human parainfluenza virus 3]	AGT75210.1

TABLE 7-continued

PIV3 NCBI Accession Numbers (Nucleic Acid and Amino Acid Sequences)	
Description	GenBank Accession
D protein [Human parainfluenza virus 3]	AHX22393.1
D protein [Human parainfluenza virus 3]	AGT75258.1
D protein [Human parainfluenza virus 3]	AHX22345.1
D protein [Human parainfluenza virus 3]	AGT75250.1
D protein [Human parainfluenza virus 3]	AHX22113.1
D protein [Human parainfluenza virus 3]	AGW51232.1
D protein [Human parainfluenza virus 3]	AHX22057.1
D protein [Human parainfluenza virus 3]	AHX22209.1
D protein [Human parainfluenza virus 3]	AGW51056.1
D protein [Human parainfluenza virus 3]	AHX22161.1
D protein [Simian Agent 10]	ADR00402.1
D protein [Human parainfluenza virus 3]	AHX22361.1
D protein [Human parainfluenza virus 3]	AGW51281.1
D protein [Human parainfluenza virus 3]	AGW51184.1
D protein [Human parainfluenza virus 3]	AGW51160.1
D protein [Human parainfluenza virus 3]	AHX22465.1
D protein [Human parainfluenza virus 3]	AHX22329.1
D protein [Human parainfluenza virus 3]	AGW51064.1
D protein [Human parainfluenza virus 3]	AGW51040.1
D protein [Human parainfluenza virus 3]	AGT75226.1
D protein [Human parainfluenza virus 3]	AHX22425.1
D protein [Human parainfluenza virus 3]	AHX22305.1
D protein [Human parainfluenza virus 3]	AGW51249.1
D protein [Human parainfluenza virus 3]	AHX22481.1
D protein [Human parainfluenza virus 3]	AHX22281.1
D protein [Human parainfluenza virus 3]	AGW51048.1
D protein [Human parainfluenza virus 3]	AHX22297.1
D protein [Human parainfluenza virus 3]	AGW51088.1
D protein [Human parainfluenza virus 3]	AGT75305.1
D protein [Human parainfluenza virus 3]	AHX22185.1
D protein [Human parainfluenza virus 3]	AGW51104.1
D protein [Human parainfluenza virus 3]	AHX22081.1
D protein [Human parainfluenza virus 3]	AGW51192.1
D protein [Human parainfluenza virus 3]	AHX22489.1
D protein [Human parainfluenza virus 3]	AHX22441.1
D protein [Human parainfluenza virus 3]	AHX22409.1
D protein [Human parainfluenza virus 3]	AHX22369.1
D protein [Human parainfluenza virus 3]	AHX22321.1
D protein [Human parainfluenza virus 3]	AHX22073.1
D protein [Human parainfluenza virus 3]	AGW51152.1
D protein [Human parainfluenza virus 3]	AGW51072.1
D protein [Human parainfluenza virus 3]	AGT75321.1
D protein [Human parainfluenza virus 3]	AHX22257.1
D protein [Human parainfluenza virus 3]	AHX22129.1
D protein [Human parainfluenza virus 3]	AHX22417.1
D protein [Human parainfluenza virus 3]	AGT75218.1
D protein [Human parainfluenza virus 3]	AHX22265.1
D protein [Human parainfluenza virus 3]	AGT75178.1
D protein [Human parainfluenza virus 3]	AHX22433.1
D protein [Human parainfluenza virus 3]	AGW51273.1
D protein [Human parainfluenza virus 3]	AGW51208.1
D protein [Human parainfluenza virus 3]	AGT75170.1
D protein [Human parainfluenza virus 3]	AGT75162.1
D protein [Human parainfluenza virus 3]	AGW51257.1
D protein [Human parainfluenza virus 3]	AGW51200.1
D protein [Human parainfluenza virus 3]	AGW51176.1
D protein [Human parainfluenza virus 3]	AGT75186.1
D protein [Human parainfluenza virus 3]	AGW51265.1
D protein [Human parainfluenza virus 3]	AGW51168.1

TABLE 8

Signal Peptides		
Description	Sequence	SEQ ID NO:
HuIgG _k signal peptide	METPAQLLFLLLLWLPDTTG	15
IgE heavy chain epsilon-1 signal peptide	MDWTWILFLVAAATRVHS	16
Japanese encephalitis PRM signal sequence	MLGSNSGQRVVFILLVAPAYS	17
VSVg protein signal sequence	MKCLLYLAFLFIGVNCA	18
Japanese encephalitis JEV signal sequence	MWLVSLAIVTACAGA	19

TABLE 9

hMPV/PIV Cotton Rat Challenge Study Design					
Group	n	Test Article	[conc]/μg	Route	Challenge
1	5	Placebo	n/a	IM	hMPV/A2
2	5	hMPV vaccine mRNA	30	IM	hMPV/A2
3	5	hMPV vaccine mRNA	15	IM	hMPV/A2
4	5	hMPV vaccine mRNA	10	IM	hMPV/A2
5	5	hMPV/PIV3 vaccine mRNA (15/15)	30	IM	hMPV/A2
6	5	FI-hMPV	n/a	IM	hMPV/A2
7	5	Placebo	n/a	IM	PIV3
8	5	PIV3 vaccine mRNA	30	IM	PIV3
9	5	PIV3 vaccine mRNA	15	IM	PIV3
10	5	PIV3 vaccine mRNA	10	IM	PIV3
11	5	hMPV/PIV3 vaccine mRNA (15/15)	30	IM	PIV3
12	5	FI-PIV3	n/a	IM	PIV3
60					

TABLE 10

Betacoronavirus Nucleic Acid Sequence		
Strain	Nucleic Acid Sequence	SEQ ID NO:
gb KJ156934.1 : 21405-25466 Middle East respiratory syndrome coronavirus isolate Riyadh_14_2013, spike protein (nucleotide)	ATGATACACTCAGTGTTCCTACTGATGTTCTTGTTAAACACC TACAGAAAGTTACGTTGATGTAGGGCCAGATTCTGTTAAG TCTGCTTGTATTGAGGTTGATATACAACAGACCTTCTTTGA TAAACTTGGCCTAGGCCAATTGATGTTTCTAAGGCTGAC GGTATTATATACCCCTCAAGGCCGTACATATTCTAACATAA CTATCACTTATCAAGGTTCTTTTCCCTATCAGGGAGACCAT GGTGATATGTATGTTTACTCTGCAGGACATGCTACAGGCA CAACTCCACAAAAGTTGTTTGTAGCTAACTATTCTCAGGA CGTCAACAGTTTGCTAATGGGTTTGTCGTCGGTATAGGA GCAGCTGCCAATTCACCTGGCAGCTGTTATTATTAGCCATC TACCAGCGCTACTATACGAAAAATTACCCGTGCTTTTATGC TGGGTTCTTCAGTTGGTAATTTCTCAGATGGTAAATGGG CCGCTTCTTCAATCATACTCTAGTTCTTTTGCCCGATGGAT GTGGCACTTTACTTAGAGCTTTTATTGTATTCTAGAGCCT CGCTCTGGAAATCATGTCTGCTGGCAATTCCTATACTTC TTTTGCCACTTATCACACTCCTGCAACAGATTGTCTGATG GCAATTACAATCGTAATGCCAGTCTGAACCTTTTAAAGGA GTATTTAATTTACGTAACGACCTTTATGTACACTTATA ACATTACCGAAGATGAGATTTTAGAGTGGTTGGCATTAC ACAAACTGCTCAAGGTGTTACCTCTTCTCATCTCGGTATG TTGATTTGTACGGCGGCAATATGTTTCAATTTGCCACCTTG CCTGTTTATGATACTATTAGTATTATTCTATCATTCCTCA CAGTATTCGTTCTATCCAAAGTGATAGAAAAGCTTGGGCT GCCTTCTACGTATATAAACTTCAACCGTTAACTTTCTGTT GGATTTTCTGTTGATGGTTATATACGCAGAGCTATAGACT GTGGTTTAAATGATTGTGCACAACTCCACTGCTCATATGAA TCCTTCGATGTTGAATCTGGAGTTTATTCAGTTTCTGCTTT CGAAGCAAAACCTTCTGGCTCAGTTGTGGAACAGGCTGAA GGTGTTGAATGTGATTTTTCACCTCTTCTGCTGGCACACC TCCTCAGGTTTATAATTTCAAGCGTTTGGTTTTTACCAATT GCAATTATAATCTTACCAAAATGCTTTCACTTTTTTCTGTG AATGATTTTACTTTAGTCAAAATATCTCCAGCAGCAATTGC TAGCAACTGTTATTCTTCACTGATTTTGGATTATTTTCAT ACCCACTTAGTATGAAATCCGATCTCAGTGTAGTTCTGCT GGTCCAATATCCAGTTTAAATTATAAACAGTCCTTTTCTAA TCCACATGTTTGTCTTAGCGACTGTTCCCTACAACCTTA CTACTATTACTAAGCCTCTTAAGTACAGCTATATTAACAA GTGCTCTCGTCTTCTTTCTGATGATCGTACTGAAGTACCTC AGTTAGTGAACGCTAATCAATACTCACCTGTGTATCCATT GTCCCATCCACTGTGTGGGAAGACGGTGATTATTATAGGA AACAACTATCTCCACTTGAAGGTGGTGGCTGGCTTGTTC TAGTGGCTCAACTGTTGCCATGACTGAGCAATTACAGATG GGCTTTGGTATTACAGTTCAATATGGTACAGACCAATA GTGTTTGGCCCAAGCTTGAATTTGCTAATGACACAAAAT	20

TABLE 10-continued

Betacoronavirus Nucleic Acid Sequence		
Strain	Nucleic Acid Sequence	SEQ ID NO:
	TGCCCTCTCAATTAGGCAATTGCGTGGAAATATTCCCTCTATG GTGTTTCGGGCCGTGGTGTTCCTCAGAAATGCACAGCTGTA GGTGTTTCGACAGCAGCGCTTTGTTTATGATGCGTACCAGA ATTTAGTTGGCTATTATTCTGATGATGGCACTACTACTGT CTGCGTGCTTGTGTTAGTGTTCCTGTTTCTGTCATCTATGA TAAAGAACTAAACCCACGCTACTCTATTTGGTAGTGT GCATGTGAACACATTTCTTCTACCATGTCTCAATACTCCCG TTCTACGCGATCAATGCTTAAACGGCGAGATTCTACATAT GGCCCCCTTCAGACACCTGTTGGTTGTCTCCTAGGACTTGT TAATTCCTCTTTGTTTCGTAGAGGACTGCAAGTTGCTCTCG GTCAATCTCTCTGTGCTCTTCTGACACACCTAGTACTCTC ACACCTCGCAGTGTGCGCTCTGTGCGAGGTGAAATGCGCT TGGCATCCATTGCTTTTAAATCATCCATTACAGGTTGATCAA CTTAATAGTAGTATTTTAAATTAAGTATACCCACTAATTT TTCTTTGGTGTGACTCAGGAGTACATTGAGACACCATTC AGAAAGTTACTGTTGATTGTAACAGTACGTTTGCAATGG TTTCAGAAAGTGTGAGCAATTACTGCGCGAGTATGGCCAG TTTTGTTCAAAATAAACAGGCTCTCCATGGTGCCAAATT ACGCCAGGATGATTCTGTACGTAATTTGTTTGCGAGCGTG AAAAGCTCTCAATCATCTCTATCATACAGGTTTGGAG GTGACTTTAATTGACACTTCTAGAACCTGTTTCTATATCT ACTGGCAGTCGTAGTGACGTAAGTCTATTGAGGATTTGC TATTTGACAAAGTCACTATAGCTGATCCTGGTTATATGCA AGGTTACGATGATTGTATGACGCAAGGTCCAGCATCAGCT CGTGATCTTATTTGTGCTCAATATGTGGCTGGTTATAAAGT ATTACCTCCTCTTATGGATGTTAATATGGAAGCCGCGTATA CTTCATCTTTGCTTGGCAGCATAGCAGGTGTTGGCTGGACT GCTGGCTTATCCTCCTTTGCTGCTATTCATTGACACAGAG TATYTTTTATAGGTTAAACGGTGTGGCATTACTCAACAG GTTCTTTCAGAGAACCAAAGCTTATTGCCAATAAGTTTA ATCAGGCTCTGGGAGCTATGCAACAGGCTTCACTACAAC TAATGAAGCTTTTCGGAAGGTTACAGGATGCTGTGAACAC AATGCACAGGCTCTATCAAATTAGCTAGCAGCTATCTA ATACTTTTGGTGCTATTTCCGCCCTCTATTGGAGACATCATA CAACGTCTTGATGTTCTCGAACAGGACGCCAAATAGACA GACTTATTAATGGCCGTTTGACAACACTAAATGCTTTTGTT GCACAGCAGCTTGTTCTGTTCCGAATCAGCTGCTCTTTCCGC TCAATTGGCTAAAGATAAAGTCAATGAGTGTGTCAAGGCA CAATCCAAGCGTTCTGGATTTTGCAGTCAAGGCACACATA TAGTGTCTTTGTTGTAATGCCCCCTAATGGCCTTTACTTT ATGCATGTTGGTTATTACCCTAGCAACCACATTGAGGTTGT TTCTGCTTATGGTCTTTGCGATGCAGCTAACCTACTAATT GTATAGCCCCGTTAATGGCTACTTTATTAACAACTAATAAC ACTAGGATTGTTGATGAGTGGTCATATACTGGCTCGTCCTT CTATGCACCTGAGCCCATCACCTCTCTAATACTAAGTATG TTGCACCAAGGTGACATACCAAAACATTTCTACTAACCT CCTCTCTCTCTCTCGGCAATTCACCGGGATTGACTTCC AAGATGAGTTGGATGAGTTTTCAAAATGTTAGCACCAG TATACCTAATTTGGTCTCTAACAACAGATTAACTACTACAT TACTCGATCTTACCTACGAGATGTTGTCTCTTCAACAAGTT GTTAAAGCCCTTAATGAGTCTTACATAGACCTTAAAGAGC TTGGCAATTATACTATTACAACAAATGGCCGTGGTACAT TTGGCTTGGTTTCATTGCTGGGCTTGTGCTTAGCTCTAT GCGTCTTCTCATACTGTGCTGCACTGGTTGTGGCACAAAC TGTATGGGAAAACCTAAGTGTAATCGTTGTTGTGATAGAT ACGAGGAATACGACCTCGAGCTGCATAAGGTTTCATGTTCA CTAA	
MERS S FL SPIKE 2cEMC/2012 (XBai change(T to G)) (nucleotide)	ATGATACACTCAGTGTTCCTACTGATGTTCTTGTAAACAC TACAGAAAGTTACGTTGATGTAGGCCAGATTCTGTAAAG TCTGCTTGATTTGAGGTTGATATACAACAGACTTTCTTTGA TAAACTTGGCCTAGGCCAATTGATGTTTCTAAGGCTGAC GGTATTATATACCTCAAGGCCGTACATATTCTAACATAA CTATCACTTATCAAGGCTTTTTTCCCTATCAGGGAGACCAT GGTGATATGATGTTTACTCTGCAGGACATGCTACAGGCA CAACCTCCACAAAGTTGTTTGTAGCTAACTATTCTCAGGA CGTCAACACAGTTTGCTAATGGGTTTGTGCTCCGTATAGGA GCAGCTGCCAATTCCACTGGCACTGTATTATTAGCCCATC TACCAGCGCTACTATACGAAAATTTACCTGCTTTTATGC TGGGTTCTTCAGTTGGTAATTTCTCAGATGGTAAATGGG CCGCTTCTCAATCATACTCTAGTTCTTTGCCCCGATGGAT GTGGCACTTACTTAGAGCTTTTATTGTATTCTGGAGCCT	21

TABLE 10-continued

Betacoronavirus Nucleic Acid Sequence		
Strain	Nucleic Acid Sequence	SEQ ID NO:
	CGCTCTGGAAATCATTGTCCTGCTGGCAATTCCCTATACTTC TTTTGCCACTTATCACACTCCTGCAACAGATTGTTCTGATG GCAATTACAATCGTAATGCCAGTCTGAACTCTTTTAAGGA GTATTTTAATTTACGTAACGACCTTTATGTACACTTATA ACATTACCGAAGATGAGATTTTAGAGTGGTTTGGCATTAC ACAACTGCTCAGGTGTTACCTCTTCTCATCTCGGTATG TTGATTTGTACGGCGGCAATATGTTCAATTTGCCACCTTG CCTGTTTATGATACTATTAAGTATTATTCTATCATTCTCA CAGTATTCTGTTCTATCCAAAGTGATAGAAAAGCTTGGGCT GCCTTCTACGTATATAAACTTCAACCGTTAACTTTCCCTGTT GGATTTTTCTGTTGATGGTTATATACGCAGAGCTATAGACT GTGGTTTTAATGATTGTGCACAACTCCACTGCTCATATGAA TCCTTCGATGTTGAATCTGGAGTTTATTGAGTTTCGTCTTT CGAAGCAAAACCTTCTGGCTCAGTTGTGGAACAGGCTGAA GGTGTGAATGTGATTTTACCTCTTCTGTCTGGCACACC TCCTCAGGTTTATAATTTCAAGCGTTTGGTTTTTACCAATT GCAATTATAATCTTACCAATTTGCTTTCACTTTTTCTGTG AATGATTTTACTTGTAGTCAAATATCTCCAGCAGCAATTGC TAGCAACTGTTATTCTTCACTGATTTGGATTACTTTTCAT ACCCACTTAGTATGAAATCCGATCTCAGTGTAGTTCTGCT GGTCCAATATCCAGTTTAAATTATAAACAGTCCTTTCTAA TCCCACATGTTGATTTTAGCGACTGTTCCCTATAACCTTA CTACTATTACTAAGCCTCTTAAGTACAGCTATATTAACAA GTGCTCTCGTCTTCTTTCTGATGATCGTACTGAAGTACCTC AGTTAGTGAACGCTAATCAATACTCACCTGTGTATCCATT GTCCCATCCACTGTGTGGGAAGACGGTGATTATTATAGGA AACAACATCTCCACTTGAAGGTGGTGGCTGGCTTGTTC TAGTGGCTCAACTGTTGCCATGACTGAGCAATTACAGATG GGCTTTGGTATTACAGTTCAATATGGTACAGACACCAATA GTGTTTGCCCCAAGCTTGAATTTGCTAATGACACAAAAT TGCCCTCTCAATTAGGCAATTGCGTGGAATATCCCTCTATG GTGTTTCGGGCCGTGGTGTGTTTTCAGAAATGACAGCTGTA GGTGTTCGACAGCAGCGCTTTGTTTATGATGCGTACCAGA ATTTAGTTGGCTATTATTCTGATGATGGCAACTACTACTGT TTGCGTGTGTTGTTAGTGTTCCTGTTTCTGTCATCTATGAT AAAGAACTAAAACCCACGCTACTCTATTTGGTAGTGTG CATGTGAACACATTTCTTCTACCATGTCTCAATACTCCCGT TCTACGCGATCAATGCTTAAACGGCGAGATTCTACATATG GCCCCCTTCAGACACCTGTTGGTTGTGCTTAGGACTTGT AATTCCCTCTTTGTTTCGTAGAGGACTGCAAGTTGCCTCTTG TCAATCTCTCTGTGCTCTTCTGACACACCTAGTACTCTCA CACCTCGCAGTGTGCGCTCTGTTCCAGGTGAAATGCGCTT GGCATCCATTGCTTTTAAATCATCTTATTGAGTTGATCAAC TTAATAGTAGTTATTTTAAATTAAGTATACCCACTAATTTT TCCTTTGGTGTGACTCAGGAGTACATTGAGCAACCATTC AGAAAGTTACTGTTGATTGTAAACAGTACGTTTGAATGG TTTCCAGAAGTGTGAGCAATTACTGCGCGAGTATGGCCAG TTTTGTTCCAAAATAAACAGGCTCTCCATGGTGCCAATTT ACGCCAGGATGATTCTGTACGTAATTTGTTTGCAGCGGTG AAAAGCTCTCAATCATCTCTATCATACAGGTTTGGAG GTGACTTTAATTTGACACTTCTGGAACCTGTTCTATATCT ACTGGCAGTCGTAGTGCACGTAGTGCTATTGAGGATTGTC TATTTGACAAAGTCACTATAGCTGATCCTGGTTATATGCA AGGTTACGATGATTGCATGCAGCAAGGTCCAGCATCAGCT CGTGATCTTATTTGTGCTCAATATGTGGCTGGTTACAAAGT ATTACCTCCTCTTATGGATGTTAATATGGAAGCCGCGTATA CTTCATCTTTGCTTGGCAGCATAGCAGGTGTTGGCTGGACT GCTGGCTTATCCTCCTTTGCTGCTATTCCATTGACAGAG TATCTTTTATAGGTTAAACGGTGTGGCATTACTCAACAGG TTCTTTGAGAAACCAAAGCTTATGCCAAATAAGTTTAA TCAGGCTCTGGGAGCTATGCAACAGGCTTCACTACAAC AATGAAGCTTTTCAAGAGTTTCAAGATGCTGTGAACAACA ATGCACAGGCTCTATCCAAATTAGCTAGCGAGCTATCTAA TACTTTGGTGCTATTTCCGCTCTATTGGAGACATCATAC AACGTCCTGATGTTCTCGAACAGGACGCCAAATAGACAG ACTTATTAATGGCCGTTTGACAACTAAATGCTTTTGTG CACAGCAGCTTGTTCGTTCCGAATCAGCTGCTCTTTCCGCT CAATTGGCTAAAGATAAAGTCAATGAGTGTGCAAGGCAC AATCCAAGCGTTCTGATTTTGCAGTCAAGGCACACATAT AGTGCTCTTTGTTGTAATGCCCTAATGGCCTTTACTTCA TGCATGTTGGTTATTACCCTAGCAACCAATTGAGGTTGTT TCTGCTTATGGTCTTTGCGATGCAGCTAACCTACTAATTG	

TABLE 10-continued

Betacoronavirus Nucleic Acid Sequence		
Strain	Nucleic Acid Sequence	SEQ ID NO:
	TATAGCCCTGTTAATGGCTACTTTATTAATACTAATAACA CTAGGATTGTTGATGAGTGGTCATATACTGGCTCGTCCTTC TATGCACCTGAGCCATTACCTCCCTTAATACTAAGTATGT TGCACCACAGGTGACATACAAAACATTCTACTAACCTC CCTCCTCCTCTTCTCGGCAATTCACCGGGATTGACTTCCA AGATGAGTTGGATGAGTTTTCAAAATGTTAGCACCAGT ATACCTAATTTTGGTTCCTTAACACAGATTAATACTACATT ACTCGATCTTACCTACGAGATGTTGTCTCTCAACAAGTTG TTAAAGCCCTTAATGAGTCTTACATAGACCTTAAAGAGCT TGGCAATTATACCTATTACAACAAATGGCCGTGGTACATT TGGCTTGGTTTCATTGCTGGGCTTGTGCTTAGCTCTATG CGTCTTCTCATACTGTGCTGCACTGGTGTGGCACAACCT GTATGGGAAAACCTAAGTGTAATCGTTGTTGTGATAGATA CGAGGAATACGACCTCGAGCCGATAAGGTTTATGTTTAC TAA	
Novel_MERS_S2_subunit_trimeric vaccine (nucleotide)	ATGATCCACTCCGTGTTCTCTCATGTTCTGTTGACCCC CACTGAGTCAGACTGCAAGCTCCCGTGGGACAGTCCCTG TGTGCGCTGCCTGACACTCCTAGCACTGACCCACGCTC CGTGCGGTGCGTGCCTGGCGAAATGCGCTGGCCTCCATC GCCTTCAATCACCCAATCCAACTGGATCAGCTGAATAGCT CGTATTTCAAGCTGTCCATCCCGCAAGTCTCTGTTCCGGG GTCACCCAGGAGTACATCCAGACCACAATTGAGAAGGTCA CCGTCGATTGCAAGCAATACGTGTGCAACGGCTTCCAGAA GTGCGAGCAGCTGCTGAGAGAATACGGGCAGTTTTCAGC AAGATCAACAGGCGCTGCATGGAGCTAACTTGCGCCAGG ACGACTCCGTGCGCAACCTCTTGCCTCTGTGAAGTCATCC CAGTCTCCCAATCATCCCGGATTCGGAGGGGACTTCA ACCTGACCCTCCTGGAGCCCGTGTGATCAGCACCAGGTAG CAGATCGGCGCTCAGCCATTGAAGATCTTCTGTTTCGAC AAGGTCACCATCGCCGATCCCGGCTACATGCAAGGATACG ACGACTGTATGCAAGCAGGACAGCCTCCGCGAGGGACCT CATCTGCGCGCAATACGTGGCCGGGTACAAAGTGTGCTC CCTCTGATGGATGTGAACATGGAGGCCGCTTATACTTCGT CCTGCTCGGCTCTATCGCCGGCTGGGGTGGACCGCCGG CCTGTCTCTTCCGCGCTATCCCTTTGCACAATCCATT TCTACCGCTCAACGGCGTGGGCATTACTCAACAAGTCTT GTCGAGAACAGAAAGTTGATCGCAACAAGTTCAATCA GGCCCTGGGGGCTATGCAAGTGGATTCACTACGACTAAC GAAGCGTTCCAGAAGGTCCAGGACGCTGTGAACAACAAC GCCAGGCGCTCTCAAGCTGGCCTCCGAACCTCAGCAACA CCTTCGGAGCCATCAGCGCATCGATCGGTGACATAATTCA GCGGCTGGACGTGCTGGAGCAGGACGCCAGATCGACCG CCTCATCAACGACGGCTGACCACTTGAATGCCCTTCGTG GCACAACAGCTGGTCCGGAGCGAATCAGCGGCATTTCCG CCCAACTCGCCAAGGACAAAGTCAACGAATGCGTGAAG CCCAGTCCAAGAGTCCGTTTCTGCGGTCAAGGAACCCA TATTGTGTCTTCGTGTAACGCGCCCAACGGTCTGTACT TTATGCACGTGGCTACTACCCGAGCAATCATATCGAAGT GGTGTCCGCTACGGCTGTGCGATGCCGCTAACCCACT AACTGTATTGCCCTGTGAACGGATATTTATTAAGACCA ACAACACCCGCTATTGTGACGAATGGTCATACACCGGTT GTCTTCTACGCGCCGAGCCCATCACTTCACTGAACACC AAATACGTGGCTCCGCAAGTGACCTACCAGAACATCTCCA CCAATTTGCCGCGCGCTGCTCGGAAACAGCACCGGAAT TGATTTCAAGATGAAGTGGACGAATTTCTCAAGAACGTG TCCACTTCCATTCCCAACTTCGGAAGCCTGACACAGATCA ACACCACCTTCTCGACCTGACCTACGAGATGCTGAGCCT TCAACAAGTGGTCAAGGCCCTGAACGAGAGCTACATCGAC CTGAAGGAGCTGGGCAACTATACCTACTACAACAAGTGGC CGGACAAGATTGAGGAGATTCTGTGAAAATCTACCACAT TGAAAACGAGATCGCCAGAATCAAGAAGCTTATCGGCGA AGCC	22
MERS_S0_Full-length Spike protein (nucleotide, codon optimized)	ATGGAACCCCTGCCAGCTGCTGTTCTGCTGCTGCTGTG GCTGCTGATACACCGCGAGCTATGTGGACGTGGGCCCC GATAGCGTGAAGTCCGCTGTATCGAAGTGGACATCCAGC AGACCTTTTTCGACAAGACCTGGCCAGACCCATCGACGT GTCCAAGGCCGACGCATCATATCCACAAGGCCGAGACC TACAGCAACATCACCATTACCTACAGGGCCTGTTCCCAT ATCAAGGCCACACGGCGATATGTACGTGACTCTGCGCG CCACGCCACCGGCACACACCCAGAACTGTTCTGTGGCC	23

TABLE 10-continued

Betacoronavirus Nucleic Acid Sequence		
Strain	Nucleic Acid Sequence	SEQ ID NO:
	AACTACAGCCAGGACGTGAAGCAGTTCGCCAACGGCTTCG TCGTGCGGATTGGCGCCGCTGCCAATAGCACCGGCACAGT GATCATCAGCCCCAGCACCAGCGCCACCATCCGGAAGATC TACCCCGCCTTCATGCTGGGCAGCTCCGTGGGCAATTTCA GCGACGGCAAGATGGGCGGTTCTTCAACCACACCTGGT GCTGCTGCCCGATGGCTGTGGCAGCTGCTGAGAGCCTTC TACTGCATCCTGGAACCCAGAAGCGGCAACCACTGCCCTG CCGGCAATAGCTACACCAGCTTCGCCACCTACCACACACC CGCCACCGATTGCTCCGACGGCAACTACAACCGGAACGCC AGCCTGAACAGCTTCAAAGAGTACTTCAACCTGCGGAAC GCACCTTCATGTACACCTACAATATCACCAGGACGAGAT CCTGGAATGGTTCCGCATCACCCAGACCGCCAGGGCGTG CACCTGTTTCAGCAGCAGATACGTGGACCTGTACGGCGGCA ACATGTTCCAGTTTGCCACCCCTGCCCGTGTACGACACCATC AAGTACTACAGCATCATCCCCACAGCATCCGGTCCATCC AGAGCGACAGAAAAGCCTGGGCCGCTTCTACGTGTACAA GCTGCAGCCCCGACCTTCTGCTGGACTTCAGCGTGGAC GGCTACATCAGACGGGCCATCGACTGCGGCTTCAACGACC TGAGCCAGCTGCACTGCTCCTACGAGAGCTTCGACGTGGA AAGCGGCGTGTACAGCGTGTCCAGCTTCGAGGCCAAGCCT AGCGGCAGCGTGGTGAACAGGCTGAGGGCGTGAATGC GACTTCAGCCCTCTGCTGAGCGGCACCCCTCCCCAGGTGT ACAACTTCAAGCGGCTGGTGTTCACCAACTGCAATTACAA CCTGACCAAGCTGCTGAGCCTGTTCTCCGTGAACGACTTC ACCTGTAGCCAGATCAGCCCTGCCGCCATTGCCAGCAACT GCTACAGCAGCCTGATCCTGGACTACTTCAGCTACCCCT GAGCATGAAGTCCGATCTGAGCGTGTCTCCGCCGACCC ATCAGCCAGTTCAACTACAAGCAGAGCTTCAGCAACCCTA CCTGCCTGATTCTGGCCACCGTGCCCAATCTGACCAC CATCACCAGCCCTGAAGTACAGCTACATCAACAGTGC AGCAGACTGCTGTCCGACGACCGGACCGAAGTGGCCAGC TCGTGAACGCCAACCAGTACAGCCCTGCGTGTCCATCGT GCCCAGCACCGTGTGGAGGACGGCGACTACTACAGAAA GCAGCTGAGCCCCCTGGAAGGCGGCGGATGGCTGGTGGCT TCTGGAAGCACAGTGGCCATGACCGAGCAGCTGCAGATG GGCTTTGGCATCACCGTGCAGTACGGCACCGACCAACA GCGTGTGCCCCAAGCTGGAATTCGCCAATGACACCAAGAT CGCCAGCCAGCTGGGAAACTGCGTGGAACTACTCCCTGTAT GGCGTGTCCGGACGGGCGTGTCCAGAATTGCACAGCAG TGGGAGTGCAGCAGCAGAGATTCTGTGTACGATGCTACCA GAACCTCGTGGGCTACTACAGCGACGACGCAATTACTAC TGCTTGCGGGCTGTGTGTCCGTGCCCGTGTCCGTGATCTA CGACAAAGAGACAAAGACCCACGCCCACTGTTCCGGCTCC GTGGCCTGCAGCACATCAGCTCCACCATGAGCCAGTACT CCGCTCCACCGGTCCATGCTGAAGCGGAGAGATAGCAC CTACGGCCCCCTGCAGACACCTGTGGGATGTGTGCTGGGC CTCGTGAACAGCTCCCTGTTGTGGAAGATTGCAAGCTGC CCCTGGGCCAGAGCCTGTGTGCCCTGCCAGATACCCCTAG CACCCTGACCCCTAGAAGCGTGCCTCTGTGCCCGGGCAA ATGCGGCTGGCCTCTATCGCCTTCAATCACCCATCCAGGT GGACCACTGAACCTCAGCTACTTCAAGCTGAGCATCCCC ACCAACTTCAGCTTCGGCGTGACCCAGGAGTACATCCAGA CCACAATCCAGAAAGTGACCGTGGACTGCAAGCAGTACGT GTGCAACGGCTTTCAGAAGTGCGAACAGCTGCTGCGCGAG TACGGCCAGTTCTGCAGCAAGATCAACCAAGGCCCCGACG GCGCCAACCTGAGACAGGATGACAGCGTGCGGAACCTGTT CGCCAGCGTGAAAAGCAGCAGTCCAGCCCCATCATCCCT GGCTTCGGCGGCGACTTTAACCTGACCCCTGCTGGAACCTG TGTCCATCAGCACCGGCTCCAGAAGCGCCAGATCCGCCAT CGAGGACCTGTGTTGACAAAGTGACCATTGCCGACCCC GGCTACATGCAGGGCTACGACGATTGCATGCAGCAGGGCC CAGCCAGCGCCAGGGATCTGATCTGTGCCAGTATGTGGC CGGCTACAAGGTGCTGCCCCCTGATGGACGTGAACATG GAAGCCGCTACACCTCCAGCTGCTGGGCTCTATTGCTG GCGTGGGATGGACAGCCGCGCTGTCTAGCTTTGCGGCCAT CCCTTTGCGCCAGAGCATCTTCTACCGGCTGAACGGCGTG GGCATCACACAACAGGTGCTGAGCGAGAACCAGAAGCTG ATCGCCAACAAGTTTAAACAGGCACTGGGCGCATGCAGA CCGGCTTCACCAACCAACGAGGCTTTCAGAAAGGTGCA GGACGCCGTGAACAACAACGCCAGGCTCTGAGCAAGCT GGCTTCGAGCTGAGCAATACCTTCGGCGCATCAGCGCC TCCATCGGCGACATCATCCAGCGGTGGACGTGCTGGAAC	

TABLE 10-continued

Betacoronavirus Nucleic Acid Sequence		
Strain	Nucleic Acid Sequence	SEQ ID NO:
	AGGACGCCCAGATCGACGGCTGATCAACGGCAGACTGA CCACCCTGAACGCTTCGTGGCACAGCAGCTCGTGCGGAG CGAATCTGCCGCTCTGTCTGCTCAGCTGGCCAAGGACAAA GTGAACGAGTGCCTGAAGGCCAGTCCAAGCGGAGCGGC TTTTGTGGCCAGGGCACCACATCGTGTCTTCGTCTGTGAA TGCCCCAACGGCCTGTACTTTATGCACGTGGCTATTACC CCAGCAACACATCGAGGTGGTGTCCGCCTATGGCCTGTG CGACGCGCCAATCCTACCAACTGTATCGCCCCCGTGAAC GGCTACTTTCATCAAGACCAACACACCCGGATCGTGGACG AGTGGTCTTACACAGGCAGCAGCTTCTACGCCCCGAGCC CATCACCTCCCTGAACACCAATACGTGGCCCCCAAGTG ACATACCAGAACATCTCCACCAACCTGCCCCCTCCACTGC TGGGAAATTCCACCGGCATCGACTTCCAGGACGAGCTGGA CGAGTTCTTCAAGACGTGTCCACCTCCATCCCCAACTTCG GCAGCCTGACCAGATCAACACCACTCTGCTGGACCTGAC CTACGAGATGCTGTCCCTGCAACAGGTCTGAAAGCCCTG AACGAGAGCTACATCGACCTGAAAGAGCTGGGGAACCTAC ACCTACTACAACAAGTGGCCTTGGTACATTTGGCTGGGCT TTATCGCCGGCTGGTGGCCCTGGCCCTGTGCGTGTCTTC ATCCTGTGCTGCACCGGCTGCGGACCAATTGCATGGGCA AGCTGAAATGCAACCGGTGCTGCGACAGATACGAGGAAT ACGACCTGGAACCTCACAAGTGCATGTGCAC	
Betacoronavirus mRNA Sequences		
gb KJ156934.1 : 21405-25466 Middle East respiratory syndrome coronavirus isolate Riyadh_14_2013, spike protein (nucleotide)	AUGAUACACUCAGUGUUUCUACUGAUGUUCUUGUUAAC ACCUACAGAAAGUUAUGUAGUGAGGGCCAGAUUCUG UUAAGUCUGCUUGUAUUGAGGUUGAUUAACAACAGACC UUCUUUGAUAAAACUUGGCCUAGGCCAAUUGAUGUUUC UAAGCGUGACGGUAUUUAUUAUCCCUAAGGCCGUACAU AUUCUAACUAACUACUUAUUAAGGUCUUUUUCCCU AUCAGGGAGACCAUGGUGUAUUGUAGUUUACUCUGCA GGACAUGCUCAGGCACAACUCCACAAAAGUUGUUUGU AGCUAAUAUUCUCAGGACGUAACAGUUUGCUAAUG GGUUUGUCGUCGUAUAGGAGCAGUCGCAAUUCCACUG GCACUGUUUAUUAUAGCCCAUCUACAGCGCUACUAUAC GAAAAAUUUAACCCUGCUUUUAUGCUGGGUUCUUCAGUU GGUAUUUUUCAGAUUGUAUUAUGGCCGCUUCUUCAA UCAUACUCUAGUUCUUUUGCCGAUGGAUGUGGCACUU UACUAGAGCUUUUAUUGUAUUCUAGAGCCUCGCUUCU GGAAAUCAUUGCCUGCUGGCAAUUCUUAUACUUCUU UGCCACUUAUCACACUCCUGCAACAGAUUGUUUGAUGG CAAUUAACUAGUAAUGCCAGUCUAGAACUUUUUAAGG AGUAUUUUAAUUUACGUAACUGCACCUUAUGUACACU UAUAACAUUACCGAAGAUAGAUUUUAGAGUGGUUUGG CAUUAACAAAACUGCUAAGGUGUACCCUUCUUCUACU UCGUAUUGUUAUUUGUACGGCGGCAAUAGUUUCAAU UUGCCACCUUGCCUGUUUAUGAUACUAUUAAGUAUUAU UCUAUCAUUCUACAGUAUUCGUUCUAUCCAAAGUGAU AGAAAAGCUUGGGCUGCCUUCUACGUAUAUAAACUUCA ACCGUUAACUUCUUGGUUGGAUUUUUCUGUUGAUGGUU AUUAACGCAGACUAUAGACUGUGUUUUAAUGAUUUG UCACAAUCUCCACUGCUCAUAGAAUCCUUCGAUGUUGAA UCUGGAGUUUAUUCAGUUUCGUCUUUCGAAGCAAAACC UUCUGGCUAGUUGGGAACAGGCUAGAGGUUGUAU GUGAUUUUUACCUUCUUCUGUCUGGCACACUCCUCAGG UUUAUAUUUUAAGCGUUUGUUUUUACCAAUUGCAAU UAUAAUCUUACCAAUUGCUUUCACUUUUUUUCUGUGAA UGAUUUUAUUUGUAGUCAAUUAUCCAGCAGCAUUG CUAGCAACUGUUAUUCUACUGAUUUUUGGAUUAUUUU UCAUACCCACUUAGUAUGAAUCCGAUCACAGUUGUAG UUCUGCUGGUCAAUAUCCAGUUUAUUUAUAAACAGU CCUUUUUAUAAUCCCAUGUUUGAUUUUAGCGACUGUUC CUCAUAACCUUAUCUAUUUAAGCCUUCUUAAGUACA GCUAUAUUAAAGUGCUUCUGCUUCUUUUUGAUGAU CGUACUGAAGUACCUAGUUAUGAAGCUAAUCAAUA CUCACCCUGUGUAUCCAUUGUCCAUCCACUGUGUGGGA AGACGGUGAUUAUUUAGGAAACAAUUCUCCACUUG AAGGUGGUGGUGGCUUGUUGCUAGUGGCUCAACUGUU GCCAUGACUGAGCAAUUAAGAUUGGCUUUGUUAUUAC AGUUCAAUAGGUACAGACACCAAUAGUUUGGCCCA AGCUUGAAUUUGCUAUGACAAAUAUUGCCUUCUCAA	65

TABLE 10-continued

Betacoronavirus Nucleic Acid Sequence		
Strain	Nucleic Acid Sequence	SEQ ID NO:
MERS S FL SPIKE 2cEMC/2012 (XBai change(U to G)) (nucleotide)	UUAGGCAAUUGCGUGGAAUUAUCCCUUAUGGUGUUUC GGGCCGUGGUGUUUUUCAGAAUUGCACAGCUGUAGGUG UUCGACAGCAGCGCUUUGUUUAUGAUGCGUACCAGAAU UUAGUUGGCUAUUAUUCUGAUGAUGGCAACUACUACUG UCUGCGUGCUUGUGUUAGUUGUCUGUUUCUGUCAUCU AUGAUAAAGAAACUAAAACCCACGCUACUCUAUUUGGU AGUGUUGCAUGUGAACACAUUUCUUCUACCAUGUCUCA AUACUCCCGUUCUACGCGAUCAAUGCUUAAACGGCGAGA UUCUACAUAUGCCCCCUUCAGACACCGUUGGUUGUGU CCUAGGACUUGUUAUUCUUCUUGUUCGUAGAGGACU GCAAGUUGCCUCUCGGUCAUUCUCUGUGUCUUCUCUG ACACACCUAGUACUCUCACACUCUCGAGUGUGCGUCUG UGCCAGGUGAAUGCGCUUGGCAUCCAUUGCUUUUAU CAUCCAUUCAGGUUGAUCACUUAUAUAGUAGUUUUU UAAAUUAAGUAUACCCACUAAUUUUCCUUUGGUGUGA CUCAGGAGUACAUCAGACAACCAUUCAGAAAGUUAUCU GUUGAUUGUAAACAGUACGUUUGCAAUGGUUUCAGAA GUGUGAGCAAUACUGCGCGAGUAUGGCCAGUUUUGUU CCAAUAUAAACAGGCUCUCCAUGGUGCCAAUUUACGCC AGGAUGAUUCUGUACGUAAUUUGUUUGCGAGCGUGAAA AGCUCUCAUACUUCUUAUCUACACAGGUUUUGAGGU GACUUUAUUUGACACUUCUAGAACCUGUUUCUAUAUC UACUGGCAGUCGUAGUGCACGUAGUGCUAUUGAGGAUU UGCUAUUUGACAAAGUCACUAUAGCUGAUUCUGGUUAU AUGCAAGGUUACGAUGAUUGUAUGCAGCAAGGUCAGC AUCAGCUCGUAUCUUAUUUGUGCUCAAUAUGUGGCU GUUAUAAAGUAUUAUACUCCUUAUGGAUGUUAUAUG GAAGCCGCGUAUACUUAUCUUGCUUGGCAGCAUAGCA GGUGUUUGGCUAGCUGGCUUAUCCUCCUUUGCUGCU AUUCCAUUUGCACAGAUUUAUUUAUAGGUUAAACGG UGUUGGCAUUAUACAAACAGGUUCUUUCAGAGAACCAAA AGCUUAUUGC CAAUAAGUUUAUACAGGCUCUGGGAGCU AUGCAAACAGGCUCACUAACAUAUGAAGCUUUUCG GAAGGUUCAGGAUGCUGUGAACAAUUGCAGAGGCUC UAUCCAAUUAGCUAGCGAGCUAUCUAAUAUUUUGGU GCUAUUUCCGCCUUAUUGGAGACUACUACAACGUCUU GAUGUUUCGAAACAGGACGCCCAAUAGACAGACUUUA UAAUGGCCGUUUGACAAACUAAUAGCUUUUUGUUGCAC AGCAGCUUGUUCGUUCCGAUACAGCUGCUCUUUCCGCU AAUUGGCUAAAGAUAAAGUCAAUAGAGUGUCAAGGCA CAAUCCAAGCGUUCUGGAUUUUGCGGUCAGGCAACAU AUAGUGUCUUUUGUUGAAUUGCCCUAAUUGGCCUUUA CUUAUGCAUGUUGGUUAUUAUCCUAGCAACCAUAUUG AGGUUGUUUCUGCUUAUGGUCUUUGCGAUGCAGCUAAC CCUACUAAUUGUAUAGCCCUUGUAAUGGCUACUUUAU UAAAACUAAUAACACUAGGAUUGUUGAUGAGUGGUCU AUACUGGCUCGUCUUAUGCACCUGAGCCCAUACCU CUCUUAUACUAAUAGUUGUACACAGGUGACAUACC AAAACAUUUCUACUAAACUCCUCCUCCUUCUUGCGCA AUUCCACCGGAUUGACUUC CAGAUGAUUGGAUGAG UUUUUCAAAAUUGUAGCACCAGUAUACCUAAUUUUGG UUCUCUAAACAGAUUAUACUACUUAUCUGAUUUUAC CUACGAGAUUGUUCUUCUACAAGUUUUUAAAGCCC UUAUUGAGUCUUACAUAAGCCUUAAGAGCUUGGCAAU UAUACUUAUUAACAACAAUUGGCCGUGGUACAUUUGGCU UGGUUUCAUUGCUGGGCUUGUUGCCUAGCUCUAUGCG UCUCUUCUAUCUGUGCUGCUCUGUUGUGGCACAAACU GUAUGGGAAAAUUAAGUGUAAUUGUUGUGAUAAGA UACGAGGAUACGACCUAGAGCCGAUAAGGUUACUAGU UCACUAA	66
	AUGAUACACUCAGUGUUUCUACUGAUGUUCUUGUUAAC ACCUACAGAAAGUUAUGUAGUAGGCGCAGAUUCUG UUAAGUCUGCUUGUAUUGAGGUUGAUUAACAACAGACU UUCUUUGAUAAACUUGGCCUAGGCCAAUUGAUGUUUC UAAGGCUAGCGGUUAUUAUACCCUAAAGGCCGUACAU AUUCUAAACUAACUACUUAUACAAGGUCUUUUUCCCU AUCAGGAGACCAUGGUGUAUGUAUGUUUACUCUGCA GGACAUUCUACAGGCACACUCCACAAAAGUUUUUGU AGCUAAAUUUCUAGGACGUCAAACAGUUUGCUAAUG GGUUUGUCGUCGUUAAGGAGCAGCUGCCAAUUCACUG GCACUGUUUAUUAAGCCCAUUCACAGCGCUACUUAUC	

TABLE 10-continued

Betacoronavirus Nucleic Acid Sequence		
Strain	Nucleic Acid Sequence	SEQ ID NO:
	GAAAAUUUACCCUGCUUUUAUGCUGGGUUCUUCAGUU GGUAUUUUCAGAUUGGUAUAAUUGGCCGCUUCUCAA UCAUACUCUAGUUCUUUUGCCGAUGGAUGGGCACUU UACUUAGAGCUUUUUUAUUGUAUUCUGGAGCCUCGCUCU GGAAAUCAUUGCCUGCUGGCAAUUCCUAUACUUCUUU UGCCACUUAUCACACUCCUGCAACAGAUUGUUCUGAUGG CAAUUAACAUCGUAUUGCCAGUCUGAACUUCUUUAAGG AGUAUUUUAAUUUACGUAACUGCACCUUUUAUGUACACU UAUAACAUAUACCGAAGAUAGAUUUUAGAGUGGUUUUG CAUUAACACAAACUGCUCAGGUGUUCACCUUCUCAUC UCGUAUUGUUAUUUACGGCGGCAUAUUGUUCAAU UUGCCACCUUGCCUGUUUAUGAUACUAUUAAGUAUUAU UCUAUCAUUCUCACAGUAUUUGUUCUAUCCAAAGUGAU AGAAAGCUUUGGGCUGCCUUCUACGUAUAUAAACUUCA ACCGUUAACUUUCCUGUUGGAUUUUUCUGUUGAUGGUU AUAUACGCAGAGCUAUGAGCUGUGGUUUUAUUGAUUUU UCACAAUCCACUGCUCUAUAGAAUCCUUCGAGUUGGAA UCUGGAGUUUAUUCAGUUUCGUCUUUCGAGCAAAACC UUCUGGCUCAGUUGGGAACAGGCUGAAGGUUGUAAU GUGAUUUUUCACCUUCUUCUGUCUGGCACACUCCUCAGG UUUUAUAUUUCAAAGCUUUUGUUUUUACCAAUUGCAAU UAUAUUCUUAACCAAUUGCUUCACUUUUUUCUGUGAA UGAUUUUACUUGUAGUCAAAUAUCCACAGCAAAUUG CUAGCAACUGUUAUUCUACUGAUUUUUGGAUUACUUU UCAUACCCACUUAUGUAUGAAUCCGAUCUCAGUUGUAG UUCUGCUGGUCCAAUAUCCAGUUUAUUAUAAACAGU CCUUUUCAAUCCCAUGUUUGAUUUUAGCGACUGUUC CUCAUAACCUUACUACUAUUAUAGCCUUCUUAAGUACA GCUAUAUUAACAAGUCUUCUGUUCUUUUUUGAUGAU CGUACUGAAGUACCUAGUUAUGAAGCUAAUCAAUA CUCACCCUGUGUAUCCAUGUCCAUCCACUGUGUGGGA AGACGGUGAUUAUUAUAGGAAACAACUUCUCCACUUG AAGGUGGUGGCGUGCUUGUUGCUAGUGGCUCAACUGUU GCCAUGACUGAGCAAUACAGAUUGGCUUUGGUUUUAC AGUUCAAUAUGGUACAGACACCAAUAGUUUUGCCCA AGCUUGAAUUUGCUAAGACACAAAUUUGCCUUCUAA UUAGGCAAUUGCGUGGAUAUUCUUAUGGUGUUUC GGGCCGUGGUGUUUUUACAGAAUUGCACAGCUGUAGGUG UUCGACAGCAGCGCUUUUUUAUGAUGCGUACCAAGAU UUAGUUGGCUAUAUUUCUGAUGAUGGCAACUACUACUG UUUGCGUGCUUGUUGUAGUUCUUGUUUCUGUCAUCU AUGAUAAAGAAACUAAACCCACGCUACUUAUUUGGU AGUGUUGCAUGUGAACACAUUUCUUAACCAUGUCUCA AUACUCCCGUUCUACGCGAUCAAUGCUUAAACGGCGAGA UUCUACAUAUGGCCCUUCAGACACCUUGUUGGUUGUGU CCUAGGACUUGUUAUUCCUUCUUGUUCGUAGAGGACU GCAAUUGCCUUCUUGGUCAAUCUUCUGUGUCUUCUUG ACACACCUAGUACUCUACACCUCCAGUGUGCGUCUCUG UUCAGGUGAAUUGCGCUUGGCAUCCAUUGCUUUUAU CAUCCUAUUCAGGUUGAUCAACUUAUAUAGUUAUUU UAAAUUAAGUAUACCCACUAUUUUUCCUUUGGUGUGA CUCAGGAGUACAUAUCAGACAACCAUUCAGAAAGUUAU GUUGAUUGUAAACAGUACGUUUGCAAUGGUUUCCAGAA GUGUGAGCAAUUACUGCGCAGUAUGGCCAGUUUUUGU CCAAAUUAACACAGGCUCUCCAUUGGUGCCAAUUUACGCC AGGAUGAUUCUGUACGUAUUUUGUUUGCAGCGUGAUA AGCUUCUAAUACUUCUUAUACUACAGGUUUUGGAGGU GACUUUAUUUGACACUUCUGGAACUGUUUCUAUAUC UACUGGCAUUCGUAGUGCACGUAUGCUAUUGAGGAUU UGCUAUUUGACAAAGUACUAUAGCUGAUCCUGGUUAU AUGCAAGGUUACGAUAUUGCAUGCAGCAAGGUCAGC AUCAGCUCUGAUUCUUAUUUGGCUCAAUAUGGCGUG GUUAACAAAGUAUACCUCCUUAUUGGAUGUUAAUUG GAAGCCGCGUAUAUCUUAUCUUGCUUGGCAGCAUAGCA GGUGUUUGGUGGACUGCUGGCUUAUCCUCCUUUGCUGCU AUUCCAUUUGCACAGAGUAUCUUUAUAGGUUAACGG UGUUGGCAUUAUCUAAACAGGUUCUUUCAGAGAACCAA AGCUUAUUUGCAAUAAGUUUAUACAGGCUUCGGGAGCU AUGCAAACAGGCUUCACUACAACUAAUGAAGCUUUUCA GAAGGUUCAGGAUGCUGUAGAACAAUUGCAGAGGCUC UAUCCAAUAUAGCUAGCGAGCUAUCUAUAUUAUUUGU GCUAUUUCCGCCUCUAUUGGAGACAUAUACACAGUCUU	

TABLE 10-continued

Betacoronavirus Nucleic Acid Sequence		
Strain	Nucleic Acid Sequence	SEQ ID NO:
	GAUGUUCUCGAACAGGACGCCCCAAUAGACAGACUUAU UAAUGGCCGUGUUGACACACUAAUUGCUUUUGUUGCAC AGCAGCUUGUUCGUUCCGAUAGCUGUCUUCUCCGUC AAUUGGCUAAAGAUAAAGUCAUAGAGUGUGUCAAGGCA CAAUCCAGCGUUCUGGAUUUUGCGGUCAGGACACAU AUAGUGUCUUGUUGUAUAGCCCUAAUGGCCUUUA CUUCAUGCAUGUUGGUUAUACCUAGCAACACAUUGA GGUUGUUUCUGCUUAUGGUUUUGCGAUGCAGCUAAC CUACUAAUUGUAUAGCCCCUGUUAAUGGCUACUUUAU AAAACUAAUACACUAGGAUUUGUAGUAGUGGUCAUA UACUGGCUUGUCUUUAUGCACCUGAGCCAUUACCU CCUUAUAUCUAAGUAUGUUGCACCAGGUGACAUAACA AAACAUUUUCUACUAAACUCCUCCUCCUUCUCCGCAA UCCACCGGGAUUGACUUCACAGAUAGUUGGAUGAGU UUUUCAAAAGUUGUAGCACCAGUAUACCUAAUUUUGGU UCCCUAACACAGAUUAUACUACUUAUCGACUUCUAC UACGAGAUUGUUCUUCUACAGUUGUUAAGCCCU UAAUGAGUCUUAACUAGACCUUAAAGAGCUUGGCAU AUACUUUAUACAAACAAUGGCCGUGGUACAUUUGGCU GGUUUCAUUGCUGGGCUUGUUGCUUAGCUUAUGCGU CUUCUUAUACUGUGCUGCACUGGUUGGCAAAACUG UAUGGGAACCUAAGUGUAAUCGUUGUUGAUAGAU ACGAGGAUACGACCUAGCCGCAUAGGUUCAUGUUC ACUAA	
Novel_MERS_S2_subunit_trimeric vaccine (nucleotide)	AUGAUCCACUCCGUGUCCUCCUUAUGUCCUGUUGACC CCACUGAGUCAGACUGCAAGCUCCCGUGGGACAGUCC CUGUGUGCGCUGCCUGACACUCCUAGCACUCUGACCCCA CGCUCGUGCGGUGCGGUGCCUGGCGAAUUGCGGUGGCC UCCAUCCGCUUCAAUACCCAAUCCAGUGGAUACGUG AAUAGCUCGUUUUUAAGCUGUCCAUCCACGAACUUC UCGUUCGGGUCACCCAGGAGUACUCCAGACCAAAU CAGAAGGUCACCGUCGAUUGCAAGCAUACGUGGCAAC GGCUUCCAGAGUGCGAGCAGCUGCUGAGAGAAUACGG GCAGUUUUGCAGCAAGAUCAACAGCGCUGCAUGGAGC UAAUUGCGCCAGGACGACUCCGUGCGCAACCUUUUGC CUCUGUAGUACAUCACAGUCCUCCCAAUACUCCGGG AUUCGGAGGGGACUUAACCUAGACCUCUGGAGCCCGU GUCGAUCAGCACCGUAGCAGAUCCGCGCGCUCAGCCAU UGAAGAUCUUUGUUCGACAAGGUCACCAUCGCCGAUCC GGGCUACAUGCAGGGAUACGACGACUGUAUGCAGCAGG GACCAGCCUCCGCGAGGGACCUCAUCUGCGCGCAUACG UGGCCGGGUACAAAGUGCUGCCUCCUUGAUGGAUGUG AACAUGGAGGCGCUUAUACUUCGUCCUGCUGGCUUCU AUCGCCGGCGUGGGUGGACCGCGCCUGUCUCCUUC GCCGCUAUCCCUUUUGCAUUAUCCAUUUUUAACGGGCU AACGGCGUGGGCAUUAUACAAAGUCCUGUCGGAGAAC CAGAAGUUGAUCGCAAAACAAGUUAUACAGGCCUUGG GGCCAUGCAGACUGGAUUCACUACGACUAAACGAAGCGU CCAGAAGGUCCAGGACGCUUGAACAACAACGCCCAGGC GCUUCAAGCUGGCCUCCGAACUAGCAACACCUUCGG AGCCAUCAGCGCAUCGAUCGUGACAUAAUUCAGCGGCU GGACGUGCUGGAGCAGGACGCCAGAUACGCCGCUCAU CAACGGACGGCUGACCAUUGAAUGCCUUCGUGGCACA ACAGCUGGUCCGGAGCGAAUACGCGGACUUCUCCGCCA ACUCGCCAAGGACAAAGUCAAGAAUGCGUGAAGGCCCA GUCCAAGAGGUCGGUUUCUGCGUCAAGGAACCAUAU UGUGUCCUUCGUGCGUAACGCGCCAAACGGUCUGUACU UAUGCAGUCGGCUACUACCCGAGCAAUCAUACGAAGU GGUGUCCGCCUACGGCCUGUGCGAUGCCGCUAACCCAC UAACUGUAUUGCCCCUGUAAACGGAUUAUUUAAGA CCAACAACACCCGCAUUGUGGACGAAUGGUCAUACCCG GUUCGUCCUUCACGCGCCGAGCCCAUACUUCACUGA ACACCAAUAACGUGGCUCCGCAAGUGACCUACGAGAAC UCUCCACCAAUUUGCCGCGCGCGUGUCGGAACAGCA CCGGAUUGAUUUCCAAGAUAAUGGACGAUUAUUCU AAGAACGUGUCCAUUCCAUUCCAAUUCGGAAGCCUG ACACAGAUCAACACCAUCCUUCGACCUAGACCUACGAG AUGCUGAGCCUUAACAAGUGGUCAAGGCCUGAACGAG	67

TABLE 10-continued

Betacoronavirus Nucleic Acid Sequence		
Strain	Nucleic Acid Sequence	SEQ ID NO:
MERS_S0_Full-length Spike protein (nucleotide, codon optimized)	AGCUACAUCGACCUGAAGGAGCUGGGCAACUAUACCUAC UACAACAAGUGGCCGGACAAGAUUGAGGAGAUUCUGUC GAAAUCUACCAUUGAAAACGAGAUCGCCAGAAUCA AGAAGCUUAUCGGCGAAGCC	68
	AUGGAAACCCUGCCAGCUGUGUCCUGCUGCUGCUG UGGCUGCCUGAUACACCGGCAGCUAUGUGGACGUGGGC CCCGAUAGCGUGAAGUCCGCCUGUAUCGAAGUGGACAUC CAGCAGACCUUUUCGACAAGACCUGGCCAGACCCAUUC GACGUGUCCAGGCGCGAGCAUCUUAUCCACAAGGC CGGACCUACAGCAACAUCACCAUUAUCCAGGGCCUG UUCCCAUAUCAAGGCGACCACGGCGAUUUGUACGUGUAC UCUGCCGGCCACGCCACCGGCACACCCAGAAAACUG UUCGUGGCCAACUACAGCCAGGACGUGAAGCAGUUCGCC AACGGCUUCGUCGUGCGGAUUGGCCCGCUGCCAUAAGC ACCGGCACAGUGAUCUAGCCCGCAGCACCAGCGCCACC AUCCGGAAGAUUACCCGCCUUAUGCUGGGCAGCUCC GUGGGCAAUUUCAGCGACGGCAAGUUGGGCCGGUUCUU CAACCACACCCUGGUGCUGCUGCCGAUGGCGUGGGCAC ACUGCUGAGAGCCUUCUACUGCAUCCUGGAACCCAGAAG CGGCACCAUGCCCGGCCGCAUAGCUACACCGCUU CGCCACCUACACACACCCGCCACCGAUUUGCUGGACGG CAACUACAACCGGAACGCCAGCCUGAACAGCUUCAAAGA GUACUUAACUGCGGAACUGACCUUUAUGUACACCUA CAAUUAUACCCGAGGACGAGAUCCUGGAUUGGUUCGGCA UCACCCAGACCGCCAGGGCGUGCACCUUUCAGCAGCA GAUACGUGGACUGUACGGCGGCAACAUUUCAGUUU GCCACCCUGCCCGUGUACGACACCAUCAAGUACUACGC AUCAUCCCCACAGCAUCCGGUCCAUCCAGAGCGACAGA AAAGCCUGGGCCGCCUUCUACUGUACAAAGCUGCAGCCC CUGACCUUCCUGCUGGACUUCAGCGUGGACGGCUACUUC AGACGGGCCAUUCGACUGCGGCUUCAAACGACUGAGCCAG CUGCACUGCUCCUACGAGAGCUUCGACGUGGAAAGCGGC GUGUACAGCGUGCCAGCUUCGAGGCCAAGCCUAGCGGC AGCGUGGUGGAACAGGCUAGAGGGCGUGGAUUGCGACUU CAGCCCUUCUGCUGAGCGGCACCCUCCCCAGGUGUACAA CUUCAAGCGCGUGGUGUACCAACUGCAAUUAACAACCU GACCAAGCUGCUGAGCCUGUUCUCCGUGAACGACUUCAC CUGUAGCCAGAUCAGCCUGCCGCCAUUGCCAGCAACUG CUACAGCAGCCUGAUCCUGGACUACUUCAGCUACCCCU GAGCAUGAAGUCCGAUUCGAGCGUGUCCUCCGCCGGACC CAUCAGCCAGUUAACUACAAGCAGAGCUUCAGCAACCC UACCUGCCUGAUUUGGCCACCGUGCCCAAAUCUGAC CACCACUACCAAGCCCUUAGAGUACAGCUACUACAACAA GUGCAGCAGACUGCUGUCCGACGACCGGACCGAAGUGCC CCAGCUCUGAAGCGCAACAGUACAGCCCGCUGCGUGUC CAUCGUGCCAGCACCGUGUGGAGGACGGCGACUACUA CAGAAAGCAGCUGAGCCCCUGGAAGGCGGCGGAUGGCU GGUGGCUUCUGGAAGCACAGUGGCCAUGACCGAGCAGCU GCAGAUUGGCUUUGGCAUACCGUGCAGUACGGCACCGA CACCACAGCGUGUGCCCAAGCUGGAUUCGCCAAUGA CACCAGAUCCGCCAGCCAGCUGGGAAACUGCGUGGAUA CUCCCUUAUGGCGUGUCCGGACGGGGCGUGUUCAGAA UUGCACAGCAGUGGGAGUGCGGCAGCAGAGAUUCGUGU ACGAUGCCUACCAAGACCUUGUGGGCUACUACAGCGAGC ACGGCAAUUAUACUGCCUGCGGGCCUGUGUUCGUGC CCGUGUCCGUGAUCUACGACAAAGAGACAAGACCCACG CCACACUGUUCGGUCCUGGGCCUGCGAGCAUACAGCU CCACCAUGAGCCAGUACUCCCGUCCACCCGGUCCAUUC UGAAGCGGAGAGAUAGCACUACGGCCCCUGCAGACAC CUGUGGGAUGUGUGUGGGCCUUGGAACAGCUCCUGU UUGUGGAAGAUGCAAGCUGCCCGGGCCAGAGCCUGU GUGCCUGCCAGAUACCCUAGCACCCUGACCCUAGAA GCGUGCGCUCUGUGCCCGGCGAAUGCGGCGUGGCCUUA UCGCCUUAUACACCCAUCCAGGUGGACAGCUGAACU CCAGCUACUUAAGCUGAGCAUCCACCAACUUCAGCU UCGGCGUGACCCAGGAGUACAUCAGACCAAAUCCAGA AAGUGACCGUGGACUGCAAGCAGUACGUGGCAACGGC UUUCAGAGUGCGAACAGCUGCUGCGGAGUACGGCCAG UUCUGCAGCAAGAUAACAGGCCUUGCACGGCGCCAAC CUGAGACAGGAUGACAGCGUGCGGAACCUUUCGCCAGC GUGAAAAGCAGCCAGUCCAGCCCCAUCAUCCUGGCUUC	

TABLE 10-continued

Betacoronavirus Nucleic Acid Sequence		
Strain	Nucleic Acid Sequence	SEQ ID NO:
	GGCGGCGACUUUAACCGACCCUGCUGGAACCGUGUCC AUCAGCACCGGCUCCAGAAGCGCCAGAUCCGCCAUCGAG GACCUGCUGUUCGACAAGGUGACCAUUGCCGACCCCGGC UACAUGCAGGGCUACGACGAUUGCAUGCAGAGGGCCCA GCCAGCGCCAGGGAUCUGAUCUGUGCCAGUAUGUGGCC GGCUACAAGGUGCUGCCCCCUGAUGGACGUGAACAU GAAGCCGCCUACACCCAGCCUGCUGGGCUCUAUUGCU GGCGUGGGAUGGACAGCCGGCCUGUCUAGCUUUGCCGCC AUCCCUUUCGCCCAGAGCAUCUUAACCGGCUGAACGGC GUGGGCAUCACACAACAGGUGCUGAGCGAGAACAGAA GCUGAUCGCCAACAGUUUAACAGGCACUGGGCGCCAU GCAGACCGGCUUACACCCACCAACGAGGCCUUCAGAAA GGUGCAGGACGCCGUGAACCAACGCCCCAGGCUCUGAG CAAGCUGGCCUCCGAGCUGAGCAUACCUUCGGCGCCAU CAGCGCCUCCAUCCGCGCAUCAUCCAGCGCUGGACGU GCUGGAACAGGACGCCAGAUCCAGCGCUGAUCAACGG CAGACUGACCACCCUGAACGCCUUCGUGGCACAGCAGCU CGUGCGGAGCGAAUCUGCCGUCUGUCUGCUCAGCUGGC CAAGGACAAAGUGAACGAGUGCGUGAAGGCCCAGUCCA AGCGGAGCGCCUUUUGUGGCCAGGGCACCCAUUCGUGU CCUUCGUCUGAAUGCCCCAACGGCCUGUACUUUAUGC ACGUGGGCUAUUACCCAGCAACCAUCGAGGUGGUGU CCGCCUAUGGCCUGUGCGACGCCGCCAAUCCUACCAACU GUUACGCCCCCGUGAACGGCUACUUAUCAAAGACCAACA ACACCCGGAUCGUGGACGAGUGGUCUACACAGGCAGCA GCUUCUACGCCCCCGAGCCAUACCUCCUGAACACCA AAUACGUGGCCCCCAAGUGACAUACAGAACAUCCCA CCAACCGUCCCCCUCACUGCUGGGAUUAUCCACCGGCA UCGACUUCGAGGACGAGCUGGACGAGUUCUUAAGAAGC UGUCCACCUCUACUCCCCAACUUCGGCAGCCUGACCCAGA UCAACACCACUCUGCUGGACCGUACGAGAUUGCUGU CCUGCAACAGGUCUGAAAGCCUGAACGAGAGCUACA UCGACCGUAAAGAGCUGGGGAACUACACCUACUACAACA AGUGGCCUUGGUACAUUUGGCUGGGCUUUAUCGCCGCC UGGUGGCCUGGCCUGUGCGUGUUCUUAUCCUGUGCU GCACCGGCUUGCGCACCAAUUGCAUGGGCAAGCUGAAAU GCAACCGGUGCUGGACAGAUACGAGAAUACGACCUGG AACCUCACAAAGUGCAUGGAC	

TABLE 11

Betacoronavirus Amino Acid Sequences		
Strain	Amino Acid Sequence	SEQ ID NO:
gb KJ156934.1 : 21405-25466 Middle East respiratory syndrome coronavirus isolate Riyadh_14_2013, spike protein (amino acid)	MIHSVFLLMFLLTPTESYVDVGPDSVKSACIEVDIQQTFFDKT WPRPIDVSKADGIIYPQGRYSNITITYQGLFPYQGDHGDY VYSAGHATGTTpQKLFVANYSDVKQFANGFVVRIGAAANS TGTVIIISPSTSATIRKIYPAPMLGSSVGNFSDGKMGRFFNHTL VLLPDGCGTLRLAFYCILEPRSGNHCPAGNSYTSFATYHTPA TDCSDGNYNRNASLNSFKEYFNLRNCTFMYTYNITEDEILEW FGITQTAQGVHLFSSRYVDLYGNNMFQFATLPVYDTIKYYSII PHSIRSIQSDRKAAAFVYVKLQPLTFLDLSVDGYIRRAIDC GFNDLSQLHCSYESFDVESGVYSVSFEAKPSGVSVEQAEGV ECDPSPLLSGTPPQVYNFKRLVFTNCYNLTKLKLSLVNDFC CSQISPAIASNCYSSLILDYFSYPLSMKSDLSVSSAGPISQFN YKQSFNPTCLILATVPHNLTTITKPLKYSYINKSRLSDDR EVPQLVNAQYSPCVSIVPSTVWEDGDYRKQLSPLEGGW LVASGLTVAMTEQLQMGFGITVQYGTDTNSVCPKLEFANDT KIASQLGNVCVEYSLYGVSGRGVFQNTAVGVRQQRFFVDA YQNLVGYSDDGNYCLRACVSPVSVIYDKETKTHATLFG SVACEHISSTMSQYRSRSTRMLKRRDSTYGPLQTPVGCVLGL VNSSLFVEDCKLPLGQSLCALPDTPTSTLTPRSVRVSPGEMRLA SIAFNHPIQVDQLNSSYFKLSIPTNFSFGVTQEYIQTIIQKVT DCKQYVCNGFQKCEQLLREYGFQCSKINQALHGANLRQDDS VRNLFASVKSSQSSPIIPGFGDFNLTLLEPVSIISTGSRARS EDLLFDKVTIADPGYMQYDDCMQGGPASARDLIQAQYVA GYKVLPLMDVNMEAAAYTSSLGSIAGVGWTAGLSSFAAIPF	24

TABLE 11-continued

Betacoronavirus Amino Acid Sequences		
Strain	Amino Acid Sequence	SEQ ID NO:
	<p>AQSIFYRLNGVGITQQVLSNQKLIANKFNQALGAMQTGFTT TNEAFKQVQDAVNNNAQALSKLASELSNTFGAISASIGDIIQR LDVLEQDAQIDRLINGRLTTLNAFVAQQLVRSESAALSAQLA KDKVNECVKAQSKRSGFCGQGTHIVSFVFNAPNGLYFMHV GYPPSNHIEVVSAYGLCDAANPTNCIAPVNGYFIKTNNTRIV DEWSTGSSFFYAPEPITSLNTKYVAPQVTYQNI STNLPPPLLG NSTGIDFQDELDEFFKNVSTSI PNFGSLTQINTTLLDLTYEMLS LQQVVKALNESYIDLKELGNYTYYNKWPYIWLGFIAGLVA LALCVFFILCCTGCGTNCMGKLCNRCCDRYEYDLEPHKV HVV</p>	
MERS S FL SPIKE 2cEMC/2012 (XbaI change (T to G)) (amino acid)	<p>MIHSVFLLMFLLTPTESYVDVGPDSVKSACIEVDIQQTFFDKT WPRPIDVSKADGIIYPQGRITYSNITITYQGLFPYQGDHGDY VYSAGHATGTTTPQKLFVANYSDVKQFANGFVVRIGAAANS TGTVII SPSTSATIRKIYPAFMLGSSVGNFSDGKMGRFFNHTL VLLPDGCGTLLRAFYCILEPRSGNHCPAGNSYTSFATYHTPA TDCSDGNYNRNASLNSFKEYFNLRNCTFMYTYNITEDEILEW FGITQTAQGVHLFSSRYVDLYGGMFQFATLPVYDTIKYYSII PHSIRSIQSDRKAWAAFVYVKLQPLTFLDFSVDGYIRRAIDC GFNDLSQLHCSYESFDVESGVYSVSFEAKPSGSVVEQAEGV ECDFSPLLSGTTPQVYNFKRLVFTNCNYNLTCLLSLFSVNDFT CSQISPAAIASNCYSSLILDYFSYPLSMKSDLSSVSSAGPISQFN YKQSFNPTCLILATVPHNLTITKPLKYSYINKCSRLSDDRT EVPQLVNAQYSPCVSIVPSTVWEDGDYRQKLSPLEGGGW LVASGSTVAMTEQLQMGFGITVQYGTDTNSVCPKLEFANDT KIASQLGNCVEYSLYGVSGRGVFQNCITAVGVRQRFVYDA YQNLVGYSDDGNYCLRACVSPVSVIYDKETKTTHATLFG SVACEHISSTMSQYSRSTRSMKRRDSTYGPLQTPVGCVLGL VNSSLFVEDCKLPLGQSLCALPDTPTSTLTPRSVRSPVGMRLA SIAFNHPIQVDQLNSSFYKLSIPTNFSFGVTQEQYIQTTIQKVTV DCKQYVCNGFQKCEQLLREYGFQCSKINQALHGANLRQDDS VRNLFASVKSQSSPIIPGFGGDFNLTLLEPVSI STGSRARSASAI EDLLFDKVTIADPGYMQGYDDCMQGPASARDLICAQYVA GYKVLPPMLMDVNMEAAYTSSLGSIAGVGWTAGLSSFAAIPF AQSIFYRLNGVGITQQVLSNQKLIANKFNQALGAMQTGFTT TNEAFKQVQDAVNNNAQALSKLASELSNTFGAISASIGDIIQR LDVLEQDAQIDRLINGRLTTLNAFVAQQLVRSESAALSAQLA KDKVNECVKAQSKRSGFCGQGTHIVSFVFNAPNGLYFMHV GYPPSNHIEVVSAYGLCDAANPTNCIAPVNGYFIKTNNTRIV DEWSTGSSFFYAPEPITSLNTKYVAPQVTYQNI STNLPPPLLG NSTGIDFQDELDEFFKNVSTSI PNFGSLTQINTTLLDLTYEMLS LQQVVKALNESYIDLKELGNYTYYNKWPYIWLGFIAGLVA LALCVFFILCCTGCGTNCMGKLCNRCCDRYEYDLEPHKV HVV</p>	25
Novel_MERS_S2_subunit_trimeric vaccine (amino acid)	<p>MIHSVFLLMFLLTPTESDCKLPLGQSLCALPDTPTSTLTPRSVR SVPGEMLASIAFNHPIQVDQLNSSFYKLSIPTNFSFGVTQEQYI QTTIQKVTV DCKQYVCNGFQKCEQLLREYGFQCSKINQALH GANLRQDSSVRNLFASVKSQSSPIIPGFGGDFNLTLLEPVSI TGSRSARSASAI EDLLFDKVTIADPGYMQGYDDCMQGPASAR DLICAQYVAGYKVLPPMLMDVNMEAAYTSSLGSIAGVGWTA GLSSFAAIPFAQSIFYRLNGVGITQQVLSNQKLIANKFNQAL GAMQTGFTTNEAFKQVQDAVNNNAQALSKLASELSNTFG AISASIGDIIQR LDVLEQDAQIDRLINGRLTTLNAFVAQQLVRS ESAALSAQLAKDKVNECVKAQSKRSGFCGQGTHIVSFVNA PGLYFMHVGYPPSNHIEVVSAYGLCDAANPTNCIAPVNGY FIKTNNTRIVDEWSTGSSFFYAPEPITSLNTKYVAPQVTYQNI STNLPPPLLG NSTGIDFQDELDEFFKNVSTSI PNFGSLTQINTTLL DLTYEMLS LQQVVKALNESYIDLKELGNYTYYNKWPDKIE EILSKIYHIENIARIKKLIGEA</p>	26
Isolate Al- Hasa_1_2013 (NCBI accession #AGN70962)	<p>MIHSVFLLMFLLTPTESYVDVGPDSVKSACIEVDIQQTFFDKT WPRPIDVSKADGIIYPQGRITYSNITITYQGLFPYQGDHGDY VYSAGHATGTTTPQKLFVANYSDVKQFANGFVVRIGAAANS TGTVII SPSTSATIRKIYPAFMLGSSVGNFSDGKMGRFFNHTL VLLPDGCGTLLRAFYCILEPRSGNHCPAGNSYTSFATYHTPA TDCSDGNYNRNASLNSFKEYFNLRNCTFMYTYNITEDEILEW FGITQTAQGVHLFSSRYVDLYGGMFQFATLPVYDTIKYYSII PHSIRSIQSDRKAWAAFVYVKLQPLTFLDFSVDGYIRRAIDC GFNDLSQLHCSYESFDVESGVYSVSFEAKPSGSVVEQAEGV ECDFSPLLSGTTPQVYNFKRLVFTNCNYNLTCLLSLFSVNDFT CSQISPAAIASNCYSSLILDYFSYPLSMKSDLSSVSSAGPISQFN</p>	27

TABLE 11-continued

Betacoronavirus Amino Acid Sequences		
Strain	Amino Acid Sequence	SEQ ID NO:
	YKQSFNSPTCLILATVPHNLTTITKPLKYSYINKCSRLSDSDRT EVPQLVNAHQYSPCVSIVPSTVWEDGDYRKQLSPLEGGGW LVASGSTVAMTEQLQMGGFITVQYGTDTNSVCPKLEFANDT KIASQLGNCVEYSLYGVSGRGVFQNTAVGVRQQRFFVYDA YQNLVGYYSDDGNYCLRACVSPVSVIYDKETKTHATLFG SVACEHISSTMSQYSRSTRSMLKRRDSTYGPLQTPVGCVLGL VNSSLFVEDCKLPLGQSLCALPDTPSTLTPRSVRVSPGEMRLA SIAFNHPIQVDQLNSSYFKLSIPTNFSFGVTQEYIQTTIQKVTV DCKQYVCNGFQKCEQLLREYGFQCSKINQALHGANLRQDDS VRNLFASVKSSQSSPIIPGFGGDFNLTLLEPVSI STGSRARSASAI EDLLFDKVTIADPGYMGGYDDCMQGGPASARDLICAQYVA GYKVLPLPLMDVNMEAAYTSSLGSIAGVGWTAGLSSFAAIPF AQSIFYRLNGVGITQQVLS ENQKLIANKFNQALGAMQTGFST TNEAFRKVQDAVNNAQALSKLASELSNTFGAISASIGDIIQR LDVLEQDAQIDRLINGRLTTLNAFVAQQLVRSESAALSAQLA KDKVNECVKAQSKRSGFCGQGTTHIVSFVNAPNGLYFMHV GYYPSNHIEVVSAYGLCDAANPTNCIAPVNGYFIKTNNTRIV DEWSTGSSFFYAPEPITSLNTKYVAPHVITYQNI STNLPPPLLG NSTGIDFQDELDEFFKNVSTSI PNFGSLTQINTTLLDLTYEMLS LQQVVKALNESYIDLKELGNYTYNKPWYIWLGFIAGLVA LALCVFFILCCTGCGTNCMGKLCNRCCDRYEEYDLEPHKV HVH	
Middle East respiratory syndrome coronavirus S protein UniProtKB- R9UQ53	MIHSVFLLMFLLTPTESYVDVGPDSVKSACIEVDIQOTFFDKT WPRPIDVSKADGIIYPQGRITYSNITITYQGLFPYQGDHGDY VYSAGHATGTTQKLEFVANYSDVKQFANGFVVRIGAAANS TGTVII SPSTSATIRKIYPAFMLGSSVGNFSDGKMRFFNHTL VLLPDGCGTLLRAFICYILEPRSGNHCPAGNSYTSFATYHTPA TDCSDGNYNRNASLNSFKKEYFNLRNCTFMYTYNITTEDEILEW FGITQTAQGVHLFSSRYVDLYGGMFQFATLPVYDTIKYYSII PHSIRSIQSDRKAAAFVYVKLQPLTFLDFSVDGYIRRAIDC GFNDLSQLHCSYESPDVESGVSVSFEAKPSGSVVEQAEGV ECDFFSPLLSGTPPQVYNFKRLVFTNCNYNLTCLLSLFSVNDFT CSQISPAAIASNCYSSLLIDYFSYPLSMKSDLSVSSAGPISQFN YKQSFNSPTCLILATVPHNLTTITKPLKYSYINKCSRLSDSDRT EVPQLVNAHQYSPCVSIVPSTVWEDGDYRKQLSPLEGGGW LVASGSTVAMTEQLQMGGFITVQYGTDTNSVCPKLEFANDT KIASQLGNCVEYSLYGVSGRGVFQNTAVGVRQQRFFVYDA YQNLVGYYSDDGNYCLRACVSPVSVIYDKETKTHATLFG SVACEHISSTMSQYSRSTRSMLKRRDSTYGPLQTPVGCVLGL VNSSLFVEDCKLPLGQSLCALPDTPSTLTPRSVRVSPGEMRLA SIAFNHPIQVDQLNSSYFKLSIPTNFSFGVTQEYIQTTIQKVTV DCKQYVCNGFQKCEQLLREYGFQCSKINQALHGANLRQDDS VRNLFASVKSSQSSPIIPGFGGDFNLTLLEPVSI STGSRARSASAI EDLLFDKVTIADPGYMGGYDDCMQGGPASARDLICAQYVA GYKVLPLPLMDVNMEAAYTSSLGSIAGVGWTAGLSSFAAIPF AQSIFYRLNGVGITQQVLS ENQKLIANKFNQALGAMQTGFST TNEAFRKVQDAVNNAQALSKLASELSNTFGAISASIGDIIQR LDVLEQDAQIDRLINGRLTTLNAFVAQQLVRSESAALSAQLA KDKVNECVKAQSKRSGFCGQGTTHIVSFVNAPNGLYFMHV GYYPSNHIEVVSAYGLCDAANPTNCIAPVNGYFIKTNNTRIV DEWSTGSSFFYAPEPITSLNTKYVAPHVITYQNI STNLPPPLLG NSTGIDFQDELDEFFKNVSTSI PNFGSLTQINTTLLDLTYEMLS LQQVVKALNESYIDLKELGNYTYNKPWYIWLGFIAGLVA LALCVFFILCCTGCGTNCMGKLCNRCCDRYEEYDLEPHKV HVH	28
Human SARS coronavirus (SARS-CoV) (Severe acute respiratory syndrome coronavirus) Spike glycoprotein UniProtKB- P59Q54	MFIFLLFLTLTSGSGLDRCTTFDDVQAPNYTQHTSSMRGVY PDEIFRSDTLTYLTQDLFLFPYSNVTFGHITNHTFGNPVIFPKDG IYFAATEKSNVVRGWVFGSTMNKKSQSVII INNSTNVVIRAC NFELCDNPPFAVSKPMGTQTHMTMIFDNAFNCTFEYISDAFSLD VSEKSGNFKHLREFVFNKDGFLYVYKGYQPIDVVRDLPSGF NTLKPIFKLPLGINITNFRAILTAFSPAQDIWGTSAAYFVGYL KPTTFMLKYDENGITDAVDCSQNPLAELKCSVKSFEIDKGI YQTSNFRVPSGDVVRFPNITNLCPFGEVFNATKPPSVYAW RKKISNCVADYSVLNSTFFSTFKCYGVSATKLNLCFNSVY ADSFVVKGDDVRQIAPGQGTGVADYNYKLPDDFMGCVLAW NTRNIDATSTGNYNYKYRLRHGKLRPFERDISNVPFSPDGK PCTPPALNCYWPLNDYGYFTTTGIGYQPYRVVLSFELLNAP ATVCGPKLSTDLIKNQCVNFNENGLTGTGVLTPSSKRFQPFQ QFGRDVSDFDTSVRDPKTSSEILDISPSCFSGGVSVITPGTNASSE VAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTQAG	29

TABLE 11-continued

Betacoronavirus Amino Acid Sequences		
Strain	Amino Acid Sequence	SEQ ID NO:
	CLIGAEHVDTSYECDIPIGAGICASYHTVSLRSTSQKSIVAYT MSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMKTSVDCN MYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTREV FAQVKQMYKPTPLKYFGGFNFSQLPDLKPTKRSFIEDLLFN KVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLL TDDMIAAYTAALVSGTATAGWTFGAGAAQIPFAMQMAYR FNGIGVTQNVLYENQKQIANQFNKAI SQIQESLTTTSTALGKL QDVVNQNAQALNTLVKQLSSNFGAISVNLNDILSRLDKVEAE VQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSEC VLGQSKRVDFCGKGYHLMSFPQAAPHGVVFLHVTVYVPSQER NFTTAPAI CHEGKAYFPREGVVFVNGTSWFITQRNFFSPQIIT DNTFVSGNCDVVGIGIINNTVYDLPQPELDSFKEELD KYFKNH TSPVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQE LGKYEQYIKWPWYVWLGFIAGLIAIVMVTILLCCMTSCCSCS KGACSCGSCCKFDEDDSEPVLLKGVKLHYT	
Human coronavirus OC43 (HCoV-OC43) Spike glycoprotein UniProtKB- P36334	MFLILLISLPTAFAVIGDLKCTSDNINDKDTGPPPISTDTVDVT NGLGTYVVLDRVYLLNTTFLNGYPTSGSTYRNMALKGSVL LSRLWFKPPFLSDFINGIFAKVKNTKVIKDRVMYSEFPATIGS TFVNTSYSVVVQPTINSTQDGNLQGLLEVSVQYNMCE YPQTICHPNLGNHRKELWHLDTGVVSCLYKRNFTYDVNAD YLYPHFYQEGGTFYAYFTDTGVVTKFLPNVYLGMAISHYYV MPLTCNSKLTLEYWVTPLTSRQYLLAFNQDGIIFNAEDCMSD FMSEIKCKTQSIAPPTGVYELNGYTVQPIADVRRKPNLPNC NIEAWLNDKSVSPPLNWERKTFSNCFNMSSLSMFIQADSFT CNNIDAAKIYGMCFSSITIDKFAIPNGRKVDLQGLNGLYLQSF NYRIDTTATSCQLYYNLPAAVSVSRFPSTWNKRFGFIEDS VFKPRPAGVLTNHDVVYAQHCFAKPNKPCCKLNGSCVGS PGKNNIGTCTPAGTNYLTCDNLCTPDPI TFTGTYKCPQTKSL VGIGEHCSGLAVKSDYCGGNSCTCRPQAFLGWSADSCLOGD KCNIFANFILHDVNSGLTCTDLQKANTDILGVCVNYDLYGI LGQGI FVEVNATYYNSWQNLLYDSNGNLYGFRDYIINRTFMI RSCYSGRVSAAFHANSSEPALFRNICKNYVFNNSLTRQLQPI NYFDSYLGCVVNAYNSTAISVQTCDLTVGSGYCVDYSKNRR SRGAITTYGRFTNFEPFTVNSVNDSELPVGGLYEIQIPSEFTIG NMVEFIQTSSPKVTIDCAAFVCGDYAACKSQLVEYGSFCDNI NAILTEVNELDDTTQLQVANS LMNGVTLSTKLKDG VNFNVD DINFSPVLGCLGSECSKASSRAIEDLLFDKVKLSDVGFVEAY NNCTGGAEIRDLCVQSYKGIKVLPPLLSENQISGYTLAATSA SLFPPWTAAGVPFYLNVQYRINGLGVMTDVLSSQNQKLIAN AFNNALYAIQEGFDATNSALVKIQAVVNANAEALNNLLQQL SNRFGAISAQLQELSRDLAEAEQIDRLINGRLTALNAYVS QQLSDSTLVKFSAAQAMEKVNCEKVSQSSRINFCGNGNHIIS LVQNAPYGLYFIHFSYVPTKYVTARVSPGLCTAGDRGIAPKS GYFVNVMNTWMTGSGYYPPEPI TENNVVMSTCAVNYTK APYVMLNTSIPNLPDFKEELDQWFKNQT SVAPDLSLDYINVT FLDLQVEMNRLQEAIKVLNQSYINLKDIGTYEYVYKWPWYV WLLICLAGVAMLVLLFFICCTGCGTSCFKKCGGCCDDYTG YQELVIKTS HDD	30
Human coronavirus HKU1 (isolate N5) (HCoV- HKU1) Spike glycoprotein UniProtKB- Q0ZME7	MFLIIFILPTTAVIGDFNCTNSFINDYNKTI PRISEDVVDVSLG LGTYVVLNRVYLLNTTLLFTGYFPKSGANFRDLALKGSYILST LWYKPPFLSDFNNGIFSKVKNTKLYVNNLTLYSEFSTIVIGSVF VNTSYTIVVQPHNGILEITACQYTMCEYPHTVCKSKGSIRNES WHIDSSEPLCLFKKNFTYNSADWLYPHFYQERGVFYAYYA DVGMPPTFLFSYLGTLTILSHYVMPLTCAISSNTDNETLEY WVTPLSRRQYLLNFDEHGVITNAVDCSSSFLSEIQCKTQSFAP NTGVYDLSGFTVKPVATVYRRIPNLPDCDIDNWLNNVSPSP LNWERRIFSNCFNLSTLLRLVHVDVFSFNNLKD SKIFGSCFN SITVDKFAIPNRRRDDQLGSSGFLQSSNYKIDISSSSCQLYYS LPLNVNTIMNFPNPSWNNRYGFGS FNLSSYDVVYSDHCFSVN SDFPCADPSVNVNSCAKSKPPSAICPAGTKYRHCDLDTLYV KNWCRCSCLPDP ISTYSPNTCPQKKVVVGIGEHCPGLGINEE KCGTQLNHSSCFPCSPDAFLGWSFDCISNNRNCIFSNFIFNGIN SGTTCSNDLLYSNTEISTGVCVNYDLYGITGQGI FKEVSAAY YNNWQNLLYDSNGNIIGFKDFLTNKTYTILPCYSGRVSAAFY QNSSSPALLYRNLCYVLLNNISFISQPFYFDSYLGCVLNAV LTSYVSSCDLRMGSGFCIDYALPSSRRKRRGISSPYRFVTPEP FNVSVFVND SVETVGLFELIPIPTNFTIAGHEEFIQTS SPKVTIDC SAFVCSNYAACHDLLSEYGTFCDNINSILNEVNDLLDITQLQV ANALMQGVTLSSNLNTNLHSDVDNIDFKSLGCLGSQCGSSS RSLLEDLLFNKVKLSVDFVEAYNNCTGGSEIRDLLCVQSFN	31

TABLE 11-continued

Betacoronavirus Amino Acid Sequences		
Strain	Amino Acid Sequence	SEQ ID NO:
	GIKVLPPILSETQISGYTTAATVAAMFPPWSAAAGVPFSLNVQ YRINGLGVTMDVLNKNQKLIANAFNKALLSIQNGFTATNSAL AKIQSVVNANAQALNSLLQQLFNKPGAISSSLQEILSRDLNLE AQVQIDRLINGRTALNAYVSQQLSDITLIKAGASRAIEKVN CVKSQSPRINFCGNGNHILSLVQNAPYGLLFHFSYKPTSFKT VLVSPGLCLSGDRGIAPKQGYFIKQNDWMFTGSSYYYPEPIS DKNVVMNSCSCVNFTKAPFIYLNNSIPNLSDFEAELESLWFKN HTSIAPNLTFSNHNATFLDLYEMNVIQESIKSLNSSFINLKEI GTYEMYVKNPWYIWLILVILFIIFLMILFFICCTGCGSACFSK CHNCCDEYGGHNDVFIKASHDD	
Novel_SARS_S2	MFIFLLFLTTLTSGSDLDRLASGIAAEQDRNTREVFAQVKQMY KTPTLKYPGGFNFSQILPDPLKPTKRSFIEDLLFNKVTADAG FMKQYGECLGDINARDLCAQKFNGLTVLPPLTDDMIAAYT AALVSGTATAGWTFGAGALQIPFAMQMAYRFGNGIGVTQN VLYENQKQIANQFNKAISSQIESLTTTSTALGKLQDVVNQNA QALNTLVKQLSSNFGAISVSLNDILSRDKVEAEVQIDRLITG RLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRV DFCGKGYHLMSPQAAPHGVVFLHVTVYVPSQERNFTTAPAI HEGKAYFPREGVVFVNGTSWFIQNRNFFSPQIITDNTFVSGN CDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPDVLG DISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYI KWPWYVWLGFIAGLIAIVMVTILLCCMTSCCSCCLKGACSCGS CCKFDEDDSEPVLGKVKLHYT	32
Novel_MERS_S2	MIHVSFLLMFLLTPTESDCKLPLGQSLCALPDTPTLTSPRSVR SVPGEMLASIAFNHPIQVDQLNSSYFKLSIPTNFSFGVTQYEYI QTTIQKVTVDCQYVYVNGFQKCEQLLREYGFQPCSKINQALH GANLRQDDSVRNLFASVKSQSSPIIPGFGGDFNLTLLEPVSI TGSRSARSAIEDLLPDKVTIADPGYMQGYDDCMQGPASAR DLICAQYVAGYKVLPLMDVNMEEAYTSSLLGSIAGVGWTA GLSSFAAIPFAQSIFYRLNGVGIQQLVSENQKLIANKFNQAL GAMQTGFTTTNEAFQKVQDAVNNAQALSKLASELSNTFG AISASIGDIIQRLDVLEQDAQIDRLINGRLTTLNAPVAQQLVRS ESAALSAQLAKDKVNECVKAQSKRSFGCGGTHIVSFVNA PNGLYFMHVGYYPSNHI EVVSAYGLCDAANPTNCIAPVNGY FIKTNNTRIVDEWYSYTGSSFYAPEPITSLNTKYVAPQVYQNI STNLPPPLNGSTGIDFQDELDEFFKNVSTSI PNFGSLTQINTTL LDLTYEMLSLQQVVKALNESYIDLKELGNYTYYNKWP	33
Novel_Trimeric_SARS_S2	MFIFLLFLTTLTSGSDLDRLASGIAAEQDRNTREVFAQVKQMY KTPTLKYPGGFNFSQILPDPLKPTKRSFIEDLLFNKVTADAG FMKQYGECLGDINARDLCAQKFNGLTVLPPLTDDMIAAYT AALVSGTATAGWTFGAGALQIPFAMQMAYRFGNGIGVTQN VLYENQKQIANQFNKAISSQIESLTTTSTALGKLQDVVNQNA QALNTLVKQLSSNFGAISVSLNDILSRDKVEAEVQIDRLITG RLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRV DFCGKGYHLMSPQAAPHGVVFLHVTVYVPSQERNFTTAPAI HEGKAYFPREGVVFVNGTSWFIQNRNFFSPQIITDNTFVSGN CDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPDVLG DISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYI KWPWYVWLGFIAGLIAIVMVTILLCCMTSCCSCCLKGACSCGS CCKFDEDDSEPVLGKVKLHYT	34

TABLE 12

Full-length Spike Glycoprotein Amino Acid Sequences (<i>Homo sapiens</i> strains)				
GenBank Accession	Country	Collection Date	Release Date	Virus Name
AFY13307	United Kingdom	2012 Sep. 11	2012 Dec. 5	Betacoronavirus England 1, complete genome
AFS88936		2012 Jun. 13	2012 Sep. 27	Human betacoronavirus 2c EMC/2012, complete genome
AGG22542	United Kingdom	2012 Sep. 19	2013 Feb. 27	Human betacoronavirus 2c England-Qatar/2012, complete genome
AHY21469	Jordan	2012	2014 May 4	Human betacoronavirus 2c Jordan-N3/2012 isolate MG167, complete genome

TABLE 12-continued

Full-length Spike Glycoprotein Amino Acid Sequences (<i>Homo sapiens</i> strains)				
GenBank Accession	Country	Collection Date	Release Date	Virus Name
AGH58717	Jordan	2012 April	2013 Mar. 25	Human betacoronavirus 2c Jordan-N3/2012, complete genome
AGV08444	Saudi Arabia	2013 May 7	2013 Sep. 17	Middle East respiratory syndrome coronavirus isolate Al-Hasa_12_2013, complete genome
AGV08546	Saudi Arabia	2013 May 11	2013 Sep. 17	Middle East respiratory syndrome coronavirus isolate Al-Hasa_15_2013, complete genome
AGV08535	Saudi Arabia	2013 May 12	2013 Sep. 17	Middle East respiratory syndrome coronavirus isolate Al-Hasa_16_2013, complete genome
AGV08558	Saudi Arabia	2013 May 15	2013 Sep. 17	Middle East respiratory syndrome coronavirus isolate Al-Hasa_17_2013, complete genome
AGV08573	Saudi Arabia	2013 May 23	2013 Sep. 17	Middle East respiratory syndrome coronavirus isolate Al-Hasa_18_2013, complete genome
AGV08480	Saudi Arabia	2013 May 23	2013 Sep. 17	Middle East respiratory syndrome coronavirus isolate Al-Hasa_19_2013, complete genome
AGN70962	Saudi Arabia	2013 May 9	2013 Jun. 10	Middle East respiratory syndrome coronavirus isolate Al-Hasa_1_2013, complete genome
AGV08492	Saudi Arabia	2013 May 30	2013 Sep. 17	Middle East respiratory syndrome coronavirus isolate Al-Hasa_21_2013, complete genome
AHI48517	Saudi Arabia	2013 May 2	2014 Feb. 6	Middle East respiratory syndrome coronavirus isolate Al-Hasa_25_2013, complete genome
AGN70951	Saudi Arabia	2013 Apr. 21	2013 Jun. 10	Middle East respiratory syndrome coronavirus isolate Al-Hasa_2_2013, complete genome
AGN70973	Saudi Arabia	2013 Apr. 22	2013 Jun. 10	Middle East respiratory syndrome coronavirus isolate Al-Hasa_3_2013, complete genome
AGN70929	Saudi Arabia	2013 May 1	2013 Jun. 10	Middle East respiratory syndrome coronavirus isolate Al-Hasa_4_2013, complete genome
AGV08408	Saudi Arabia	2012 Jun. 19	2013 Sep. 17	Middle East respiratory syndrome coronavirus isolate Bisha_1_2012, complete genome
AGV08467	Saudi Arabia	2013 May 13	2013 Sep. 17	Middle East respiratory syndrome coronavirus isolate Buraidah_1_2013, complete genome
AID50418	United Kingdom	2013 Feb. 10	2014 Jun. 18	Middle East respiratory syndrome coronavirus isolate England/2/2013, complete genome
AJD81451	United Kingdom	2013 Feb. 10	2015 Jan. 18	Middle East respiratory syndrome coronavirus isolate England/3/2013, complete genome
AJD81440	United Kingdom	2013 Feb. 13	2015 Jan. 18	Middle East respiratory syndrome coronavirus isolate England/4/2013, complete genome
AHB33326	France	2013 May 7	2013 Dec. 7	Middle East respiratory syndrome coronavirus isolate FRA/UAE, complete genome
AIZ48760	USA	2014 June	2014 Dec. 14	Middle East respiratory syndrome coronavirus isolate Florida/USA-2_Saudi Arabia_2014, complete genome
AGV08455	Saudi Arabia	2013 Jun. 4	2013 Sep. 17	Middle East respiratory syndrome coronavirus isolate Hafr-Al-Batin_1_2013, complete genome
AHI48561	Saudi Arabia	2013 Aug. 5	2014 Feb. 6	Middle East respiratory syndrome coronavirus isolate Hafr-Al-Batin_2_2013, complete genome
AHI48539	Saudi Arabia	2013 Aug. 28	2014 Feb. 6	Middle East respiratory syndrome coronavirus isolate Hafr-Al-Batin_6_2013, complete genome

TABLE 12-continued

Full-length Spike Glycoprotein Amino Acid Sequences (<i>Homo sapiens</i> strains)				
GenBank Accession	Country	Collection Date	Release Date	Virus Name
AIZ74417	France	2013 Apr. 26	2015 Mar. 10	Middle East respiratory syndrome coronavirus isolate Hu-France (UAE) - FRA1__1627-2013__BAL__Sanger, complete genome
AIZ74433	France	2013 May 7	2015 Mar. 10	Middle East respiratory syndrome coronavirus isolate Hu-France - FRA2__130569-2013__IS__HTS, complete genome
AIZ74439	France	2013 May 7	2015 Mar. 10	Middle East respiratory syndrome coronavirus isolate Hu-France - FRA2__130569-2013__InSpu__Sanger, complete genome
AIZ74450	France	2013 May 7	2015 Mar. 10	Middle East respiratory syndrome coronavirus isolate Hu-France - FRA2__130569-2013__Isolate__Sanger, complete genome
AKK52602	Saudi Arabia	2015 Feb. 10	2015 Jun. 8	Middle East respiratory syndrome coronavirus isolate Hu/Riyadh_KSA__2959__2015, complete genome
AKK52612	Saudi Arabia	2015 Mar. 1	2015 Jun. 8	Middle East respiratory syndrome coronavirus isolate Hu/Riyadh_KSA__4050__2015, complete genome
AHN10812	Saudi Arabia	2013 Nov. 6	2014 Mar. 24	Middle East respiratory syndrome coronavirus isolate Jeddah_1__2013, complete genome
AID55071	Saudi Arabia	2014 Apr. 21	2014 Nov. 12	Middle East respiratory syndrome coronavirus isolate Jeddah_C10306/KSA/2014-04-20, complete genome
AID55066	Saudi Arabia	2014	2014 Nov. 12	Middle East respiratory syndrome coronavirus isolate Jeddah_C7149/KSA/2014-04-05, complete genome
AID55067	Saudi Arabia	2014	2014 Nov. 12	Middle East respiratory syndrome coronavirus isolate Jeddah_C7569/KSA/2014-04-03, complete genome
AID55068	Saudi Arabia	2014 Apr. 7	2014 Nov. 12	Middle East respiratory syndrome coronavirus isolate Jeddah_C7770/KSA/2014-04-07, complete genome
AID55069	Saudi Arabia	2014 Apr. 12	2014 Nov. 12	Middle East respiratory syndrome coronavirus isolate Jeddah_C8826/KSA/2014-04-12, complete genome
AID55070	Saudi Arabia	2014 Apr. 14	2014 Nov. 12	Middle East respiratory syndrome coronavirus isolate Jeddah_C9055/KSA/2014-04-14, complete genome
AHE78108	Saudi Arabia	2013 Nov. 5	2014 May 1	Middle East respiratory syndrome coronavirus isolate MERS-CoV-Jeddah-human-1, complete genome
AKL59401	South Korea	2015 May 20	2015 Jun. 9	Middle East respiratory syndrome coronavirus isolate MERS-CoV/KOR/KNH/002__05__2015, complete genome
ALD51904	Thailand	2015 Jun. 17	2015 Jul. 7	Middle East respiratory syndrome coronavirus isolate MERS-CoV/THA/CU/17__06__2015, complete genome
AID55072	Saudi Arabia	2014 Apr. 15	2014 Nov. 12	Middle East respiratory syndrome coronavirus isolate Makkah_C9355/KSA/Makkah/2014-04-15, complete genome
AHC74088	Qatar	2013 Oct. 13	2013 Dec. 23	Middle East respiratory syndrome coronavirus isolate Qatar3, complete genome

TABLE 12-continued

Full-length Spike Glycoprotein Amino Acid Sequences (<i>Homo sapiens</i> strains)				
GenBank Accession	Country	Collection Date	Release Date	Virus Name
AHC74098	Qatar	2013 Oct. 17	2013 Dec. 23	Middle East respiratory syndrome coronavirus isolate Qatar4, complete genome
AHI48572	Saudi Arabia	2013 Aug. 15	2014 Feb. 6	Middle East respiratory syndrome coronavirus isolate Riyadh_14_2013, complete genome
AGV08379	Saudi Arabia	2012 Oct. 23	2013 Sep. 17	Middle East respiratory syndrome coronavirus isolate Riyadh_1_2012, complete genome
AID55073	Saudi Arabia	2014 Apr. 22	2014 Nov. 12	Middle East respiratory syndrome coronavirus isolate Riyadh_2014KSA_683/KSA/2014, complete genome
AGV08584	Saudi Arabia	2012 Oct. 30	2013 Sep. 17	Middle East respiratory syndrome coronavirus isolate Riyadh_2_2012, complete genome
AGV08390	Saudi Arabia	2013 Feb. 5	2013 Sep. 17	Middle East respiratory syndrome coronavirus isolate Riyadh_3_2013, complete genome
AHI48605	Saudi Arabia	2013 Mar. 1	2014 Feb. 6	Middle East respiratory syndrome coronavirus isolate Riyadh_4_2013, complete genome
AHI48583	Saudi Arabia	2013 Jul. 2	2014 Feb. 6	Middle East respiratory syndrome coronavirus isolate Riyadh_5_2013, complete genome
AHI48528	Saudi Arabia	2013 Jul. 17	2014 Feb. 6	Middle East respiratory syndrome coronavirus isolate Riyadh_9_2013, complete genome
AHI48594	Saudi Arabia	2013 Jun. 12	2014 Feb. 6	Middle East respiratory syndrome coronavirus isolate Taif_1_2013, complete genome
AHI48550	Saudi Arabia	2013 Jun. 12	2014 Feb. 6	Middle East respiratory syndrome coronavirus isolate Wadi-Ad-Dawasir_1_2013, complete genome
AIY60558	United Arab Emirates	2014 Mar. 7	2014 Dec. 6	Middle East respiratory syndrome coronavirus strain Abu Dhabi/Gayathi_UAE_2_2014, complete genome
AIY60538	United Arab Emirates	2014 Apr. 10	2014 Dec. 6	Middle East respiratory syndrome coronavirus strain Abu Dhabi_UAE_16_2014, complete genome
AIY60528	United Arab Emirates	2014 Apr. 10	2014 Dec. 6	Middle East respiratory syndrome coronavirus strain Abu Dhabi_UAE_18_2014, complete genome
AIY60588	United Arab Emirates	2014 Apr. 13	2014 Dec. 6	Middle East respiratory syndrome coronavirus strain Abu Dhabi_UAE_26_2014, complete genome
AIY60548	United Arab Emirates	2014 Apr. 19	2014 Dec. 6	Middle East respiratory syndrome coronavirus strain Abu Dhabi_UAE_30_2014, complete genome
AIY60568	United Arab Emirates	2014 Apr. 17	2014 Dec. 6	Middle East respiratory syndrome coronavirus strain Abu Dhabi_UAE_33_2014, complete genome
AIY60518	United Arab Emirates	2014 Apr. 7	2014 Dec. 6	Middle East respiratory syndrome coronavirus strain Abu Dhabi_UAE_8_2014, complete genome
AIY60578	United Arab Emirates	2013 Nov. 15	2014 Dec. 6	Middle East respiratory syndrome coronavirus strain Abu Dhabi_UAE_9_2013, complete genome
AKJ80137	China	2015 May 27	2015 Jun. 5	Middle East respiratory syndrome coronavirus strain ChinaGD01, complete genome

TABLE 12-continued

Full-length Spike Glycoprotein Amino Acid Sequences (<i>Homo sapiens</i> strains)				
GenBank Accession	Country	Collection Date	Release Date	Virus Name
AHZ64057	USA	2014 May 10	2014 May 14	Middle East respiratory syndrome coronavirus strain Florida/USA-2_Saudi Arabia_2014, complete genome
AKM76229	Oman	2013 Oct. 28	2015 Jun. 23	Middle East respiratory syndrome coronavirus strain Hu/Oman_2285_2013, complete genome
AKM76239	Oman	2013 Dec. 28	2015 Jun. 23	Middle East respiratory syndrome coronavirus strain Hu/Oman_2874_2013, complete genome
AKI29284	Saudi Arabia	2015 Jan. 6	2015 May 27	Middle East respiratory syndrome coronavirus strain Hu/Riyadh-KSA-2049/2015, complete genome
AKI29265	Saudi Arabia	2015 Jan. 21	2015 May 27	Middle East respiratory syndrome coronavirus strain Hu/Riyadh-KSA-2343/2015, complete genome
AKI29255	Saudi Arabia	2015 Jan. 21	2015 May 27	Middle East respiratory syndrome coronavirus strain Hu/Riyadh-KSA-2345/2015, complete genome
AKI29275	Saudi Arabia	2015 Jan. 26	2015 May 27	Middle East respiratory syndrome coronavirus strain Hu/Riyadh-KSA-2466/2015, complete genome
AKK52582	Saudi Arabia	2015 Feb. 10	2015 Jun. 8	Middle East respiratory syndrome coronavirus strain Hu/Riyadh_KSA_2959_2015, complete genome
AKK52592	Saudi Arabia	2015 Mar. 1	2015 Jun. 8	Middle East respiratory syndrome coronavirus strain Hu/Riyadh_KSA_4050_2015, complete genome
AHZ58501	USA	2014 Apr. 30	2014 May 13	Middle East respiratory syndrome coronavirus strain Indiana/USA-1_Saudi Arabia_2014, complete genome
AGN52936	United Arab Emirates	2013	2013 Jun. 10	Middle East respiratory syndrome coronavirus, complete genome

TABLE 13

MeV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO :
GC_F_MEASLES_B3.1 Sequence, NT (5' UTR, ORF, 3' UTR) Sequence Length: 1864	TCAAGCTTTTGGACCTCGTACAGAAGCTAATACGACT CACTATAGGGAAATAAGAGAGAAAAGAAGTAAGAA GAAATATAAGAGCCACCATGGGTCTCAAGGTGAACGTC TCTGCCGTATTCATGGCAGTACTGTAACTCTCCAACA CCCGCCGGTCAAATTCATTGGGGCAATCTCTAAGAT AGGGGTAGTAGGAATAGGAAGTGCAGCTACAAAGTT ATGACTCGTTCAGCCATCAATCATTAGTCATAAAATT AATGCCCAATATAACTCTCCTCAATAACTGCACGAGGG TAGAGATTGCAGAAATACAGGAGACTACTAAGAACAGTT TTGGAACCAATTAGGGATGCACCTAATGCAATGACCCA GAACATAAGGCCGGTTCAGAGCGTAGCTTCAAGTAGGA GACACAAGAGATTTGCGGGAGTAGTCTGGCAGGTGCG GCCCTAGGTGTTGCCACAGCTGCTCAGATAACAGCCGG CATTGCACCTTCAACGGTCCATGCTGAATCTCAGGCCAT CGACAATCTGAGAGCGAGCCTGGAACCTACTAATCAGG CAATTGAGGCAATCAGACAAGCAGGGCAGGAGATGAT ATTGGCTGTTCAAGGTGTCCAAGACTACATCAATAATG AGCTGATACCGTCTATGAACCAGCTATCTGTGATCTA ATCGGTCAGAGCTCGGGCTCAAATTGCTTAGATACTA TACAGAAATCCTGTCTATTATTGGCCCCAGCCTACGGG ACCCCATATCTGCGGAGATATCTATCCAGGCTTTGAGTT ATGCACTTGGAGGAGATATCAATAAGGTGTTAGAAAAG	35

TABLE 13-continued

MeV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO.
GC_F_MEASLES_B3.1 ORF Sequence, NT	CTCGGATACAGTGGAGGCGATTTACTAGGCATCTTAGA GAGCAGAGGAATAAAGGCTCGGATAACTCACGTCGAC ACAGAGTCTACTTCATAGTCTCAGTATAGCCTATCCG ACGCTGTCCGAGATTAAGGGGTGATTGCCACCGGCT AGAGGGGGTCTCGTACAACATAGGCTCTCAAGAGTGGT ATACCACTGTGCCCCAAGTATGTTGCAACCCAGGGTAC CTTATCTCGAATTTTGATGAGTCATCATGTACTTTCATG CCAGAGGGGACTGTGTGCAGCCAAAATGCCTTGACCC GATGAGTCTCTGCTCCAAGATGCCTCCGGGGTCCA CCAAGTCTGTGCTCGTACACTCGTATCCGGGTCTTTTG GGAACCGGTTCAATTTATCACAAGGGAACCTAATAGCC AATTGTGCATCAATCTTTGTAGTGTTACACAACAGGT ACGATTATTAATCAAGACCCGTGACAAGATCCTAACATA CATTGCTGCCGATCGCTGCCCGTAGTCGAGGTGAACG GCGTGACCATCCAAGTCCGGAGCAGGAGGTATCCAGA CGCTGTGTACTTGCACAGAATTGACCTCGGTCTCCCAT ATCATTTGGAGAGGTTGGACGTAGGGACAAATCTGGGG AATGCAATTGCCAAATTTGAGGATGCCAAGGAATTGTT GGAATCATCGGACCAGATATTGAGAAGTATGAAAGGTT TATCGAGCACTAGCATAGTCTACATCCTGATTGCAGTG TGTCTTGAGGGTTGATAGGATCCCCACTTAAATATGT TGCTGCAGGGGGCGTTGTAACAAAAGGGAGAACAG TTGGTATGTCAAGACCAGGCCATAAGCCTGACCTTACA GGAACATCAAATCCTATGTAAGATCGCTTTGATGATA ATAGGCTGGAGCCTCGGTGGCCAAGCTTCTTGCCCTT GGGCTCCCCCAGCCCTCTCCCTTCTGCACCCGT ACCCCGTGGTCTTTGAATAAGTCTGAGTGGGCGGC	36
	ATGGGTCTCAAGGTGAACGTCTCTGCCGTATTCATGGC AGTACTGTAACTCTCCAAACACCCGCGGTCAAATTC ATTGGGGCAATCTCTCTAAGATAGGGGTAGTAGGAATA GGAAGTGCAAGCTACAAAGTTATGACTCGTTCAGCCA TCAATCATTAGTCATAAAATTAATGCCAATATAACTCT CCTCAATAAATGCACGAGGGTAGAGATTGCAGAATACA GGAGACTACTAAGAACAGTTTGGAAACCAATTAGGGAT GCACTTAATGCAATGACCCAGAACATAAGGCCGGTTCA GAGCGTAGCTTCAAGTAGGAGACACAAGAGATTTGCG GGAGTAGTCTTGGCAGGTGCCGCCCTAGGTGTTGCCAC AGCTGCTCAGATAACAGCCGGCATTGCACCTCACCAGT CCATGCTGAACCTCTCAGGCCATCGACAATCTGAGAGCG AGCCTGGAACTACTAATCAGGCAATTGAGGCAATCAG ACAAGCAGGGCAGGAGATGATATTGGCTGTTGAGGGTG TCCAAGACTACATCAATAATGAGCTGATACCGTCTATG AACCAGCTATCTTGTGATCTAATCGGTGAGAAGCTCGG GCTCAAATTGCTTAGATACTATACAGAAATCCTGTCATT ATTTGGCCCCAGCCTACGGGACCCCATCTGCGGAGA TATCTATCCAGGCTTTGAGTTATGCACTTGGAGGAGAT ATCAATAAGGTGTTAGAAAAGCTCGGATACAGTGGAG GCGATTTACTAGGCATCTTAGAGAGCAGAGGAATAAAG GCTCGGATAACTCAGTCGACACAGAGTCTTACTTCAT AGTCTCAGTATAGCCTATCCGACGCTGTCCGAGATTA AGGGGGTGATTGTCCACCGGTAGAGGGGGTCTCGTAC AACATAGGCTCTCAAGAGTGGTATACCCTGTGCCAA GTATGTTGCAACCCAGGGTACCTTATCTCGAATTTGA TGAGTCATCATGTACTTTTCATGCCAGAGGGGACTGTGT GCAGCAAAATGCCCTTGTACCCGATGAGTCTCTGCTC CAAGAATGCCCTCCGGGGGTCCACCAAGTCTGTGCTCG TACACTCGTATCCGGGTCTTTGGGAACCGGTTCAATTT ATCACAAGGGAACCTAATAGCCAATTGTGCATCAATTC TTTGTAAAGTTACACAACAGGTACGATTATTAATCAA GACCTTGACAAGATCCTAACATACATTGCTGCCGATCG CTGCCCGGTAGTCGAGGTGAACGGCGTGACCATCCAAG TCGGGAGCAGGAGGTATCCAGACGCTGTGTACTTGAC AGAATTGACCTCGGTCTCCCATATCATTGGAGAGGTT GGACGTAGGGACAAATCTGGGGAATGCAATTGCCAAA TTGGAGGATGCCAAGGAATTGTTGGAATCATCGGACCA GATATTGAGAAGTATGAAAGGTTTATCGAGCACTAGCA TAGTCTACATCTGATTGCAGTGTGCTTTGGAGGGTTGA TAGGGATCCCCACTTAAATATGTTGCTGCAGGGGGCGT TGTAACAAAAGGGAGAACAAAGTTGGTATGTCAAGAC CAGGCCTAAAGCCTGACCTTACAGGAACATCAAAATCC TATGTAAGATCGCTTTGA	

TABLE 13-continued

MeV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO.
GC_F.MEASLES_B3.1 mRNA Sequence (assumes T100 tail) mRNA Sequence Length: 1925	G*GGGAAATAAGAGAGAAAAGAAGAGTAAGAAGAAAT ATAAGAGCCACCATGGGTCTCAAGGTGAACGTCTCTGC CGTATTCATGGCAGTACTGTAACTCTCCAAACACCCG CCGGTCAAATTCATTGGGGCAATCTCTCTAAGATAGGG GTAGTAGGAATAGGAAGTGCAAGCTACAAAGTTATGA CTCGTTCCAGCCATCAATCATTAGTCATAAAATTAATGC CCAATATAACTCTCCTCAATAACTGCACGAGGGTAGAG ATTGCAGAATACAGGAGACTACTAAGAACAGTTTGGGA ACCAATTAGGGATGCACCTAATGCAATGACCCAGAACA TAAGGCCGGTTCAGAGCGTAGCTTCAAGTAGGAGACAC AAGAGATTGCGGGAGTAGTCCTGGCAGGTGCGGCCCT AGGTGTTGCCACAGCTGCTCAGATAACAGCCGGCATTG CACTTCACCGGTCCATGCTGAACCTCTCAGGCCATCGAC AATCTGAGAGCGAGCCTGGAACTACTAATCAGGCAAT TGAGGCAATCAGACAAGCAGGGCAGGAGATGATATTG GCTGTTCAAGGTGTCCAAGACTACATCAATAATGAGCT GATACCGTCTATGAACAGCTATCTGTGATCTAATCG GTCAGAAGCTCGGGCTCAAATTGCTTAGATACTATACA GAAATCCTGTCAATTATTTGGCCCCAGCCTACGGGACCC CATATCTGCGGAGATATCTATCCAGGCTTTGAGTTATGC ACTTGGAGGAGATCAATAAGGTGTTAGAAAAGCTCG GATACAGTGGAGGCGATTACTAGGCATCTTAGAGAGC AGAGGAATAAAGGCTCGGATAACTCACGTCGACACAG AGTCCTACTTCATAGTCTCTCAGTATAGCCTATCCGACGC TGTCCGAGATTAAAGGGGTGATTGTCCACCGCTAGAG GGGGTCTCGTACAACATAGGCTCTCAAGAGTGGTATAC CACTGTGCCCCAAGTATGTTGCAACCCAAGGGTACCTTA TCTCGAATTTTGATGAGTCATCATGTACTTTCATGCCAG AGGGGACTGTGTGCAGCCAAATGCCTTGTACCCGATG AGTCCTCTGCTCCAAGAATGCCTCCGGGGTCCACCAA GTCCTGTGCTCGTACACTCGTATCCGGGTCTTTTGGGAA CCGGTTCATTTATCACAAGGGAACCTAATAGCCAATT GTGCATCAATTCTTTGTAAGTGTACACAACAGGTACG ATTATTAATCAAGACCCCTGACAAGATCCTAACATACAT TGCTGCCGATCGCTGCCCGTAGTCGAGGTGAACGGCG TGACCATCCAAGTCGGGAGCAGGAGGTATCCAGACGCT GTGTACTTGCACAGAATTGACCTCGGTCTCCCATATCA TTGGAGAGGTGGACGTAGGGACAATCTGGGGAAATG CAATTGCCAAATTGGAGGATGCCAAGGAATTGTTGGAA TCATCGGACCATATTTGAGAAGTATGAAAGGTTTATC GAGCACTAGCATAGTCTACATCCTGATTGCAGTGTGTC TTGGAGGGTTGATAGGGATCCCCACTTTAATATGTTGCT GCAGGGGGCGTTGTAAACAAAAGGGAGAACAAGTTGG TATGTCAAGACCAGGCCTAAAGCCTGACCTTACAGGAA CATCAAAATCCTATGTAAGATCGCTTTGATGATAATAG GCTGGAGCCTCGGTGGCCAAGCTTCTTGCCTTGGGC CTCCTCCAGCCCCCTCCTCCCTTCTGACCCGTACCC CCGTGGTCTTTGAATAAAGTCTGAGTGGGCGGCAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAACTAG	37
GC_F.MEASLES_D8 Sequence, NT (5' UTR, ORF, 3' UTR) Sequence Length: 1864	TCAAGCTTTTGGACCCTCGTACAGAAGCTAATACGACT CACTATAGGGAAATAAGAGAGAAAAGAAGTAAGAA GAAATATAAGAGCCACCATGGGTCTCAAGGTGAACGTC TCTGTCAATTCATGGCAGTACTGTAACTCTTCAACA CCCACCGGTCAAATCCATTGGGGCAATCTCTAAGAT AGGGGTGTTAGGGGTAGGAAGTGCAAGCTACAAAGTT ATGACTCGTTCAGCCATCAATCATAGTCATAAAGTT AATGCCCAATATAACTCTCCTCAACAATTGCACGAGGG TAGGGATTGCAGAAATACAGGAGACTACTGAGAACAGTT CTGGAACCAATTAGAGATGCATTAATGCAATGACCCA GAATATAAGACCGGTTCAAGAGTGTAGCTTCAAGTAGGA GACACAAGAGATTGCGGGAGTTGTCTTGGCAGGTGCG GCCCTAGGCGTTGCCACAGCTGCTCAAATAACAGCCGG TATTGCACCTTACCAGTCCATGCTGAACCTCTCAAGCCAT CGACAACTGAGAGCGAGCCTAGAACTACTAATCAGG CAATTGAGGCAATCAGACAAGCAGGGCAGGAGATGAT ATTGGCTGTTCAAGGTGTCCAAGACTACATCAATAATG AGCTGATACCGTCTATGAATCAACTATCTGTGATTTAA TCGGCCAGAAGCTAGGGCTCAAATTGCTCAGATACTAT	38

TABLE 13-continued

MeV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO:
GC_F_MEASLES_D8 ORF Sequence, NT	ACAGAAATCCTGTCATTATTTGGCCCCAGCTTACGGGA CCCCATATCTGCGGAGATATCTATCCAGGCTTTGAGCT ATGCCGCTTGGAGGAGATATCAATAAGGTGTTGGAAAAG CTCGGATACAGTGGAGGTGATCTACTGGGCATCTTAGA GAGCAGAGGAATAAAGGCCCGGATAACTCAGTCGAC ACAGAGTCCTACTTCATTGTACTCAGTATAGCCTATCCG ACGCTATCCGAGATTAAGGGGTGATTGCCACCGGCT AGAGGGGGTCTCGTACAACATAGGCTCTCAAGAGTGGT ATACCACTGTGCCCCAAGTATGTTGCAACCCAGGGTAC CTTATCTCGAATTTTGATGAGTCATCATGCACCTTTCATG CCAGAGGGGACTGTGTGCAGCCAGAATGCCTGTACCC GATGAGTCCTCTGCTCCAAGATGCCTCCGGGGTCCA CTAAGTCCTGTGCTCGTACACTCGTATCCGGGTCTTTCG GGAACCGGTTCAATTTATCACAGGGGAACCTAATAGCC AATTGTGCATCAATCCTTTGCAAGTGTTACACAACAGG AACAATCATTAAATCAAGACCTGACAAGATCCTAACAT ACATTGCTGCCGATCACTGCCCGGTGGTCGAGGTGAAT GGCGTGACCATCCAAGTCGGGAGCAGGAGGTATCCGG ACGCTGTGTACTTGACAGGATTGACCTCGGTCTCTCC ATATCTTTGGAGAGGTGGACGTAGGGACAATCTGGG GAATGCAATTGCTAAGTTGGAGGATGCCAAGGAATTGT TGGAGTCATCGGACCAGATATTGAGGAGTATGAAAGGT TTATCGAGCACTAGTATAGTTTACATCCTGATTGCAGTG TGTCTTGAGGATTGATAGGGATCCCCGCTTTAATATGT TGCTGCAGGGGGCGTTGTAACAAGAAGGGAGAACAAG TTGGTATGTCAAGACCAGGCCATAAGCCTGATCTTACA GGAACATCAAATCCTATGTAAGGTCACTCTGATGATA ATAGGCTGGAGCCTCGGTGGCCAAGCTTCTTGCCCCCTT GGGCCTCCCCCAGCCCTCCTCCCTTCTGCACCCGT ACCCCGTGGTCTTTGAATAAGTCTGAGTGGGCGGC	39
	ATGGGTCTCAAGGTGAACGTCTCTGTCTATTCATGGC AGTACTGTAACTCTTCAAACACCCACCGGTCAAATCC ATTGGGGCAATCTCTCTAAGATAGGGGTGGTAGGGGTA GGAAGTGCAAGCTACAAAGTTATGACTCGTTCAGCCA TCAATCATTAGTCATAAAGTTAATGCCAATATAACTCT CCTCAACAATTGACGAGGGTAGGGATTGCAGAATACA GGAGACTACTGAGAACAGTTCTGGAACCAATTAGAGAT GCACTTAATGCAATGACCCAGAATATAAGACCGGTTCA GAGTGTAGCTTCAAGTAGGAGACACAAGAGATTTGCCG GAGTTGTCTGGCAGGTGCGGCCCTAGGCGTTGCCACA GCTGCTCAAATAACAGCCGGTATTGCACTTCAACAGTC CATGCTGAATCTCAAGCCATCGACAATCTGAGAGCGA GCCTAGAACTACTAATCAGGCAATTGAGGCAATCAGA CAAGCAGGGCAGGAGATGATATTGGCTGTTGAGGGTGT CCAAGACTACATCAATAATGAGCTGATACCGTCTATGA ATCAACTATCTTGTGATTAAATCGGCCAGAAGCTAGGG CTCAAATTGCTCAGATACTATACAGAAATCCTGTCAAT ATTTGGCCCCAGCTTACGGGACCCCATATCTGCGGAGA TATCTATCCAGGCTTTGAGCTATGCGCTTGAGAGGAGAT ATCAATAAGGTGTTGGAAAAGCTCGGATACAGTGGAG GTGATCTACTGGGCATCTTAGAGAGCAGAGGAATAAAG GCCCGGATAACTCAGTCGACACAGAGTCCTACTTCAT TGTACTCAGTATAGCCTATCCGACGCTATCCGAGATTA AGGGGGTGATTGTCCACCGGTAGAGGGGGTCTCGTAC AACATAGGCTCTCAAGAGTGGTATACCAGTGTGCCAA GTATGTTGCAACCCAGGGTACCTTATCTCGAATTTTGA TGAGTCATCATGCACCTTTCATGCCAGAGGGGACTGTGT GCAGCCAGAATGCCCTTGTACCCGATGAGTCCTCTGCTC CAAGAATGCCCTCGGGGGTCCACTAAGTCTGTGCTCG TACACTCGTATCCGGGTCTTTCGGGAACCGGTTCAATTT ATCACAGGGGAACCTAATAGCCAATTGTGCATCAATCC TTTGCAAGTGTTACACAACAGGAACAATCATTAAATCAA GACCTTGACAAGATCCTAACATACATTGCTGCCGATCA CTGCCCGGTGGTCGAGGTGAATGGCGTGACCATCCAAG TCGGGAGCAGGAGGTATCCGGACGCTGTGTACTTGCAC AGGATTGACCTCGTCTCCCATATCTTTGGAGAGGTT GGACGTAGGGACAAATCTGGGAATGCAATTGCTAAGT TGGAGGATGCCAAGGAATGTTGGAGTCATCGGACCAG ATATTGAGGAGTATGAAAGGTTTATCGAGCACTAGTAT AGTTTACATCCTGATTGCAAGTGTCTTGGAGGATTGAT AGGGATCCCCGCTTTAATATGTTGCTGCAGGGGGCGTT	

TABLE 13-continued

MeV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO.
	GTAACAAGAAGGGAGAACAAGTTGGTATGTCAAGACC AGGCCTAAAGCCTGATCTTACAGGAACATCAAAATCCT ATGTAAGGTCACCTCTGA	
GC_F.MEASLES_D8 mRNA Sequence (assumes T100 tail) Sequence Length: 1925	G*GGGAAATAAGAGAGAAAAGAAGTAAGAAGAAAT ATAAGAGCCACCATGGGTCTCAAGGTGAACGTCTCTGT CATATTTCATGGCAGTACTGTTAACTCTTCAAACACCCAC CGGTCAAATCCATTGGGGCAATCTCTCTAAGATAGGGG TGGTAGGGGTAGGAAGTGCAAGCTACAAGTTATGACT CGTTCCAGCCATCAATCATTAGTCATAAAGTTAATGCC CAATATAACTCTCCTCAACAATTGCACGAGGGTAGGGA TTGCAGAAATACAGGAGACTACTGAGAACAGTTCTGGAA CCAATTAGAGATGCACTTAATGCAATGACCCAGAATAT AAGACCGGTTCAAGTGTAGCTTCAAGTAGGAGACACA AGAGATTGCGGGAGTTGCTTGGCAGGTGCGGCCCTA GGCGTTGCCACAGCTGCTCAAATAACAGCCGGTATTGC ACTTCACAGTCCATGCTGAACCTCTAAGCCATCGACA ATCTGAGAGCGAGCCTAGAACTACTAATCAGGCAATT GAGGCAATCAGACAAGCAGGCGAGGATGATATTGG CTGTTCAAGGTGTCCAAGACTACATCAATAATGAGCTG ATACCGTCTATGAATCAACTATCTTGTGATTAAATCGGC CAGAAGCTAGGGCTCAAATTGCTCAGATACTATACAGA AATCCTGTCAATTATTGGCCCCAGCTTACGGGACCCCAT ATCTGCGGAGATATCTATCCAGGCTTTGAGCTATGCGC TTGGAGGAGATATCAATAAGGTGTTGGAAAAGCTCGGA TACAGTGGAGGTGATCTACTGGGCATCTTAGAGAGCAG AGGAATAAAGGCCCGGATAACTCAGTCGACACAGAG TCCTACTTCAATTGTACTCAGTATAGCCTATCCGACGCTA TCCGAGATTAAAGGGGTGATTGTCCACCGGTAGAGGG GGTCTCGTACAACATAGGCTCTCAAGAGTGGTATACCA CTGTGCCCAAGTATGTTGCAACCCAAGGGTACCTTATC TCGAATTTTGATGAGTCATCATGCACTTTCATGCCAGAG GGGACTGTGTGCAGCCAGAATGCCTTGTACCCGATGAG TCCTCTGCTCCAAGAATGCCTCCGGGGTCCACTAAGT CCTGTGCTCGTACACTCGTATCCGGGTCTTTCGGGAACC GGTTCATTTTATCAGAGGGAACCTAATAGCCAATTGT GCATCAATCCTTTGCAAGTGTTACACAACAGGAACAAT CATTAATCAAGACCCTGACAAGATCCTAACATACATTG CTGCCGATCACTGCCCGGTGGTCGAGGTGAATGGCGTG ACCATCCAAGTCGGGAGCAGGAGGTATCCGACGCTGT GTACTTGACAGGATTGACCTCGGTCCCTCCATATCTTT GGAGAGGTTGGACGTAGGGACAAATCTGGGGAATGCA ATTGCTAAGTTGGAGGATGCCAAGGAATTGTTGGAGTC ATCGGACCAGATATTGAGGAGTATGAAAGGTTTATCGA GCACTAGTATAGTTTACATCTGATTGCAGTGTGTCTTG GAGGATTGATAGGGATCCCCGCTTAAATATGTTGCTGC AGGGGGCGTTGTAAACAAGAAGGGAGAACAAAGTTGGTA TGTCAGAGCCAGGCCCTAAAGCCTGATCTTACAGGAACA TCAAAATCCTATGTAAGGTCACCTGATGATAATAGGC TGGAGCCTCGGTGGCCAAGCTTCTTGCCCTTGGGCCCTC CCCCCAGCCCCCTCCTCCCTTCCTGCACCCGTACCCCG TGGTCTTTGAATAAAGTCTGAGTGGGCGGCAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAATCTAG	40
GC_H.MEASLES_B3 Sequence, NT (5' UTR, ORF, 3' UTR) Sequence Length: 2065	TCAAGCTTTTGGACCCTCGTACAGAAGCTAATACGACT CACTATAGGGAATAAGAGAGAAAAGAAGTAAGAA GAAATATAAGAGCCACCATGTACCGCAACGAGACCG GATAAATGCCCTTCTACAAGATAACCCCTATCCCAGG GAAGTAGGATAGTTATTAACAGAGAACATCTTATGATT GACAGACCCTATGTTCTGTCTGGCTGTTCTGTTCTGTCATG TTTCTGAGCTTGATCGGATTGCTGGCAATTGCAGGCATT AGACTTCATCGGGCAGCCATCTACACCGCGGAGATCCA TAAAAGCCTCAGTACCAATCTGGATGTGACTAACTCCA TCGAGCATCAGGTCAGGACGTGCTGACACCACTCTTT AAAATCATCGGGGATGAAGTGGGCTTGAGAACACCTC AGAGATTCAGTGACCTAGTGAAATTCATCTCGGACAAG ATTAAATTCCTTAATCCGATAGGGAGTACGACTTCAG AGATCTCACTTGGTGCATCAACCCGCCAGAGAGGATCA AAGTAGATTATGATCAATACTGTGCAGATGTGGCTGCT GAAGAGCTCATGAATGCATTGGTGAACCTCACTCTACT	41

TABLE 13-continued

MeV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO.
	GGAGACCAGAACAACCACTCAGTTCCTAGCTGTCTCAA AGGGAAACTGCTCAGGGCCCACTACAATCAGAGGTCA ATTCTCAAACATGTCGCTGTCTTGTGGACTTGACTT AGGTCGAGGTACAAATGTGTCTATAGTCACTATGA CATCCAGGGAATGTATGGGGAACTACCTAGTTGAA AAGCCTAATCTGAACAGCAAAGGGTCAGAGTTGTACA ACTGAGCATGTACCGAGTGTGAGTAGGTTGTATCA GAAACCCGGGTTTGGGGGCTCCGGTGTTCATATGACA AACTATTTTGAACAACAGTCAGTAATGGTCTCGGCAA CTGTATGGTGGCTTTGGGGGAGCTCAAACCTCGCAGCCC TTTGTACAGGGGACGATTCTATCATAATCCCTATCAGG GATCAGGGAAGGTGTGAGCTCCAGCTCGTCAAGCTG GGTGTCTGGAATCCCCAACCGACATGCAATCCTGGGT CCCCTTATCAACGGATGATCCAGTGGTAGACAGGCTTT ACCTCTCATCTCACAGAGGTGTATCGCTGACAAATCAA GCAAAATGGGCTGTCCGACAACACGAACAGATGACA AGTTGCGAATGGAGACATGCTTCAGCAGGCGTGTAAA GGTAAATCCAGCACTCTGCGAGAATCCCGAGTGGGT ACCATGGAAGGATAACAGGATTCCTTCATACGGGGTCC TGTCTGTTGATCTGAGTCTGACGGTTGAGCTTAAATCA AAATTGCTTCGGGATTCGGGCCATTGATCACACAGGC TCAGGGATGGACCTATACAAATCCAACGCAACATGT GTATTGGCTGACTATTCGCGCAATGAGAAATCTAGCCT TAGGCGTAATCAACACATTGGAGTGGATACCGAGATTC AAGGTTAGTCCCAACCTCTTCACTGTCCCAATTAAGGA AGCAGGCGAAGACTGCGCATGCCCCAACATACCTACCTG CGGAGGTGGACGGTGATGTCAAACCTCAGTTCCAACCTG GTGATTCTACCTGGTCAAGATCTCCAATATGTTTTGGCA ACCTACGATACCTCCAGGTTGAGCATGCTGTGGTTTA TTACGTTTACAGCCCAAGCCGCTCATTTCTTACTTTTA TCCTTTTAGGTTGCCATAAAGGGGGTCCCAATCGAAC TACAAGTGGAATGCTTCACATGGGATCAAAACTCTGG TGCCGCTCACTTCTGTGTCTGCGGACTCAGAAATCCGGT GGACTTATCACTCACTCTGGGATGGTGGGCATGGGAGT CAGCTGCACAGCTACCGGGAAGATGGAACCAATCGC AGATAATGATAATAGGCTGGAGCCTCGGTGGCCAGCT TCTTGCCCTTGGGCTCCCCCAGCCCTCCTCCCTT CCTGCACCCGTACCCCGTGGTCTTTGAATAAAGTCTG AGTGGGCGGC	
GC_H_MEASLES_B3 ORF Sequence, NT	ATGTCACCGCAACGAGACCGGATAAATGCCTTCTACAA AGATAACCTTATCCCAAGGGAAGTAGGATAGTTATTA ACAGAGAATCTTATGATTGACAGACCTATGTTCTG CTGGCTGTTCTGTTCTGTCATGTTTCTGAGCTTGATCGGA TTGCTGGCAATGCAAGGATAGACTTCATCGGGCAGC CATCTACACCGCGGAGATCCATAAAGCCTCAGTACCA ATCTGGATGTGACTAACTCCATCGAGCATCAGGTCAAG GACGTGCTGACACCACTCTTAAATCATCGGGGATGA AGTGGGCTGAGAACACCTCAGAGATTCAGTACCTAG TGAAATTCATCTCGGACAAGATTAAATTCCTTAATCCG GATAGGGAGTACGACTTCAGAGATCTCACTTGGTGCAT CAACCCGCGAGAGAGGATCAAACCTAGATTATGATCAAT ACTGTGCAGATGTGGCTGCTGAAGAGCTCATGAATGCA TTGGTGAACTCAACTCTACTGGAGACCAGAACCAACCAC TCAGTTCCTAGCTGTCTCAAAGGGAATGCTCAGGGC CCACTACAATCAGAGGTCAATTCTCAAACATGTCGCTG TCCTTGTGGACTTGTACTTAGGTCGAGGTACAAATGTG TCATCTATAGTCACTATGACATCCAGGGAATGTATGG GGGAACCTACCTAGTTGAAAAGCCTAATCTGAACAGCA AAGGGTCAGAGTTGTCACTGAGCATGTACCGAGTG TTTGAAGTAGGTGTGATCAGAAACCCGGGTTTGGGGC TCCGGTGTTCATATGACAACTATTTTGAACACAGCAG TCAGTAATGGTCTCGGCAACTGTATGGTGGCTTTGGGG GAGCTCAAACCTCGCAGCCCTTTGTACGGGGACGATT TATCATAATTCCCTATCAGGGATCAGGGAAGGTGTCA GCTTCAGCTCGTCAAGCTGGGTGTCTGGAATCCCCA ACCGACATGCAATCCTGGGTCCCCTTATCAACGGATGA TCCAGTGGTAGACAGGCTTACCTCTCATCTCACAGAG GTGTCTCGTACCAATCAAGCAAATGGGCTGTCCCG ACAACACGAACAGATGACAAGTTGCGAATGGAGACAT GCTTCAGCAGGCGTGTAAAGGTAAATCCAGCACTC TGCAGAAATCCCGAGTGGGTACCATTGAAGGATAACAG	42

TABLE 13-continued

[illegible]

TABLE 13-continued

MeV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO.
	CTGTGCAGATGTGGCTGCTGAAGAACTCATGAATGCAT TGGTGAACCTCAACTCTACTGGAGACCAGGGCAACCAAT CAGTTCCTAGCTGTCTCAAAGGAACTGCTCAGGGCC CACTACAATCAGAGGCCAATTCTCAAACATGTCGCTGT CCCTGTTGGACTTGTATTAAAGTCGAGGTACAAATGTGT CATCTATAGTCACTATGACATCCCAGGGAATGTACGGG GGAACCTTACCTAGTGGAAAAGCCTAATCTGAGCAGCAA AGGGTCAGAGTTGTCACAACTGAGCATGCACCGAGTGT TTGAAGTAGGTGTTATCAGAAATCCGGGTTTGGGGGCT CCGGTATTCCATATGACAACTATCTTGAGCAACCGAT CAGTAATGATTTGAGCAACTGCATGGTGGCTTTGGGGG AGCTCAAGTTCGACGCCCTCTGTACAGGGAAGATTCT ATCACAATTCCCTATCAGGGATCAGGGAAGGTGTCTAG CTTCCAGCTTGTCAAGCTAGGTGTCTGGAAATCCCAA CCGACATGCAATCCTGGGTCCCCCTATCAACGGATGAT CCAGTGATAGACAGGCTTTACCTCTCATCTCACAGAGG CGTTATCGCTGACAAATCAAGCAAAATGGGCTGTCCGA CAACACGGACAGATGACAAGTTCGGAATGGGACATG CTTCCAGCAGGCGGTAAAGGGTAAATCCAAGCACTTT GCGAGAATCCCGAGTGGACACCATTGAAGGATAACAG GATTCTTCATACGGGGTCTGTCTGTTGATCTGAGTCT GACAGTTGAGCTTAAATCAAAATGTTTCAGGATTCTG GGCCATTGATCACACACGGTTCAGGGATGGACCTATAC AAATCCAACCAACAATATGATTGGCTGACTATCCC GCCAATGAAGAACCCTGGCCTTAGGTGTAATCAACACAT TGGAGTGGATACCGAGATTCAAGGTAGTCCCAACCTC TTCCTGTTCATTAAGGAAGCAGGCGAGGACTGCCA TGCCCCAACATACCTACCTGCGGAGGTGGATGGTGATG TCAAACTCAGTTCCAATCTGGTGATTCTACCTGGTCAAG ATCTCCAATATGTTCTGGCAACCTACGATATTCAGA GTTGAACATGCTGTAGTTTATTACGTTTACAGCCCAAGC CGCTCATTTTCTTACTTTTATCCTTTTAGGTTGCCTGTAA GGGGGGTCCCCATTGAATACAAGTGAATGCTTCACA TGGGACCAAAAACCTCTGGTGCCGTCACCTTCTGTGTGCTT GCGGACTCAGAATCTGGTGGACATATCACTCACTCTGG GATGGTGGGCATGGGAGTCAGCTGCACAGCCACTCGGG AAGATGGAACCAAGCCGAGATAG	
GC_H_MEASLES_D8 mRNA Sequence (assumes T100 tail) Sequence Length: 2126	G*GGGAAATAAGAGAGAAAAGAAGAGTAAGAAGAAAT ATAAGAGCCACCATGTCAACCAACGAGACCGGATAA ATGCCTTCTACAAAGACAACCCCATCCTAAGGGAAGT AGGATAGTTATTAAAGAGAACATCTTATGATTGATAG ACCTTATGTTTTGCTGGCTGTTCTATTTCGTCATGTTTCTG AGCTTGATCGGGTTGCTAGCCATTGCAGGCATTAGACT TCATCGGGCAGCCATCTACACCGCAGAGATCCATAAAA GCCTCAGCACCACCTGAGTGAATAACTCAATCGAG CATCAGGTAAAGGACGTGTCGACACCACTCTTCAAGAT CATCGGTGATGAAGTGGGCTTGAGGACACCTCAGAGAT TCACTGACCTAGTGAAGTTCATCTCTGACAAGATTAAA TTCCTTAATCCGGACAGGGAATACGACTTCAGAGATCT CACTTGGTGATCAACCCGCCAGAGAGAATCAAATTGG ATTATGATCAATACGTGTCAGATGTGGCTGCTGAAGAA CTCATGAATGCATTGGTGAACCTCAACTCTACTGGAGAC CAGGGCAACCAATCAGTTCCTAGCTGTCTCAAAGGGAA ACTGCTCAGGGCCCACTACAATCAGAGGCCAATTCTCA AACATGTCGCTGTCCCTGTTGGACTTGTATTAAAGTCGA GGTTACAATGTGTCATCTATAGTCACTATGACATCCCA GGAATGTACGGGGGAACCTACCTAGTGGAAAAGCCT AATCTGAGCAGCAAGGGTCAGAGTTGTCACAACTGAG CATGCACCGAGTGTGTTGAAGTAGGTGTTATCAGAAATC CGGGTTTGGGGGCTCCGGTATTCCATATGACAACTAT CTTGAGCAACCAGTCAGTAATGATTTCAGCAACTGCAT GGTGGCTTTGGGGGAGCTCAAGTTCGCAGCCCTCTGTC ACAGGGAAGATTCTATCACAATCCCTATCAGGGATCA GGGAAAGGTGTCAGCTTCCAGCTTGTCAGCTAGGTGT CTGGAATCCCCAACCGACATGCAATCCTGGGTCCCC TATCAACGGATGATCCAGTGATAGACAGGCTTTACCTC TCATCTACAGAGGCGTTATCGCTGACAATCAAGCAAA ATGGGCTGTCCCGACAACACGACAGATGACAAGTTGC GAATGGAGACATGCTTCCAGCAGGCGTGAAGGGTAA AATCCAAGCACTTTGCGAGAATCCGAGTGGACACCAT TGAAGGATAACAGGATTCTTCATACGGGGTCTTGTCT	46

TABLE 13-continued

MeV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO.
	GTTGATCTGAGTCTGACAGTTGAGCTTAAAAATCAAAAT TGTTCAGGATTTCGGCCATTGATCACACACGGTTCAG GGATGGACCTATACAAATCCACCACAACATATGTAT TGGCTGACTATCCCGCCAATGAAGAACCTGGCCTTAGG TGTAATCAACACATTGGAGTGGATACCGAGATTCAGG TTAGTCCCAACCTCTTCACTGTCCAATTAAGGAAGCA GGCAGGAGCTGCCATGCCCCAACATACCTACCTGCGGA GGTGGATGGTGTGTCAAACTCAGTTCCAATCTGGTGA TTCTACCTGGTCAAGATCTCCAATATGTTCTGGCAACCT ACGATACTTCCAGAGTTGAACATGCTGTAGTTTATTAC GTTTACAGCCCAAGCCGCTCATTTTCTTACTTTTATCCT TTTAGGTTGCCCTGTAAAGGGGGTCCCCATTGAATTACA AGTGGAAATGCTTCACATGGGACCAAAACTCTGGTGCC GTCACCTCTGTGTGCTTGCAGACTCAGAATCTGGTGA CATATCACTCACTCTGGGATGGTGGGCATGGGAGTCAG CTGCACAGCCACTCGGGAAGATGGAACAGCCGCGAGA TAGTGATAATAGGCTGGAGCCTCGGTGGCCAAGCTTCT TGCCCTTGGGCCTCCCCCAGCCCTCCTCCCTTCTCT GCACCCGTACCCCGTGGTCTTTGAATAAAGTCTGAGT GGGCGGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAT CTAG	
MeV mRNA Sequences		
GC_F_MEASLES_B3.1 Sequence, NT (5' UTR, ORF, 3' UTR) Sequence Length: 1864	UCAAGCUUUUGGACCCUCGUACAGAAAGCUAAUACGAC UCACUUAUAGGGAAUAAGAGAGAAAAGAGUUAAG AAGAAUAUAAGAGCCACCAUGGGUCUACAGGUGAA CGUCUCUGCCGUUAUUAUGGAGUACUGUUAACUCUC CAAACACCCGCCGUCAAAUAUUGGGGCAUUCUCU CUAAGAUAGGGGUAGUAGGAUAUAGGAAGUGCAAGCU ACAAAAGUUAUGACUCGUUCCAGC CAUCAUUAUAGU CAUAAAAUUAUGCCCAAUAUAUCUCUCCUAUAAC UGCACGAGGUAGAGAUUGCAGAAUACAGGAGACUA CUAAGAACAGUUUUGGAACCAUUAAGGAUGCACUU AAUGCAAUGACCCAGAACAUAAGGCCGGUUCAGAGCG UAGCUUCAAGUAGGAGACACAAGAGAUUUGCGGGAG UAGUCCUGGCAGGUGCGGCCUAGGUGUUGCCACAGC UGCUACAGUAACAGCCGGCAUUGCACUUCACCGGUCC AUGCUGAACUCUCAGGCCAUCGACAAUCUGAGAGCGA GCCUGGAAACUACUAAUCAGGCAAUUGAGGCAUUCAG ACAAGCAGGGCAGGAGAUUAUUGGCUGUUCAGGG UGUCCAAGACUACAUAUAUAGAGCUGAUACCGUCU AUGAACCAGCUAUCUUGUGAUCUAAUCGGUCAGAAGC UCGGGCUCAAUUGCUUAGAUACUACAGAAAUCCU GUCAUUAUUUGGCCCAAGCCUACGGGACCCAUUAUCU GCGGAGAUUAUCUUAUCCAGGC UUUGAGUUAUGCACUU GGAGGAGAUUAUCAAUAGGUGUUAAGAAAGCUCGGA UACAGUGGAGGC GAUUUACUAGGCAUCUUAAGAGAGC AGAGGAAUAAAGGCUCGGAUAACUCACGUCGACACAG AGUCCUACUUAUAGUCCUCAGUAUAGCCUAUCCGAC GCUGUCCGAGAUUAAGGGGUGAUUUGCCACCGGCUA GAGGGGUCUCGUACAACAUAGGCUCUCAAGAGUGG UAUACCACUGGCCAAGUAUGUUGCAACCCAGGGU ACCUUAUCUCGAAUUAUUGAUGAGUCAUUAUGUACUU UCAUGCCAGAGGGGACUGUGGAGCCAAAUGCCUU GUACCCGAGUAGUCCUCUGUCCAGAAUGCCUCCGG GGGUCCACCAAGUCCUGUGCUCGUACUCUUAUCCG GGUUUUUUGGGAACCGGUUCAUUUAUACAAGGGA ACCUAAUAGCCAAUUGUGCAUAAUUCUUUGUAAGU GUUACACAACAGGUACGAUUAUUAUACAAGCCUGA CAAGAUCUAAACAUACAUUGCUGCCGAUCGUGCCCG GUAGUCGAGGUGAACGGCGUGACCAUCCAGUCCGGA GCAGGAGGUUCCAGACGUCUGUAUCUUGCACAGAAU UGACCUCGGUCCUCCAUUAUUAUUGGAGGUGUUGGAC GUAGGGACAAAUUGGGGAUGCAAUUGCCAAAUUG GAGGAUGCCAAGGAUUGUUGGAUUAUUGGACAG AUAUUGAGAAGUAUGAAAGGUUUUAUCGAGCAUAGC AUAGUCUACAUCUGAUUGCAGUGUCUUGGAGGG UUGAUAGGAUCCCAUUAUUAUUGUUGCAGAGG GGGCUUGUAACAAAAGGGAGAACAAUUGGUUAUG	69

TABLE 13-continued

MeV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO.
	UCAAGACCAGGCCUAAAGCCUGACCUACAGGAACAU CAAAAUCCUAUGUAAGAU CGCUUUGAU GAUAAUAGG CUGGAGCCUCGGUGGCCAAGCUUCUUGCCCCUUGGGC CUCCCCCAGCCCCUCCUCCCUUCCUGACCCGUACC CCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG	
GC_F_MEASLES_B3.1 ORF Sequence, NT	AUGGGUCUCAAGGUGAACGUCUCUGCCGUUUCAUGG CAGUACUGUUAACUCUCCAAACACCCGCGGUCAAAU UCAUUGGGGCAUUCUCUAAGAUAGGGUAGUAGG AAUAGGAAGUGCAAGCUACAAGUUUAGACUCGUUC CAGCCAUCAAUCAUAGUCAUAAAUAUAGCCCAAU AUAACUCUCCCAAUAACUGCACGAGGUAGAGAUUG CAGAAUACAGGAGACUACUAAGAACAGUUUUGGAAC CAAUUAGGGAUGCACUUAAGCAUAGACCAGAACAU AAGGCCGGUUCAGAGCGUAGCUUCAGUAGGAGACAC AAGAGAUUUGCGGGAGUAGUCCUGGCAGGUGCGGCC UAGGUGUUGCCACAGCUGCU CAGAUAAAGCCGGCAU UGCACUUCACCGGUCCAUGCUGAACUCUCAGGCCAUC GACAAUCUGAGAGCGAGCCUGGAAACUACUAAUCAGG CAAUUGAGGCAUUCAGACAAGCAGGCGAGGAGUA UAUUGGCUGUUCAGGGUGUCCAAGACUACAUCAAUA AUGAGCUGAUACCGUCUAUGAACAGCUAUCUUGUA UCUAAUCGGUCAGAAUCUGGGUCUCAAUUGCUUAGA UACUUAUCAGAAAUCCUGUCAUUUUUGGCCCCAGCC UACGGGACCCCAUAUCUGCGGAGAUUUAUCCAGGC UUUGAGUUAUGCACUUGGAGGAGAUUAUCAAUAGGU GUUAGAAAGCUCGGAUACAGUGGAGGCGAUUUACU AGGCAUCUUAGAGAGCAGAGGAAUAAAGGCUCGGAU AACUCACGUCGACACAGAGUCCUACUUAUAGUCCUC AGUAUAGCCUUAUCCGACGUCUGUCCAGAUUAAGGGG UGAUUGUCCACCGGCUAGAGGGGUCUCGUACAACAU AGGCUCUCAAGAGUGGUUAUCCACUGUGCCCAAGUUA GUUGCAACCCAGGGUACCUUAUCUCGAAUUUUGAU AGUCAUCAUGUACUUUAUGCCAGAGGGGACUGUGU GCAGCCAAAUGCCUUUGUACCCGAGUAGUCCUCUGCU CCAAGAAUGCCUCCGGGGUCCACCAAGUCCUGUGCU CGUACACUCGUUACCGGGUCUUUUGGGAACCGGUUCA UUUUUAUCACAAGGGAACCUAAUAGCCAAUUGUGCAUC AAUUCUUUGUAAGUGUACACAACAGGUACGAUUAU UAAUCAAGACCCUGACAAGAUCUAAUACAUUAGCU GCCGAGUCGUGCCCGGUAGUCGAGGUGAACGGCGUGA CCAUCCAAAGUCGGGAGCAGGAGGUUCCAGAGCGUGU GUACUUGCACAGAAUUGACCUGGUUCCUCCAUUAUA UUGGAGAGGUUGGACGUAGGGACAAAUUGGGGAU GCAAUUGCCAAAUUGGAGGAUGCCAAGGAAUUGUUG GAAUCAUCGACCAAGAUUUGAGAGUAUGAAGGU UUUUCGAGCAUAGCAUAGUCUACUCCUGAUUGCAG UGUGUCUUGGAGGGUUGAUAGGGAUCCCAUUAUA UAUGUUGCUGAGGGGCGUUGUAAACAAAAGGGAG AACAAGUUGGUAUGUCAAGACAGGCCUAAAGCCUGA CCUUAACAGGAACAUCAAAUCCUAUGUAAGAUCCGUU UGA	70
GC_F_MEASLES_B3.1 mRNA Sequence (assumes T100 tail) mRNA Sequence Length: 1925	G*GGGAAUAAGAGAGAAAAGAAGUAAGAAGAAA UAUAAGAGCCACCAUGGGUCUCAAGGUGAACGUCUCU GCCGUUAUUAUGGCAGUACUGUUAACUCUCCAAACAC CCGCCGGUCAAUUAUUGGGGCAUUCUCUAAGAU AGGGGUAGUAGGAAUAGGAAGUGCAAGCUACAAGU UAUGACUCGUUCCAGCCAUCAAUUAUGUAUAAAA UUAAUGCCCAAUAUACUCUCUCAAUAACUGCACGA GGGUGAGAUUGCAGAAUACAGGAGACUACUAGAA CAGUUUUUGGAACCAAUUAAGGGAUGCACUUAUGCAA UGACCAGAAUAUAAGGCCGGUUCAGAGCGUAGCUUC AAGUAGGAGACACAAGAGAUUUGCGGGAGUAGUCCU GGCAGGUUGCGGCCUAGGUGUUGCCACAGCUGCUAG AUAACAGCCGGCAUUGCACUUCACCGGUCCAUUCUGA ACUCUCAGGCCAUUCGACAAUUGAGAGCGAGCCUGGA AACUACUAAUACAGGCAAUUGAGGCAAUCAGACAAGCA GGGCAGGAGAUAGUAUUGGCUGUUCAGGGUGUCCAA GACUACAUCAAUAUAGAGCUGAUACCGUCUAUGAAC AGCUAUCUUGUAUCUAAUCCGUCAGAAAGCUGGCU CAAUUGCUUAGAUACUAUACAGAAUCCUGUCAU	71

TABLE 13-continued

MeV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO:
	AUUUGGCCCCAGCCUACGGGACCCCAUAUCUGCGGAG AUAUCUAUCCAGGCUUUGAGUUAUGCAUUGGAGGA GAUAUCAUAAGGUGUUAAGAAAGCUCGGAUACAGU GGAGGCGAUUUAUAGGCAUCUAGAGAGCAGAGGA AUAAGGCGGGAUAACUCACGUCGACACAGAGUCCU ACUUCUAUAGUCCUCAGUAUAGCCUAUCCGACGUCGUC CGAGAUUAAGGGGUGAUUGUCCACCGGCUAGAGGG GGUUCUGUACAACAUAAGGCUUCAAGAGUGGUAUACC ACUGUGCCCAAGUAUGUUGCAACCCAAGGGUACCUUA UCUCGAAUUUUGAUAGUACAUCUAGUACUUUCAUGCC AGAGGGGACUGUGGACAGCCAAAAGCCUUGUACCCG AUGAGUCCUCUGCUCCAAGAAUGCCUCGGGGGUCCA CCAAGUCCUGGUCUGUACACUCGUUACCGGGUCCUU UGGGAACCGGUUCAUUUUAUCACAGGGAACCUAAU AGCCCAAUUGUGCAUCAAUUCUUUGUAAGUGUACAC AACAGGUACGAUUAUUAUCAAAGACCCUGACAAGAU CUAACAUACAUUGCUGCCGAUCCGUGCCCGUAGUCG AGGUGAACGGCGUGACCAUCCAAGUCGGGAGCAGGAG GUAUCCAGACGUCUGUACUUGCACAGAAUUGACCTC GGUCCUCCCAUAUCAUUGGAGAGGUUGGACGUAAGGG ACAAAUUCUGGGAAUGCAAUUGCCAAUUGGAGGAU GCCAAGGAUUUGUUGGAUAUCGAGACAGAUUUG AGAAGUAUGAAAGGUUUAUCGAGCAUAGCAUAGUC UACAUCUGAUGCAGUGUGUCUUGGAGGGUUGUA GGGAUCCCCACUUUAUUGUUGCUGCAGGGGGCGUU GUAACAAAAGGGAGAACAGUUGGUUUGUCAAGAC CAGGCCUAAAGCCUGACCUUACAGGAACAUCAAAUC CUAUGUAAGAUCGCUUUGAUUAUAGGCGUGGAGC CUCGGUGGCCAAGCUUCUUGCCCCUUGGGCCUCCCC CAGCCCCUCCCCUUCUGCACCUGUACCCCCGUGG UCUUUGAAUAAAGUCUGAGUGGGCGGCAAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAUCUAG	
GC_F_MEASLES_D8 Sequence, NT (5' UTR, ORF, 3' UTR) Sequence Length: 1864	UCAAGCUUUGGACCCUGUACAGAAGCUAAUACGAC UCACUAUAGGGAAUAAGAGAGAAAAGAGUUAAG AAGAAUAUAAGAGCCACCAUGGGUCUCAAAGGUGAA CGUCUCUGUACAUAUUAUGGCAUACUUAACUCUU CAAACACCCACCGGUCAAAUCCAUGGGGCAUUCUU CUAAGAUAGGGUGGUAGGGGUAGGAAGUGCAAGCU ACAAGUUAUGACUCGUUCCAGCACAUAUUAUAGU CAUAAAGUUAUUGCCCAAUAUAUCUCCUACAACAAU UGCACGAGGUAAGGAUUGCAGAAUACAGGAGACUA CUGAGAACAGUUCUGGAACCAAUUAAGAUUGCACUU AAUGCAAUGACCCAGAAUAUAGACCGGUUCAGAGU GUAGCUUCAAGUAGGAGACACAAGAGAUUUGCGGA GUUGUCCUGGAGGUGCGGCCUAGGCGUUGCCACAG CUGUCUAAAUAACAGCCGGUAUUGCACUUCACCAGUC CAUGCUGAACUCUACAGCCAUCCGACAAUCUGAGAGCG AGCCUAGAAAUCUAAUACAGGCAAUUGAGGCAAUCA GACAAGCAGGCGAGGAGAUUAUUGGCGUUCAGG GUGUCCAAAGACUACAUCAAUAAUAGGCUGAUACCGUC UAUGAAUCAACUAUCUUGUGAUUUAUUCGGCCAGAA GCUAGGGCUCAAUUGCUCAGAUACUAACAGAAUUC CUGUCAUUAUUGGCCCAAGCUUACGGGACCCAUUAU CUGCGGAGAUUAUCUUAUCCAGGCUUUGAGCUAUGCUCU UGGAGGAGAUUAUAAAGGUGUUGGAAAGCUCGG AUACAGUGGAGGUGAUUACUGGGCAUCUUAAGAGAG CAGAGGAUUAAGGCCCGGAUAACUCACGUCGACACA GAGUCCUACUUAUUGUACUCAGUAUAGCCUAUCCGA CGCUAUCGAGAUUAAGGGGUGAUUGUCCACCGGCU AGAGGGGUGUCGUACAACAUAAGGCUUCUACAGAGUG GUUAUCCACUGGCCCAAGUAUUGUACAACCAAGGG UACCUUAUCGAAUUUUGAUAGAGUACAUCAGCACUU UCAUGCCAGAGGGGACUGUGGACGCCAGAAUGCCUU GUACCCGAGUAGUCCUCUGUCCAAAGAAUGCCUCCGG GGGUCCACUAAGUCCUGUGUCUGUACAUCGUAUCCG GGUUUUCGGGAACCGGUUCAUUUAUACAGGGGA ACCUAAUAGCCAAUUGGCAUCAUCCUUUGCAAGUG UUAACAACAGGAACAUAUUAUUAAGACCCUGAC AAGAUCUUAACAUAUUGCUGCCGAUACUGCCCGG	72

TABLE 13-continued

MeV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO.
	UGGUCGAGGUGAAUUGGCGUGACCAUCCAAGUCGGGA GCAGGAGGUAUCCGACGCGUGUACUUGCACAGGAU UGACCUCGGUCCUCCAUUAUCUUUGGAGAGGUUGGAC GUAGGGACAAAUUCUGGGGAUUGCAAUUGCUAAGUUG GAGGAUGCCAAGGAAUUGUUGGAGUCAUCGGACCAG AUUAUUGAGGAGUAUGAAAGGUUUUUCGAGCACUAGU AUAGUUUACAUCUUGAUUGCAGUGUGUCUUGGAGGA UUGAUAGGGAUCCCCGCUUUAUUAUGUUGCUGCAGG GGGCGUUGUAACAAGAGGGGAGAACAGUUGGUUUG UCAAGACCAGGCCUAAAGCCUGAUUUACAGGAACAU CAAAAUCCUAUGUAAGGUCACUCUGAUGAUAAUAGG CUGGAGCCUCGGUGGCCAAGCUUCUUGCCCCUUGGGC CUCCCCCAGCCCCUCCUCCUCCUCCGACCCCGUACC CCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG	
GC_F_MEASLES_D8 ORF Sequence, NT	AUGGGUCUCAAGGUGAACGUCUCUGUCAUAUUCUAG GCAGUACUGUUAACUCUUAACAACCCACCGGUCAAA UCCAUUGGGGCAUUCUCUUAAGAUAGGGGUGGUAG GGGUAGGAAGUGCAAGCUACAAAGUUAUGACUCGUU CCAGCCAUCAAUUAUAGUCAUAAAGUUAUUGCCCAA UAUAACUCUCCUCAACAUAUUGCACGAGGGUAGGGAUU GCAGAAUACAGGAGACUACUGAGAACAGUUCUGGAA CCAAUUAAGAGAUAGCAUUAUUGCAAUGACCCAGAAUA UAAGACCGGUUCAGAGUGUAGCUUCAAGUAGGAGAC ACAAGAGAUUUGCGGGAGUUGUCUGGCAGGUGCGG CCCUAGGCGUUGGCCACAGCUGUCUCAAUAACAGCCGG UAUUGCACUUCACCAAGUCCAUUGCUAUCUUAAGCC AUCGACAAUCUGAGAGCGAGCCUAGAAACUACUAAUC AGGCCAAUUGAGGCAAUCAAGCAAGCAGGGCAGGAGA UGAUAUUGGCGUUGCAGGGUGUCCAGAGCUACAUCA AUAUAGAGCUGAUACCGUCUAUGAAUCAAUUCUU GUGAUUUAAUCGGCCAGAAGCUAGGGCUCAAUUGC UCAGAUACUAUACAGAAAUCCUGUCAUUAUUGGCC CAGCUUACGGGACCCCAUAUCUGCGGAGAUUUAUC CAGGCUUUGAGCUAUGCGUUGGAGGAGAUUCAAU AAGGUGUUGGAAAAGCUCGGAUACAGUGGAGGUGAU CUACUGGGCAUCUUAGAGAGCAGAGGAUAAAGGCC GGAUAACUCACGUCGACACAGAGUCCUACUUAUUGU ACUCAGUAUAGCUAUCCGACGCUAUCGAGAUUAAG GGGGUGAUUGUCCACCGGCUAGAGGGGUGUCUGUACA ACAUAGGCUCUCAAGAGUGGUUAACACUGUGCCCAA GUAUGUUGCAACCCAGGGUACCUUAUCUGAAUUAU GAUGAGUCAUACUGCACUUUUAUGCCAGAGGGGACUG UGUGCAGCCAGAAUGCCUUGUACCCGAGAGUCCUCU GCUCCAAGAAUGCCUCCGGGGUCCACUAAGUCCUGU GCUCGUACACUCGUUCCGGGUCUUUCGGGAACCGGU UCAUUUUUAUCAGGGGAACCUAAUAGCCAAUUGUGC AUCAAUCCUUUGCAAGUGUUAACAACAGGAACAAUC AUUAUACAAGACCCUGACAAGAUCUAAACUACAUUG CUGCCGAUACUGCCCGGUGGUCAGGUGAAUGGCGU GACC AUCCAAGUCGGGAGCAGGAGGUUCCGGACGCU GUGUACUUGCACAGGAUUGACCUUGGUCUCCCAUAU CUUUGGAGAGGUUGGACGUAGGGAUCAAUCUGGGGA AUGCAAUUGCUAAGUUGGAGGAUGCCAAGGAUUGU UGGAGUCAUCGGACCAGAUUAUGAGGAGUAGAAAG GUUUUUCGAGCACUAGUAUAGUUUAUUAUCUGAUUG CAGUGUGUCUUGGAGGAUUGAUAGGGAUCCCGCUU UAAUAUGUUGCUGCAGGGGGCGUUGUAAACAAGAGG GAGAAACAGUUGGUUUGUUAAGACCAAGCCUAAAGCC UGAUCUUACAGGAACAUAUAAUCCUAUGUAAGGUC ACUCUGA	73
GC_F_MEASLES_D8 mRNA Sequence (assumes T100 tail) Sequence Length: 1925	G*GGGAAUAAGAGAGAAAAGAAGAGUAAGAAGAAA UUAAGAGCCACCAUGGGUCUAAGGUGAACGUCUCU GUCAUAUUAUGGCAGUACUGUUAACUCUCAAACAC CCACCGGUCAAUCCAUUGGGGCAUUCUCUUAAGAU AGGGGUGGUAGGGGUGAGGAUGCAAGCUACAAGU UAUGACUCGUUCCAGCCAUCAUUAUUGCAUAAAG UUAUUGCCCAAUAUAAUCUCCUCAACAUAUUGCACA GGUAGGGAUUGCAGAAUACAGGAGACUACUGAGAA CAGUUCUGGAACCAAUUAAGAGUACUUAUUGCAA UGACCCAGAAUAUAGACCGGUUCAGAGUGUAGCUUC	74

TABLE 13-continued

MeV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO:
	AAGUAGGAGACACAAGAGAUUUGCGGGAGUUGUCU GGCAGGUGCGGCCUAGGCGUUGCCACAGCUGCUCAA AUAACAGCCGGUAUUGCACUUCACCAGUCCAUUGCUGA ACUCUCAAGCCAUCGACAAUCUGAGAGCGAGCCUAGA AACUACUAAUCAGGCAAUUGAGGCAAUCAGACAAGCA GGGCAGGAGAUGAUAUUGGCGUUCAGGGUGUCCAA GACUACAUCAAUAAUGAGCUGAUACCGUCUAUGAAUC AACUAUCUUGUGAUUUAAUCGGCCAGAAGCUAGGGC UCAAAUUGCUCAGAUACUAUACAGAAAUCCUGUCAU AUUUGGCCCCAGCUUACGGGACCCCAUUCUGCGGAG AUAUCUAUCCAGGCUUUGAGCUAUGCUGUUGGAGGA GAUAUCAUAAGGUGUUGGAAAGCUCGGAUACAGU GGAGGUGAUUCUACUGGGCAUCUAGAGAGCAGAGGA AUAAGGGCCCGGAUAACUCACGUCGACACAGAGUCCU ACUUCAUUGUACUCAGUAUAGCCUAUCCGACGCUAUC CGAGAUUAAAGGGGUGAUUUGCCACCGGCUAGAGGG GGUCUCGUACAACAUAAGGCUUCUACAGAGUGGUAUAC ACUGUGCCCAAGUAUGUUGCAACCAAGGGUACCUUA UCUCGAAUUUUGAGUAGUCAUAGCACUUCAUGCC AGAGGGGACUGUGGACAGCCAGAAUGCCUUGUACCCG AUGAGUCCUCUGCUCACAGAAUGCCUCGGGGGUGCCA CUAAGUCCUGUGCUCGUACACUCGUUCCGGGUCUUU CGGGAACCGGUUCAUUUAUACAGGGGAACCUAAUA GCCAAUUGUGCAUCAUCCUUGCAAGUGUACACAA CAGGAACAUAUAAUAAUAGACCCUGACAAGAUCU AACAUACAUUGCUGCCGAUCACUGCCCGGUGGUCGAG GUGAAUGGCGUGACCAUCCAGUCCGGAGCAGGAGG UAUCCGGACGCGUGUACUUGCAGGAUUGACCUCG GUCCUCCCAUAUCUUUGGAGAGGUUGGACGUAGGGAC AAAUUCUGGGAAUGCAAUUGCUAAGUUGGAGGAUGC CAAGGAAUUGUUGGAGUCAUCGACCAAGAUUUGAG GAGUAUGAAAGGUUUAUCGAGCACAUGAUAGUUUA CAUCCUGAUUGCAGUGUUCUUGGAGGAUUGAUAGG GAUCCCGCUCUAAUAUGUUGCUGAGGGGCGUUGU AACAAGAAGGGAGAACAAAGUUGGUUAUGUCAAGACCA GGCUAAAGCCUGAUCUACAGGAACAUCAAAACCU AUGUAAGGUCACUCUGAUGAUAAUAGGCUAGGACCU CGGUGGCCAAGCUUCUUGCCCCUUGGGCCUCCCCCA GCCCCUCCUCCUUCUGCACCCGUAACCCCGUGGUC UUUGAAUAAAGUCUGAGUGGGCGGCAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAUCUAG	
GC_H_MEASLES_B3 Sequence, NT (5' UTR, ORF, 3' UTR) Sequence Length: 2065	UCAAGCUUUUGGACCCUGUACAGAAGCUAAUACGAC UCACUAUAGGGAAUAAGAGAGAAAGAGAGUAG AAGAAUAUAAGAGCCACCAUGUCACCCGCAACGAGAC CGGAUAAUUGCCUUCUACAAAGAUAAACCUAUCCCA AGGGAAGUAGGAUAGUUUAACAGAGAAACUUCUA UGAUUGACAGACCCUAUGUUCUGCUGGCUGUUCUGU CGUCAUGUUCUGAGCUUGAUCCGGAUUGCUGGCAAU UGCAGGCAUUAAGACUUCUACGGGACGCAUCUACACC GCGGAGAUCCAUAAAGCCUAGUACCAUUCUGGAUG UGACUAAUCUCCAUUCGAGCAUCAGGUCAAGGACGUGCU GACACCACUCUUUAAAUCAUCGGGGAUGAAGUGGGC CUGAGAACACCUCAAGAGAUUACUGACCUAGUGAAAU UCAUCUCGGACAAGAUUAAAUUCUUAUCCGGAUAG GGAGUACGACUUCAGAGAUUCACUUGGUGCAUAAAC CCGCCAGAGAGGAUCAAACUAGAUAUAGAUCAAUACU GUGCAGAUGUGGCUUGCAAGAGCUCAUGAAUGCAU UGGUGAACUCAACUCUACUGGAGACCAGAACAACAC UCAGUUCUAGCUGUCUCAAAGGGAACUGCUCAGGG CCCACUACAAUCAGAGGUCAAUUCUAAACAUUGCGC UGUCCUUGUUGGACUUGUACUAGGUCGAGGUACA AUGUGUCAUCUAUAGUACUAUGACAUCCAGGGAAU GUAUGGGGAACCUACCUAGUUGAAAGCCUAAUCU GAACAGCAAAGGGUCAGAGUUGUACAACUGAGCAU GUACCGAGUGUUUGAAGUAGGUGUGAUCAAGAAACC GGGUUUGGGGCUCCGUGUUCUUAUGACAAACUA UUUUGAGCAACAGUCAGUAUAGGUCUCGGCAACUGU AUGGUGGCUUUGGGGAGCUCAAUCGCGAGCCUUU GUCACGGGACGAUUCUAUAAUUCUUAUCAGG	75

TABLE 13-continued

MeV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO.
	AUCAGGGAAGGUGUCAGCUUCCAGCUCGUCAGCUG GGUGUCUGGAAAUCCTCAACCGACAUGCAAUCCUGGG UCCCCUUAUCAACGGAUGAUCCAGUGGUAGACAGGCU UUACCUCUCAUCUCACAGAGGUGUCAUCGUCGACAAU CAAGCAAAAUGGGCUGUCCCGACACACGAACAGAUG ACAAGUUGCGAAUGGAGACAUGCUUCCAGCAGGCGUG UAAAGGUAAAAUCCAGCACUCUGCGAGAAUCCCGAG UGGGUACCAUUGAAGGAUAACAGGAUUCUUAUAC GGGUGUCCUGUCUGUUGAUCUGAGUCUGACGGUUGAG CUUAAAAUCAAAUUGCUUCCGGGAUUCGGCCAUUG AUCACACACGGCUCAGGGAUGGACCUAUAACAAUCCA ACUGCAACAAUGUGUAUUGGUGACUAUUCGCGCAAU GAGAAAUUAGCCUUAAGGCGUAUUAACACAUUGGA GUGGAUACCGAGAUUCAAGGUUAGUCCCAACCUUUC ACUGUCCCAAUUAAGGAAGCAGGCGAAGCUGCCAUUG CCCCAACAUACCUACCUUGCGGAGGUGGACGGUGAUGU CAAACUCAGUUCACACUGGUGAUUUAACUGGUCAA GAUCUCCAAUAGUUUUGGCAACCUACGAUACCUCCA GGGUUGAGCAUGCUGUGGUUUAUACGUUUACAGCC CAAGCCGCUCAUUUUCUUAUUAUCCUUUUAGGUU GCCUAUAAGGGGGUCCAAUCGAACUACAGUGGAA UGCUUACAUGGGAUCAAACUUGGUGCCGUCACU UCUGUGUCUUGCGGACUCAGAAUCCGUGGACUUAU CACUCACUCUGGGAUGGUGGCAUGGGAGUCAGCUGC ACAGCUACCCGGGAAGAUGGAACCAUUCGAGAUAAU GAUAAUAGGCUUGGAGCCUCGUGGCGCAAGCUUCUUGC CCUUGGGCCUCCCCCAGCCCCUCCUCCCUUCCUGC ACCCGUACCCCCGUGGUUUUGAAUAAAGUCUGAGUG GGCGGC	
GC_H_MEASLES_B3 ORF Sequence, NT	AUGUCACCGCAACGAGACCGGAUAAAUGCCUUCUACA AAGAUAACCCUUAUCCCAAGGGAAGUAGGAUAGUUA UUUACAGAGAAUUAUUGAUUGACAGACCCUUAUG UUCUGCUGGCGUUUCUGUUCGUAUGUUUCUGAGCUU GAUCGGAUUGCUGGCAUUGCAGGCAUUAAGCUUCA UCGGGACGCCAUUACACCGCGAGAUCCAUAAGGC CUCAGUACCAUUCUGGAUGUGACUAACUCCAUUCGAGC AUCAGGUCAAGGACGUGCUGACACACUUAUAAAU CAUCGGGGAUGAAGUGGGCCUGAGAACCCUCAGAGA UUCACUGACCUAGUAAAUAUUAUCUGGACAGAUUA AAUUCUUAUCCGGAUAGGGAUACGACUUCAGAG AUCUCACUUGGUGCAUACACCGCCAGAGAGGAUCAA ACUAGAUAUGAUCAAUACUGGCGAUGUGGCGUC UGAAGAGCUCUAGAAUGCAUUGGUGAACUACACUCU ACUGGAGACCGAACAACCAUCAGUUCUAGCUGUC UCAAGGGGAACUGCUCAGGGCCCAUACAACAGAG GUCAAUUCUCAAACAUUGCGCUGUCCUUGUUGGACUU GUACUUAAGGUCGAGGUUACAAGUGUCUUAUAGU CACUAUGACAUCACAGGGAUGUAUGGGGGAACCUAC CUAGUUGAAAAGCCUAAUCUGAACAGCAAGGGUCA GAGUUGUCACAACUGAGCAUGUACCGAGUGUUUGAA GUAGGUGUGAUCAGAAACCCGGUUUGGGGCUCCG GUGUUCUUAUGACAAACUUAUUUGAGCAACAGUCA GUAAUGGUCUCGGCAACUGUAUGGUGCUUUUGGGG AGCUCAAACUCGACGCCUUUGUCACGGGGACGAUUC UAUCAUAUUUCCUUAUCAGGGAUCAGGGAAGGUGU CAGCUUCAGCUCGUAAGCUGGGUGUCUGGAAUCC CCAACCGACAUGCAAUCCUGGGUCCCUUAUCAACGG AUGAUCCAGUGGUAAGACAGGCUUUAACUUCUAUCU CAGAGGUGUCUUCGUGACAACAGCAAAUUGGGCU GUCCCGACAACACGAACAGAUACAAGUUGCGAAUGG AGACUUCUUCAGCAGGCGUGUAAGGUUAAAUCCA AGCACUCUGCGAGAAUCCGAGUGGGUACCAUUGAAG GAUAAACAGGAUCCUUAUACGGGUGUCUGUCUGUUG AUCUGAGUCUGACGGUUGAGCUUAAAAUCAAUUG CUUCGGGAUUCGGGCCAUUGAUCACACACGGCUCAGG GAUGGACCUUAACAAUCCACUGCAACAAGUGUUAU UGGCUAGCUUAUCCGCAAGAGAAAUUAAGCCUUG GCGUAAUCAAACAUAUUGGAGUGGAUACCGAGAUUCA AGGUUAGUCCCAACCUUUCACUGUCCCAAUUAAGGA AGCAGGCGAAGACUGCCAUUGCCCCAACAUACCUACCU GCGGAGGUGGACGGUGAUGUCAACUAGUUCCAACC	76

TABLE 13-continued

MeV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO.
	UGGUGAUUCUACCUUGGUCAGAUCUCCAAUAUGUUU UGGCAACCUACGAUACCUCCAGGGUUGAGCAUGCUGU GGUUUUAUACGUUUACAGCCCAAGCCGUCAUUUUCU UACUUUUUACUUUUAGGUUGCCUAUAAAGGGGUC CCAUUCGAACUACAAGUGGAUGCUUCACAUGGGAUC AAAAAUCUGGUGCCGUCACUUCUGUGUGCUUGCGGA CUCAGAAUCCGGUGGACUUAUCACUCACUCUGGGGAG GUGGGCAUGGGAGUCAGCUGCACAGCUACCCGGGAAG AUGGAACCAUUCGACAGUAA	
GC_H_MEASLES_B3 mRNA Sequence (assumes T100 Tail) Sequence Length: 2126	G*GGGAAUAAGAGAGAAAAGAAGAGUAAGAAGAAA UAUAAGAGCCACCAUGUCACCGCAACGAGACCGGAUA AAUGCCUUCUACAAAGAUACCCUUAUCCCAAGGGAA GUAGGAUAGUUAUUAACAGAGAAACUUAUAGAUUG ACAGACCCUAUGUUCUGCUGGCUGUUCUGUUCGUCAU GUUUCUGAGCUUGAUCGGAUUGCUGGCAUUGCAGG CAUUAAGACUUCUACCGGCGAGCCAUUACACCGCGGAG AUCCAUAAGGCCUCAGUACCAUUCUGGAUGUGACUA ACUCCAUCGAGCAUCAGGUCAGGACGUGCUGACACC ACUCUUUAAAAUCAUCGGGGAUGAAGUGGGCCUGAG AACACCUUCAGAGAUUCACUGACCUAGUGAAAUUCUUC UCGGACAAGAUUAAAUUCCUUAUCCGGAUAGGGAG UACGACUUCAGAGAUUCACUUGGUGCAUACCCGCG CAGAGAGGAUCAAACUAGAUUAUGAUCAAUACUGUG CAGAUGUGGCUGCUGAAGAGCUCAUGAAUGCAUUGG UGAACUCAAUCUACUGGAGACCAAGAAACAACACUCA GUUCCUAGCUGUCUCAAAGGGAAACUGUCUAGGGCCC ACUACAAUCAGAGGUCAAUUCUCAAACUAGUCGUGU CCUUGUUGGACUUGUACUUAAGGUCGAGGUUACAAUG UGUCAUCUUAUAGUCACUAGACAUCCAGGGAAUGUA UGGGGGAACCUACCUAGUUGAAAAGCCUAAUUCUGAAC AGCAAAGGGUCAGAGUUGUCAACUGAGCAUGUACC GAGUGUUUAGUAGUAGGUGUGAUCAGAAACCCGGU UGGGGGCUCCGGUGUUCUUAUAGACAAACUUAUUG AGCAACCAGUCAGUAAUGGUCUCGGCAACUGUAUGGU GGCUUUGGGGAGCUCAAACUCGACGCCUUUGUCAC GGGGACGAUUCUUAUCAAUUAUCCUUAUCAGGGAUCAG GGAAGGUGUCAGCUUCACGUCUGCAAGCUGGGUGU CUGGAAAUCCCAACCGACAUAGCAUUCUGGGUCCCC UUAUCAACGGAUGAUCCAGUGGUAGACAGGCUUUAAC UCUCUUCUACAGAGGUGUCUUCGUGACAAUCAAAGC AAAAUGGGCUGUCCCGACAACACGAACAGAUACAAAG UUGCGAAUGGAGACAUUCUUCAGCAGGCGUGUAAA GGUAAAAUCCAAGCACUCUGCGAGAAUCCCGAGUGGG UACC AUUGAAGAUAAACAGGAUUCUUAUACGCGGG UCCUGUCUGUUGAUUCUAGUCUGACGUGUAGCUUA AAAUCAAAUUGCUUCGGGAUUCGGGCCAUUGAUACAC ACACGGCUCAGGGAUGGACCUAUACAAUCCAAUCUGC AACAAUGUGUAUUGGCUAGCUAUUCCGCCAAUGAGA AAUCUAGCCUUAAGGCGUAAUCAACAUAUUGGAGUGG AUACCGAGAUUCAAGGUUAGUCCCAACCUUUCACUG UCCCAAUUAAGGAAGCAGGCGAAGACUGCCAUUGCCCC AACAUACCUACCUUGCGAGGUGGACGGUGAUGUCAAA CUCAGUCCAAACUGGUGAUUCUACUGGUCAGAUC UCCAAUAUGUUUUGGCAACCUACGAUACUUCAGGGU UGAGCAUGCUGUGGUUAUUAACGUUUUACGCCAAGC CGCUCAUUUUUUAUUAUCCUUUUAGGUUGCCUA UAAAGGGGUGCCAAUUCGAACUACAGUGGAAUGCU UCACAUGGGAUCAAACUUCUGGUGCCGUCACUUCUG UGUGCUUGCGGACUCAGAAUCCGGUGGACUUAUCACU CACUCUGGGAUGGUGGCAUGGGAGUCAGCUGCACAG CUACCCGGGAAGAUUGGAACCAUUCGAGAUAAUGAUA AUAGGCGGAGCCUCGUGGGCCAAGCUUUCUUGCCCU UGGGCCUCCCCCAGCCCUCCUCCCCUUCUGCACCC GUACCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCG GCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAUCUAG	77

TABLE 13-continued

MeV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO.
GC_H_MEASLES_D8 Sequence, NT (5' UTR, ORF, 3' UTR) Sequence Length: 2065	UCAAGCUUUUGGACCCUCGUACAGAAGCUAAUACGAC UCACUUAUAGGGAAUUAAGAGAGAAAAGAGUAAG AAGAAAUUAAGAGCCACCAUGUCACCACAACGAGAC CGGAUAAUAGCCUUCUACAAAGACAACCCCAUCCUA AGGGAAGUAGGAUAGUUAUUAACAGAGAACAUCUUA UGAUUGAUAGACCUUAUGUUUUGCUGGCUGUUCUUAU UCGUCAUGUUUCUGAGCUUGAUCGGGUUGCUAGCCAU UGCAGGCAUUAAGACUUCUUCGGGCAGCCAUUACACC GCAGAGAUCUAAAAGCCUCAGCACCAAUUCUGGAUG UAAUCUAAUCUAAUCGAGCAUCAGGUUAAGGACGUGCU GACACCACUCUUAAGAUAUCUGGUAUGAAGUGGGC UUGAGGACACCUAGAGAUCUACUGACCUAGUGAAGU UCAUCUCUGACAAGAUUAAAUUCUUAUCCGGACAG GGAAUACGACUUCAGAGAUCUACUUGGUGUAUCAAC CCGCCAGAGAGAAUCAAUUGGAUUAUGAUCAAUAC UGUGCAGAUUGGCUGCUGAAGAACUUAUGAAUGCA UUGGUGAAUCUACUCUACUGGAGACCAGGGCAACCA AUCAGUUCUAGCUGUCUCAAAGGGAACUGCUCAGG GCCCACUACAUCAGAGGCCAAUUCUAAACAUGUCG CUGUCCCUGUUGGACUUGUAUUUAAGUCGAGGUUAC AAUGUGUCAUCUAUAGUCACUAUGACAUCUCCAGGAA UGUACGGGGGAACUUAACUAGUGGAAAAGCCUAAUC UGAGCAGCAAAGGGUCAGAGUUGUCACAACUGAGCA UGCACCGAGUGUUUGAAGUAGGUGUUAUCAGAAAUC CGGGUUUGGGGCUCCGGUAUUCUAUAGACAACUA UCUCUGAGCAACAGUCAGUAUAGAUUUCAGCAACUGC AUGGUGGCUUUGGGGAGCUCAGUUCGAGCCUCUCU GUCACAGGGAAGAUUCUACACAUAUCCUUAUCAGGG AUCAGGGAAGGUGUCAGCUUCCAGCUUGUCAAGCUA GGUGUCUGGAAAUCUCCAAACGACAUGCAAUCCUGGG UCCCCUUAUCAAACGGAUGAUCCAGUGAUAAGACAGGCU UUACCUCUCAUCUCACAGAGGCGUUAUCGUGACAACU CAAGCAAAUUGGGCUGUCCCGACAACACGGACAGAUG ACAAGUUGCGAAUGGAGACAUGCUUCCAGCAGGCGUG UAAGGGUAAAUCUACAGCACUUUGCGAGAAUCCCGAG UGGACACCAUUGAAGGAUAACAGGAUUCUUAUACG GGGUCUUGUCUGUUUAUCUGAGUCUGACAGUUGAGC UUAUUUAUCAAUUGUUAUCAGGAUUCGGGCCAUUGA UCACACACGGUUCAGGGAUGGACCUUAUCAAUCCAA CCACAACAUAUUGUAUUGGCUAGCUAUCUCCGCCAAUG AAGAACCUUGGCCUUAAGGUGUAUUAACACAUUGGAG UGGAUACCGAGAUUAAGGUUAGUCCCAACCUUUA CUGUUCUAAUUAAGGAAGCAGGCGAGGACUGCCAUGC CCCAACAUAACUACUUGCGGAGGUGGAUGGUAUGUC AAACUCAGUUCCAAUCUGGUGAUUUAUCCUGGUCAG AUCUCAAUAUGUUUUGGCAACCUACGAUAUUAUCCAG AGUUGAAUAGUCUGUAGUUUAUUAACGUUAACAGCCC AAGCCGCUCAUUUUUAUUAUUAUCCUUUAGGUUG CCUGUAAGGGGGUCCCAUUGAAUUAUAAAGUGGAA UGCUUCAUAGGGACCAAAACUCUGGUGCCGUCACU UCUGUGUCUUGCGGACUCAGAAUCUGGUGGACUAU UCACUACUUCUGGGAUGGUGGCAUUGGAGUACAGCUG CACAGCCACUUGGGAAGAUUGGAACCAAGCCGAGAUAG UGAUAAUAGGUGGAGCCUUGGUGGCCAAGCUUCUUG CCCUUGGGCUCCCCCAGCCCCUCCUCCCUUCCUG CACCCGUACCCCGUGGUCUUUGAAUAAAGUCUGAGU GGGCGGC	78
GC_H_MEASLES_D8 ORF Sequence, NT	AUGUCACCACAACGAGACCGGAUAAAUGCCUUCUACA AAGACAACCCCAUCCUAAAGGAAGUAGGAUAGUUAU UAACAGAGAAUUAUUAUGAUUAGACCUUAUUGU UUUGCUGGCUUUAUUAUCGUAUUAUUGGAGCUU GAUCGGGUGCUAGCCAUUGCAGGCAUUAAGACUUAU CGGGCAGCCAUUAACACCGCAGAGAUUAUAAAAGCC UCAGCACCAUUCUGGAUGUAACUAACUCAAUCGAGCA UCAGGUUAAGGACGUGCUGACACCAUUAUUAAGAUC AUCGGUGAUGAAGUGGCUUGAGGACACCUAGAGA UUCACUGACCUAGUGAAGUUAUUAUUGACAAAGAUUA AAUUCUUAUUAUCCGACAGGGAUUAACAGCUUCAGAGA UUCACUUGGUGUAUUAACCCGCCAGAGAGAAUCAA UUGGAUUAUGAUCAAUACUGGUCAGAUUGGUGUCU	79

TABLE 13-continued

MeV Nucleic Acid Sequences		SEQ ID NO :
Description	Sequence	
	GAAGAACUCAUGAAUGCAUUGGUGAACUCAACUCUAC UGGAGACCAGGGCAACCAAUCAGUCCUAGCUGUCUC AAAGGGAACUGUCUACAGGGCCCAUCACAAUCAGAGGC CAAUUCUCAAAACAUUGCUCGUCGCCUGUUGGACUUGU AUUUAAGUCGAGGUUACAAGUGUCAUCAUAGUCA CUAUGACAUCCAGGGAUUGUACGGGGAAUUAACCU AGUGGAAAAGCCUAAUCUGAGCAGCAAAGGGUCAGA GUUGUCACAACUCGAGCAUGCACCGAGUGUUGAAGU AGGUGUUAUCAGAAAUCCGGGUUUGGGGGUCCGGU AUUCCAUAUGACAAACUAUCUUGAGCAACAGUCAGU AAUGAUUUUCAGCAACUGCAUGGUGGUUUUGGGGGAG CUCAGAUUCGAGCCUCUGUCACAGGGAAGAUUCUA UCACAAUUCCCUAUACAGGGAUCAGGGAAGGUGUCAG CUUCCAGCUUGUCAAGCUAGGUGUCUGGAAAUCCCCA ACCGACAUGCAAUUCCUGGGUCCCCUAUCAACGGAUG AUCCAGUGAUGAGCAGGCUUUAACCUUCAUCUCACAG AGGCGUUAUCGUCGACAUAACAGCAAAUUGGGCUGUC CCGACAACCGACAGAUGACAAGUUGCGAAUGGAGA CAUGCUCACAGCAGGCUGUUAAGGGUAAAAUCCAAGC ACUUGCGAGAAUCCGAGUGGACACCAUUGAAGGAU AACAGGAUUCUUCAUACGGGGUUCUGUCUGUUGAU UGAGUCUGACAGUUGAGCUUAAAUCAAAUUGUUU CAGGAUUCGGGCCAUUGAUCACACCGGUUCAGGGAU GGACCUAUAACAAUCCAACCAACAUAUGUAUUGG CUGACUAUCCCGCCAAUGAAGAACUUGGCCUAGGUG UAAUCAACACAUUGGAGUGGAUACCGAGAUUCAAGG UUAGUCCCAACCUUCUACUGUUCCAAUUAAGGAAGC AGGCGAGGACUGCCAUGCCCCACAUAUCCUACCGCG GAGGUGGAUGGUGAUGUCAAAUCAGUUCCAAUCUG GUGAUUCUACCGUGGCAAGAUUCUCAAUAUGUUCUGG CAACCUACGAUACUUCAGAGUUGAACAUUGCUGUAGU UUUAUACGUUUACAGCCCAAGCCGCUCAUUUUCUUA UUUUAUCCUUUAGGUUGCCUGUAAGGGGGUCCCCA UUGAAUUAACAAGUGGAAUGCUUACAUGGGGACCAA AACUCUGGUGCCGUCACUUCUGUGUCUUGCGGACUC AGAAUUCUGGUGGACAUUAUCACUCUGGGAGUGU GGGCAUGGGAGUCAGCUGCACAGCCACUCGGGAAGAU GGAACAGCCGACAGAUAG	
GC_H_MEASLES_D8 mRNA Sequence (assumes T100 tail) Sequence Length: 2126	G*GGGAAUUAAGAGAGAAAAGAAGUAAGAAGAAA UAUAAGAGCCACCAUGUCACCACACGAGACCGGAUA AAUGCCUUCUACAAAGACAACCCCAUCCUAAAGGGAA GUAGGAUAGUUAUUAACAGAGAACAUUUUAUGAUUG AUAGACCUUAUGUUUUGCUGGCUUGUUAUUCGUCA UGUUUCUGAGCUUGAUCCGGUUGCUAGCCAUUGCAG GCAUUAAGACUUAUCGGGCAGCCAUUCACACCGCAGA GAUCCAUAAAAGCCUCAGCACCAAUUGGAUGUAACU AACUCAUUCGAGCAUCAGGUUAAGGACGUGCUGACAC CACUCUUAAGAUAUCGGUGAUGAAGUGGGCUUGA GGACACCUAGAGAUUACUGACCUAGUGAAGUUAU CUCUGACAAAGAUUAAAUCCUUAUCCGGACAGGGAA UACGACUUCAGAGAUUCUACUUGGUGUAUCAACCCGC CAGAGAGAAUCAAUUGGAUUAUGAUCAAUAUCUGUG CAGAUGUGGCUGCUGAAGAACUCAUGAAUGCAUUGG UGAACUCAACUCUACUGGAGACCGGGCAACCAAUCA GUUCCUAGCUGUCUCAAAGGGAAACUGUCAGGGGCC ACUCAAAUCAGAGGCCAAUUCUCAAACAUUGCUGU CCUGUUGGACUUGUAUUUAAGUCGAGGUUACAAG UGUCAUUAUAGUCACUAUGACAUCCAGGGAUUGUA CGGGGGAACUUAUCCUAGUGGAAAAGCCUAAUUCGAGC AGCAAAGGGUCAGAGUUGUCACAACUGAGCAUGCACC GAGUGUUUAGUAGGUGUUAUCAGAAUCCGGGU UGGGGGUCUCCGUUAUCCAUAUGACAAACUAUCUUGA GCAACCAGUCAGUAUUGAUUUCAGCAACUGCAUGGUG GCUUUGGGGGAGCUCAAGUUCGACGCCUCUGUCACA GGGAAGAUUCUAUACAAAUUCCUUAUCAGGGAUCAGG GAAAGGUGUCAGCUUCAGCUUGUCAAGCUAGGUGUC UGGAAAUCCCCAACCGACAUGCAUCCUGGGUCCCC UAUCAACGGAUGAUCCAGUGAUGACAGGCUUUAACCU CUCAUCUCACAGAGGCUGUAUCGUGACAUAUACAGCA AAUUGGGCUGUCCGACAACACGGACAGAUGACAAGU UGCGAAUGGAGACAUGCUCCAGCAGGCGUGUAAGG	80

TABLE 13-continued

MeV Nucleic Acid Sequences		
Description	Sequence	SEQ ID NO:
	GUAAAAUCCAAGCACUUUGCGAGAAUCCCGAGUGGAC ACCAUUGAAGGAUAACAGGAUUCUUCUACGGGGUC UUGUCUGUUGAUUCUGAGUCUGACAGUUGAGCUUAAA AUCAAAAUUGUUUCAGGAUUCGGGCCAUUGAUCACAC ACGGUUCAGGGAUGGACCUAUACAAUCCAACCAAA CAAUAUGUAUUGGCUGACUAUCCCGCCAUGAAGAAC CUGGCCUUAGGUGUAAUACAACAUUGGAGUGGAUA CCGAGAUUCAAGGUUAGUCCCAACCUCUUCACUGUUC CAAUUAAGGAAGCAGGCGAGGACUGCCAUGCCCAAC AUACCUACCUGCGGAGGUGGUAUGUGUCAAACUC AGUUCCAAUCUGGUGAUUCUACCGGUCAAGAUCC AAUAUGUUCUGGCAACCUACGAUACUCCAGAGUUGA ACAUGCUGUAGUUUUAUACGUUUACAGCCCAAGCCGC UCAUUUUCUUAUUUUUAUCCUUUUAAGGUUGCCUGUA AGGGGGGUGCCCAUUGAAUUAACAAGUGGAUGCUUC ACAUGGGACCAAAAACUCUGGUGCCGUCACUUCUGUG UGCUUGCGGACUCAGAAUCUGGUGGACAUACACUCA CUCUGGGAUGGUGGCAUGGGAGUCAGCUGCACAGCC ACUCGGGAAGUGGAACAGCCGACAGUAGUGAUAA UAGGCUUGAGCCUCGGUGGCCAAGCUUCUUGCCCUU GGGCCUCCCCCAGCCCUCCUCCCUUCCUGCACCCG UACCCCGUGGUCUUUGAAUAAAGUCUGAGUGGGCGG CAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAUCUAG	

TABLE 14

MeV Amino Acid Sequences		
Description	Sequence	SEQ ID NO:
GC_F_MEASLES_B3.1 ORF Sequence, AA	MGLKVNVS AVFMAVLLTLQTPAGQIHWGNLSKIGVV GIGSASYKVMTRSSHQSLVIKLMPNITLLNNCTRVEIA EYRLLRTVLEPIRDALNMTQNIRPVQSVASSRRHK RFAGVVLAGAALGVATAAQITAGIALHRSMLNSQAID NLRASLETTNQAIEAIRQAGQEMILAVQGVQDYINNE LIPSMNQLSCDLIGQKLGLKLLRYYTEILSLFGPSLRDP ISAEISIQALSYALGGDINKVLEKLGYSGGDLLGILES GIKARITHVDTESYFIVLSIAYPTLSEIKGVIHVRLEGVS YNIGSQEWYTTVPKYVATQGYLISNFDSSCTFMPEG TVCSQNALYPMSPLLQECRLGSTKSCARTLVSGSFGN RFILSQGNLIANCASILCKCYTTGTIINQDPDKILTYIAA DRCPVVEVNGVTIQVGSRRYPDAVYLHRIDLGPPISE RLDVGTNLGNIAKLEDAKELLESDQILRSMKGLSST SIVYILIAVCLGGLIGIPTLICCCRGRCNKKGEQVMSR PGLKPDLTGTSKSYVRSI*	47
GC_F_MEASLES_D8 ORF Sequence, AA	MGLKVNVS VIFMAVLLTLQTPGQIHWGNLSKIGVVG VGSASYKVMTRSSHQSLVIKLMPNITLLNNCTRVGIAE YRLLRTVLEPIRDALNMTQNIRPVQSVASSRRHKK FAGVVLAGAALGVATAAQITAGIALHQSMNLNSQAIDN LRASLETTNQAIEAIRQAGQEMILAVQGVQDYINNELI PSMNQLSCDLIGQKLGLKLLRYYTEILSLFGPSLRDPIS AEISIQALSYALGGDINKVLEKLGYSGGDLLGILESRI KARITHVDTESYFIVLSIAYPTLSEIKGVIHVRLEGVSY NIGSQEWYTTVPKYVATQGYLISNFDSSCTFMPEGT VCSQNALYPMSPLLQECRLGSTKSCARTLVSGSFGNR FILSQGNLIANCASILCKCYTTGTIINQDPDKILTYIAAD HCPVVEVNGVTIQVGSRRYPDAVYLHRIDLGPPISE LDVGTNLGNIAKLEDAKELLESDQILRSMKGLSSTS IVYILIAVCLGGLIGIPALICCCRGRCNKKGEQVMSRP GLKPDLTGTSKSYVRSI*	48
GC_H_MEASLES_B3 ORF Sequence, AA	MSPQRDRINAFYKDNPPYKGSRIVINREHLMIDRPYVL LAVLFVFMFLSLIGLLAIAIGIRLHRAAIYTAIEIHKSLSTN LDVTNSIEHQVKDVLTPLFKIIGDEVGLRTPQRFTDLV KPISDKIKFLNPDRYDFRDLTWCINPPERIKLDYDQY	49

TABLE 14-continued

MeV Amino Acid Sequences		
Description	Sequence	SEQ ID NO:
	CADVAEEELMNALVNSTLLETRTTTQFLAVSKGNCS GPTTIRGQFSNMSLSLDDLVLGRGYNVSSIVTMTSQG MYGGTYLVEKPNLNSKGSLSQLSMYRVFEVGVIRNP GLGAPVFHMTNYFEQPVSNGLGNCMVALGELKLAAL CHGDDSIIPYQSGSGKGVSFQLVKLGWKSPTDMQSW VPLSTDDPVVDRLYLSSHRGVIADNQAKWAVPTTTRT DDKLRMETCFQQACKGKIQALCENPEWVPLKDNRIPS YGVLSVDLSLTVELKIKIASGFGPLITHGSGMDLYKSN CNNVYWLTIIPMRNLALGVINTLEWIPRFKVSPLFTV PIKEAGEDCHAPTYLPAEVDGDKLSSNLVILPGQDL QYVLATYDTSRVEHAVVYVYSPSRFSYFYPFRLPIK GVPIELQVECFDQKLWCRHFCVLADSESGGLITHS GMVGMGVSCATREDGTNR*	
GC_H_MEASLES_D8 ORF Sequence, AA	MSPQRDRINAFYKDNPHPKGSRIVINREHLMIDRPYVL LAVLFVMPFLSLIGLLAIAGIRLHRAAIYTAEIHKSLSTN LDVTNSIEHQVKDVLTPLFKIIGDEVGLRTPQRFDTLV KFISDKIKFLNPDREYDFRDLTWCINPERIKLDYDQY CADVAEEELMNALVNSTLLETRATNQFLAVSKGNCS GPTTIRGQFSNMSLSLDDLVLGRGYNVSSIVTMTSQGM YGGTYLVEKPNLSSKGSLSQLSMHRVFEVGVIRNPG LGAPVFHMTNYLEQPVSNDFSNCMVALGELKFAALC HREDSITIPYQSGSGKGVSFQLVKLGWKSPTDMQSW VPLSTDDPVIDRLYLSSHRGVIADNQAKWAVPTTTRTD DKLRMETCFQQACKGKIQALCENPEWTPLKDNRIPSY GVLSVDLSLTVELKIKIVSGFGPLITHGSGMDLYKSNH NNMYWLTIIPMKNLALGVINTLEWIPRFKVSPLFTV PIKEAGEDCHAPTYLPAEVDGDKLSSNLVILPGQDL QYVLATYDTSRVEHAVVYVYSPSRFSYFYPFRLPV RGVPIELQVECFDQKLWCRHFCVLADSESGGHITH SGMVGMGVSCATREDGTSRR*	50

TABLE 15

MeV NCBI Accession Numbers (Amino Acid Sequences)		
Type	Virus Name	GenBank Accession
hemagglutinin	hemagglutinin [Measles virus strain Moraten]	AAF85673.1
hemagglutinin	hemagglutinin [Measles virus strain Rubeovax]	AAF85689.1
hemagglutinin	hemagglutinin [Measles virus]	AAF89824.1
hemagglutinin	hemagglutinin protein [Measles virus]	CAA91369.1
hemagglutinin	hemagglutinin [Measles virus]	BAJ23068.1
hemagglutinin	hemagglutinin protein [Measles virus]	BAB39848.1
hemagglutinin	hemagglutinin [Measles virus]	AAA50551.1
hemagglutinin	RecName: Full = Hemagglutinin glycoprotein	P08362.1
hemagglutinin	hemagglutinin [Measles virus]	AAB63802.1
hemagglutinin	hemagglutinin [Measles virus]	AAA56650.1
hemagglutinin	hemagglutinin [Measles virus]	AAA56642.1
hemagglutinin	hemagglutinin [Measles virus]	AAA74936.1
hemagglutinin	hemagglutinin protein [Measles virus]	BAH56665.1
hemagglutinin	hemagglutinin [Measles virus]	ACC86105.1
hemagglutinin	hemagglutinin [Measles virus strain Edmonston-Zagreb]	AAF85697.1
hemagglutinin	hemagglutinin [Measles virus]	AAR89413.1
hemagglutinin	hemagglutinin [Measles virus]	AAA56653.1
hemagglutinin	RecName: Full = Hemagglutinin glycoprotein	P35971.1
hemagglutinin	Hemagglutinin [Measles virus]	CAB94916.1
hemagglutinin	hemagglutinin [Measles virus]	AAC03036.1
hemagglutinin	hemagglutinin [Measles virus]	AAF85681.1
hemagglutinin	Hemagglutinin [Measles virus]	CAB94927.1
hemagglutinin	Hemagglutinin [Measles virus]	CAB94925.1
hemagglutinin	hemagglutinin protein [Measles virus]	BAB39835.1
hemagglutinin	Hemagglutinin [Measles virus]	CAB94931.1
hemagglutinin	hemagglutinin [Measles virus genotype A]	AFO84712.1
hemagglutinin	hemagglutinin [Measles virus]	AAA56639.1
hemagglutinin	Hemagglutinin [Measles virus]	CAB94926.1
hemagglutinin	hemagglutinin protein [Measles virus]	BAB39836.1
hemagglutinin	Hemagglutinin [Measles virus]	CAB94929.1
hemagglutinin	RecName: Full = Hemagglutinin glycoprotein	P06830.1

TABLE 15-continued

MeV NCBI Accession Numbers (Amino Acid Sequences)		
Type	Virus Name	GenBank Accession
hemagglutinin	Hemagglutinin [Measles virus]	CAB94928.1
hemagglutinin	hemagglutinin protein [Measles virus]	BAB39837.1
hemagglutinin	hemagglutinin [Measles virus]	AAA74935.1
hemagglutinin	hemagglutinin protein [Measles virus]	CAB43780.1
hemagglutinin	hemagglutinin [Measles virus]	BAA09952.1
hemagglutinin	hemagglutinin protein [Measles virus]	CAB43815.1
hemagglutinin	hemagglutinin [Measles virus]	AAF28390.1
hemagglutinin	Hemagglutinin [Measles virus]	CAB94923.1
hemagglutinin	hemagglutinin protein [Measles virus]	CAB43785.1
hemagglutinin	hemagglutinin [Measles virus]	ABD34001.1
hemagglutinin	hemagglutinin protein [Measles virus]	CAB43782.1
hemagglutinin	hemagglutinin protein [Measles virus]	CAB43781.1
hemagglutinin	hemagglutinin [Measles virus]	BAH22353.1
hemagglutinin	hemagglutinin [Measles virus]	AAC35878.2
hemagglutinin	hemagglutinin protein [Measles virus]	AAL86996.1
hemagglutinin	hemagglutinin [Measles virus]	CAA76066.2
hemagglutinin	hemagglutinin [Measles virus]	AAA46428.1
hemagglutinin	hemagglutinin protein [Measles virus]	CAB43803.1
hemagglutinin	Hemagglutinin [Measles virus]	CAB94918.1
hemagglutinin	hemagglutinin [Measles virus]	AAF72162.1
hemagglutinin	hemagglutinin [Measles virus]	AAM70154.1
hemagglutinin	hemagglutinin protein [Measles virus]	CAB43776.1
hemagglutinin	hemagglutinin [Measles virus genotype D4]	ACT78395.1
hemagglutinin	hemagglutinin [Measles virus genotype D7]	AAL02030.1
hemagglutinin	hemagglutinin protein [Measles virus]	CAB43789.1
hemagglutinin	hemagglutinin protein [Measles virus]	CAB43774.1
hemagglutinin	Hemagglutinin [Measles virus]	CAB94920.1
hemagglutinin	Hemagglutinin [Measles virus]	CAB94922.1
hemagglutinin	hemagglutinin [Measles virus]	ABB59491.1
hemagglutinin	hemagglutinin protein [Measles virus]	BAB39843.1
hemagglutinin	hemagglutinin protein [Measles virus]	CAB43804.1
hemagglutinin	hemagglutinin [Measles virus]	AAX52048.1
hemagglutinin	Hemagglutinin [Measles virus]	CAB94930.1
hemagglutinin	hemagglutinin [Measles virus]	AAA74526.1
hemagglutinin	hemagglutinin protein [Measles virus]	CAB43814.1
hemagglutinin	hemagglutinin [Measles virus]	ABB59493.1
hemagglutinin	hemagglutinin [Measles virus genotype D4]	AAL02019.1
hemagglutinin	Hemagglutinin [Measles virus]	CAB94919.1
hemagglutinin	hemagglutinin protein [Measles virus]	AAL86997.1
hemagglutinin	hemagglutinin [Measles virus genotype C2]	AAL02017.1
hemagglutinin	hemagglutinin protein [Measles virus]	CAB43769.1
hemagglutinin	hemagglutinin protein [Measles virus]	CAB43808.1
hemagglutinin	hemagglutinin [Measles virus]	BAO97032.1
hemagglutinin	hemagglutinin protein [Measles virus]	CAB43805.1
hemagglutinin	hemagglutinin protein [Measles virus]	CAB43777.1
hemagglutinin	hemagglutinin [Measles virus]	AAL67793.1
hemagglutinin	hemagglutinin [Measles virus]	AAF89816.1
hemagglutinin	hemagglutinin [Measles virus genotype D4]	AAL02020.1
hemagglutinin	hemagglutinin protein [Measles virus]	CAB43786.1
hemagglutinin	hemagglutinin protein [Measles virus strain MVi/New Jersey.USA/45.05]	AEP40452.1
hemagglutinin	hemagglutinin [Measles virus]	AAA74531.1
hemagglutinin	hemagglutinin [Measles virus]	AAB63800.1
hemagglutinin	hemagglutinin [Measles virus]	AAO21711.1
hemagglutinin	hemagglutinin [Measles virus genotype D8]	ALE27189.1
hemagglutinin	hemagglutinin protein [Measles virus]	CAB43810.1
hemagglutinin	hemagglutinin [Measles virus]	AAF89817.1
hemagglutinin	hemagglutinin [Measles virus genotype D6]	AAL02022.1
hemagglutinin	hemagglutinin protein [Measles virus]	CAB43800.1
hemagglutinin	hemagglutinin protein [Measles virus genotype B3]	AGA17219.1
hemagglutinin	hemagglutinin protein [Measles virus]	CAB43770.1
hemagglutinin	hemagglutinin protein [Measles virus strain MVi/Texas.USA/4.07]	AEP40444.1
hemagglutinin	hemagglutinin [Measles virus]	AAX52047.1
hemagglutinin	hemagglutinin [Measles virus]	AAB63794.1
hemagglutinin	hemagglutinin [Measles virus]	AAB63796.1
hemagglutinin	hemagglutinin [Measles virus]	AAA74528.1
hemagglutinin	hemagglutinin [Measles virus]	AAB63774.1
hemagglutinin	hemagglutinin [Measles virus]	AAB63795.1
hemagglutinin	hemagglutinin [Measles virus]	AAA74519.1
hemagglutinin	hemagglutinin protein [Measles virus]	CAB43778.1
fusion protein	fusion protein [Measles virus strain Moraten]	AAF85672.1
fusion protein	fusion protein [Measles virus]	AAA56645.1

TABLE 15-continued

MeV NCBI Accession Numbers (Amino Acid Sequences)		
Type	Virus Name	GenBank Accession
fusion protein	fusion protein [Measles virus strain Rubeovax]	AAF85688.1
fusion protein	fusion protein [Measles virus]	AAF85680.1
fusion protein	fusion protein [Measles virus]	AEF30359.1
fusion protein	fusion protein [Measles virus]	BAA09957.1
fusion protein	fusion protein [Measles virus]	AAV84957.1
fusion protein	fusion protein [Measles virus MeV-eGFP_Edm-tag]	AI116636.1
fusion protein	fusion protein [Measles virus]	ABY58018.1
fusion protein	fusion protein [Measles virus]	BAA19838.1
fusion protein	fusion protein [Measles virus]	AAA56641.1
fusion protein	F protein [Measles virus]	ABK40529.1
fusion protein	fusion protein [Measles virus]	AAA56652.1
fusion protein	fusion protein [Measles virus]	ABY58017.1
fusion protein	fusion protein [Measles virus]	ABB71645.1
fusion protein	fusion protein [Measles virus]	NP_056922.1
fusion protein	fusion protein [Measles virus strain AIK-C]	AAF85664.1
fusion protein	fusion protein [Measles virus]	BAB60865.1
fusion protein	fusion protein [Measles virus]	BAA09950.1
fusion protein	fusion protein [Measles virus strain MVi/New York.USA/26.09/3]	AEP40403.1
fusion protein	fusion protein [Measles virus]	AAA74934.1
fusion protein	fusion protein [Measles virus]	CAB38075.1
fusion protein	fusion protein [Measles virus strain MVi/Texas.USA/4.07]	AEP40443.1
fusion protein	fusion protein [Measles virus]	AAF02695.1
fusion protein	fusion protein [Measles virus]	AAF02696.1
fusion protein	fusion protein [Measles virus]	AAT99301.1
fusion protein	fusion protein [Measles virus]	ABB71661.1
fusion protein	fusion protein [Measles virus]	BAK08874.1
fusion protein	fusion protein [Measles virus]	AAF02697.1
fusion protein	fusion protein [Measles virus genotype D4]	AFY12704.1
fusion protein	fusion protein [Measles virus strain MVi/California.USA/16.03]	AEP40467.1
fusion protein	fusion protein [Measles virus genotype D8]	AHN07989.1
fusion protein	fusion protein [Measles virus]	AAA46421.1
fusion protein	fusion protein [Measles virus]	AAA56638.1
fusion protein	fusion protein [Measles virus strain MVi/Virginia.USA/15.09]	AEP40419.1
fusion protein	fusion protein [Measles virus genotype D8]	ALE27200.1
fusion protein	fusion protein [Measles virus genotype D8]	AFY12695.1
fusion protein	fusion protein [Measles virus genotype D8]	ALE27248.1
fusion protein	fusion protein [Measles virus genotype D8]	ALE27224.1
fusion protein	fusion protein [Measles virus]	AAT99300.1
fusion protein	fusion protein [Measles virus]	BAH96592.1
fusion protein	fusion protein [Measles virus strain MVi/California.USA/8.04]	AEP40459.1
fusion protein	fusion protein [Measles virus genotype D8]	AIG94081.1
fusion protein	fusion protein [Measles virus]	BAA09951.1
fusion protein	fusion protein [Measles virus genotype D8]	ALE27194.1
fusion protein	fusion protein [Measles virus]	BAA33871.1
fusion protein	fusion protein [Measles virus strain MVi/Washington.USA/18.08/1]	AEP40427.1
fusion protein	fusion protein [Measles virus]	ABY21182.1
fusion protein	fusion protein [Measles virus genotype D8]	ALE27284.1
fusion protein	fusion protein [Measles virus]	ACA09725.1
fusion protein	fusion protein [Measles virus genotype D8]	ALE27314.1
fusion protein	fusion protein [Measles virus genotype G3]	AFY12712.1
fusion protein	fusion protein [Measles virus genotype D8]	ALE27368.1
fusion protein	RecName: Full = Fusion glycoprotein F0; Contains: RecName: Full = Fusion glycoprotein F2; Contains: RecName: Full = Fusion glycoprotein F1; Flags: Precursor	P35973.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53713.1
	unnamed protein product [Measles virus]	CAA34588.1
fusion protein	fusion protein [Measles virus]	CAA76888.1
fusion protein	fusion protein [Measles virus genotype B3.1]	AIY55563.1
fusion protein	fusion protein [Measles virus]	ADO17330.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53703.1
fusion protein	fusion protein [Measles virus genotype B3]	AGA17208.1
fusion protein	fusion protein [Measles virus]	AAL29688.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53706.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53701.1
fusion protein	fusion protein [Measles virus genotype B3]	ALE27092.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53714.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53694.1

TABLE 15-continued

MeV NCBI Accession Numbers (Amino Acid Sequences)		
Type	Virus Name	GenBank Accession
fusion protein	fusion protein [Measles virus genotype H1]	AIG53668.1
fusion protein	fusion protein [Measles virus]	ACC86094.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53670.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53707.1
fusion protein	fusion protein [Measles virus genotype B3]	AGA17216.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53671.1
fusion protein	fusion protein [Measles virus strain MVi/New Jersey.USA/45.05]	AEP40451.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53684.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53688.1
fusion protein	fusion protein [Measles virus genotype B3]	AGA17214.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53683.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53667.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53686.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53685.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53681.1
	unnamed protein product [Measles virus]	CAA34589.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53678.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53710.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53669.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53664.1
fusion protein	fusion protein [Measles virus]	AAA50547.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53679.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53709.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53672.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53697.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53689.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53676.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53675.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53663.1
fusion protein	fusion protein [Measles virus]	BAA19841.1
fusion protein	fusion protein [Measles virus]	AAF02701.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53680.1
fusion protein	fusion protein [Measles virus genotype H1]	AIG53674.1
C protein	C protein [Measles virus strain Moraten]	AAF85670.1
C protein	RecName: Full = Protein C	P03424.1
C protein	C protein [Measles virus]	ACN54404.1
C protein	C protein [Measles virus]	ACN54412.1
C protein	RecName: Full = Protein C	P35977.1
C protein	C protein [Measles virus]	AAF85678.1
C protein	C protein [Measles virus]	ABD33998.1
C protein	unnamed protein product [Measles virus]	CAA34586.1
C protein	C protein [Measles virus]	BAJ51786.1
C protein	C protein [Measles virus]	BAA33869.1
C protein	virulence factor [Measles virus]	ABO69700.1
C protein	C protein [Measles virus]	NP_056920.1
C protein	C protein [Measles virus]	ADO17333.1
C protein	C protein [Measles virus]	ACC86082.1
C protein	C protein [Measles virus]	BAA33875.1
C protein	C protein [Measles virus]	ABY21189.1
C protein	C protein [Measles virus]	BAE98296.1
C protein	C protein [Measles virus]	ADU17782.1
C protein	C protein [Measles virus strain MVi/Virginia.USA/15.09]	AEP40417.1
C protein	C protein [Measles virus]	ADU17814.1
C protein	C protein [Measles virus]	ADU17798.1
C protein	C protein [Measles virus genotype D4]	AFY12700.1
C protein	C protein [Measles virus]	ADU17784.1
C protein	C protein [Measles virus strain MVi/California.USA/16.03]	AEP40465.1
C protein	C protein [Measles virus]	ABB71643.1
C protein	C protein [Measles virus]	AEI91027.1
C protein	C protein [Measles virus]	ADU17874.1
C protein	C protein [Measles virus]	ADU17903.1
C protein	C protein [Measles virus]	CAA34579.1
C protein	C protein [Measles virus]	ADU17790.1
C protein	C protein [Measles virus]	ADU17800.1
C protein	C protein [Measles virus]	ABB71667.1
C protein	unnamed protein product [Measles virus]	CAA34572.1
C protein	C protein [Measles virus strain MVi/Arizona.USA/11.08/2]	AEP40433.1
C protein	C protein [Measles virus]	ADU17830.1
C protein	C protein [Measles virus]	ADU17947.1

TABLE 15-continued

MeV NCBI Accession Numbers (Amino Acid Sequences)		
Type	Virus Name	GenBank Accession
C protein	C protein [Measles virus]	ADU17818.1
C protein	C protein [Measles virus strain MVi/New Jersey.USA/45.05]	AEP40449.1
C protein	C protein [Measles virus strain MVi/Texas.USA/4.07]	AEP40441.1
C protein	C protein [Measles virus]	ADU17864.1
C protein	C protein [Measles virus]	ADU17838.1
C protein	C protein [Measles virus]	ADU17881.1
C protein	C protein [Measles virus strain MVi/Washington.USA/18.08/1]	AEP40425.1
C protein	C protein [Measles virus]	ADU17927.1
C protein	C protein [Measles virus]	ADU17953.1
C protein	C protein [Measles virus]	ADU17889.1
C protein	C protein [Measles virus]	ADU17963.1
C protein	C protein [Measles virus]	ADU17893.1
C protein	C protein [Measles virus]	ADU17820.1
C protein	C protein [Measles virus]	ABB71651.1
C protein	C protein [Measles virus]	ADU17786.1
C protein	C protein [Measles virus]	ADU17862.1
C protein	C protein [Measles virus]	ADU17923.1
C protein	C protein [Measles virus]	ADU17959.1
C protein	C protein [Measles virus]	ADU17951.1
C protein	C protein [Measles virus]	ADU17916.1
C protein	C protein [Measles virus]	ADU17957.1
C protein	C protein [Measles virus]	ADU17925.1
C protein	C protein [Measles virus]	ADU17901.1
C protein	C protein [Measles virus]	ADU17887.1
C protein	C protein [Measles virus]	ADU17832.1
C protein	C protein [Measles virus]	ADU17891.1
C protein	C protein [Measles virus]	ADU17961.1
C protein	C protein [Measles virus]	ADU17872.1
C protein	C protein [Measles virus]	ADU17929.1
C protein	C protein [Measles virus]	ADU17908.1
C protein	C protein [Measles virus]	ADU17910.1
C protein	C protein [Measles virus]	ADU17921.1
C protein	C protein [Measles virus]	ADU17824.1
C protein	C protein [Measles virus strain MVi/Pennsylvania.USA/20.09]	AEP40473.1
C protein	C protein [Measles virus]	ADU17828.1
C protein	C protein [Measles virus]	ADU17812.1
C protein	C protein [Measles virus genotype D8]	AFY12692.1
C protein	nonstructural C protein [Measles virus]	ABA59559.1
C protein	RecName: Full = Protein C	Q00794.1
C protein	nonstructural C protein [Measles virus]	ADO17934.1
C protein	nonstructural C protein [Measles virus]	ACJ66773.1
C protein	C protein [Measles virus genotype G3]	AFY12708.1
C protein	RecName: Full = Protein C	P26035.1
C protein	C protein [Measles virus]	BAA84128.1
nucleoprotein	RecName: Full = Nucleoprotein; AltName: Full = Nucleocapsid protein; Short = NP; Short = Protein N	Q77M43.1
nucleoprotein	nucleocapsid protein [Measles virus strain Rubeovax]	AAF85683.1
nucleoprotein	RecName: Full = Nucleoprotein; AltName: Full = Nucleocapsid protein; Short = NP; Short = Protein N	Q89933.1
nucleoprotein	nucleocapsid protein [Measles virus strain AIK-C]	AAF85659.1
nucleoprotein	nucleoprotein [Measles virus]	AB154102.1
nucleoprotein	nucleoprotein [Measles virus]	AAA56643.1
nucleoprotein	nucleoprotein [Measles virus]	AAC03050.1
nucleoprotein	nucleoprotein [Measles virus]	AAA18990.1
nucleoprotein	nucleoprotein [Measles virus]	AAA56640.1
nucleoprotein	RecName: Full = Nucleoprotein; AltName: Full = Nucleocapsid protein; Short = NP; Short = Protein N	P35972.1
nucleoprotein	RecName: Full=Nucleoprotein; AltName: Full = Nucleocapsid protein; Short = NP; Short = Protein N	P10050.1
nucleoprotein	N protein [Measles virus]	BAB60956.1
nucleoprotein	RecName: Full = Nucleoprotein; AltName: Full = Nucleocapsid protein; Short = NP; Short = Protein N	B1AAA7.1
nucleoprotein	nucleoprotein [Measles virus]	AAA18991.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46894.1

TABLE 15-continued

MeV NCBI Accession Numbers (Amino Acid Sequences)		
Type	Virus Name	GenBank Accession
nucleoprotein	nucleoprotein [Measles virus]	CAB46871.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46872.1
nucleoprotein	nucleoprotein [Measles virus]	ABU49606.1
nucleoprotein	nucleocapsid protein [Measles virus]	AAA75494.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46883.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46892.1
nucleoprotein	unnamed protein product [Measles virus]	CAA34584.1
nucleoprotein	nucleoprotein [Measles virus]	AAA18997.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46863.1
nucleoprotein	nucleoprotein [Measles virus]	AEF30352.1
nucleoprotein	nucleoprotein [Measles virus]	ABI54103.1
nucleoprotein	nucleocapsid protein [Measles virus]	AAA46433.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46902.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46873.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46906.1
nucleoprotein	nucleoprotein [Measles virus]	AAA74547.1
nucleoprotein	nucleoprotein [Measles virus]	AAA74537.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46862.1
nucleoprotein	nucleocapsid protein [Measles virus]	BAA09961.1
nucleoprotein	nucleoprotein [Measles virus]	AAO15875.1
nucleoprotein	nucleoprotein [Measles virus]	AAO15871.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46882.1
nucleoprotein	nucleoprotein [Measles virus]	CAB60124.1
nucleoprotein	nucleoprotein [Measles virus]	ABI54104.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46869.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46880.1
nucleoprotein	nucleoprotein [Measles virus]	AAA74541.1
nucleoprotein	nucleocapsid protein [Measles virus strain MVi/New Jersey.USA/45.05]	AEP40446.1
nucleoprotein	nucleoprotein [Measles virus]	ABI54110.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46903.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46899.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46901.1
nucleoprotein	nucleocapsid protein [Measles virus]	ABB71640.1
nucleoprotein	nucleoprotein [Measles virus]	CAB60113.1
nucleoprotein	nucleoprotein [Measles virus]	CAB60114.1
nucleoprotein	nucleoprotein [Measles virus]	CAB60116.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46895.1
nucleoprotein	nucleoprotein [Measles virus]	CAB60121.1
nucleoprotein	nucleoprotein [Measles virus]	ABI54111.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46889.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46898.1
nucleoprotein	nucleoprotein [Measles virus genotype B3]	ALE27083.1
nucleoprotein	nucleoprotein [Measles virus]	CAB60118.1
nucleoprotein	nucleocapsid protein [Measles virus]	CAA34570.1
nucleoprotein	nucleoprotein [Measles virus]	AAC29443.1
nucleoprotein	nucleocapsid protein [Measles virus strain MVi/Washington.USA/18.08/1]	AEP40422.1
nucleoprotein	nucleoprotein [Measles virus]	AAO15872.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46874.1
nucleoprotein	nucleoprotein [Measles virus]	AAA74550.1
nucleoprotein	nucleocapsid protein [Measles virus]	ABB71648.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46900.1
nucleoprotein	nucleoprotein [Measles virus]	BAH22440.1
nucleoprotein	nucleocapsid protein [Measles virus]	AAA46432.1
nucleoprotein	nucleocapsid protein [Measles virus]	BAA33867.1
nucleoprotein	nucleoprotein [Measles virus]	AAA74539.1
nucleoprotein	nucleoprotein [Measles virus]	CAB60115.1
nucleoprotein	nucleoprotein [Measles virus]	CAB60123.1
nucleoprotein	nucleocapsid protein [Measles virus]	ABB71664.1
nucleoprotein	nucleoprotein [Measles virus]	CAB60125.1
nucleoprotein	nucleoprotein [Measles virus]	AAA74546.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46886.1
nucleoprotein	nucleoprotein [Measles virus]	BAH22350.1
nucleoprotein	nucleoprotein [Measles virus]	CAB46867.1
nucleoprotein	nucleocapsid protein [Measles virus]	BAA09954.1
nucleoprotein	nucleoprotein [Measles virus]	AAO15873.1
nucleoprotein	nucleocapsid protein [Measles virus]	AEP95735.1
nucleoprotein	nucleoprotein [Measles virus]	AAL37726.1
nucleoprotein	nucleoprotein [Measles virus]	AAA74549.1
nucleoprotein	RecName: Full = Nucleoprotein; AltName: Full = Nucleocapsid protein; Short = NP; Short = Protein N	P26030.1

TABLE 15-continued

MeV NCBI Accession Numbers (Amino Acid Sequences)		
Type	Virus Name	GenBank Accession
nucleoprotein	nucleoprotein [Measles virus ETH55/99]	AAK07777.1
nucleoprotein	nucleoprotein [Measles virus genotype B3]	AGA17238.1
nucleoprotein	nucleoprotein [Measles virus]	AEF30351.1
nucleoprotein	nucleoprotein [Measles virus genotype B3]	AGA17242.1
nucleoprotein	nucleoprotein [Measles virus ETH54/98]	AAK07776.1
nucleoprotein	nucleoprotein [Measles virus]	AAA74548.1
nucleoprotein	nucleoprotein [Measles virus]	AAA19221.1
nucleoprotein	nucleoprotein [Measles virus]	AAC03039.1
nucleoprotein	nucleoprotein [Measles virus]	AAA19223.1
nucleoprotein	nucleoprotein [Measles virus genotype B3]	AGA17241.1
nucleoprotein	nucleoprotein [Measles virus]	CAB60122.1
nucleoprotein	nucleoprotein [Measles virus]	CAC34599.1
nucleoprotein	nucleoprotein [Measles virus]	AAC03042.1
nucleoprotein	nucleoprotein [Measles virus]	CAC34604.1
nucleoprotein	nucleoprotein [Measles virus]	AAA74544.1
nucleoprotein	nucleocapsid protein [Measles virus]	NP_056918.1
V Protein	RecName: Full = Non-structural protein V	Q9IC37.1
V Protein	RecName: Full = Non-structural protein V	Q9EMA9.1
V Protein	V protein [Measles virus]	ACN54411.1
V Protein	V protein [Measles virus]	ACN54403.1
V Protein	V protein [Measles virus]	AEP95742.1
V Protein	V protein [Measles virus strain MVi/Virginia.USA/15.09]	AEP40416.1
V Protein	V protein [Measles virus]	ADU17801.1
V Protein	V protein [Measles virus]	ADU17849.1
V Protein	V protein [Measles virus]	ABB71642.1
V Protein	V protein [Measles virus genotype D8]	AFY12693.1
V Protein	V protein [Measles virus]	YP_003873249.2
V Protein	V protein [Measles virus strain MVi/Arizona.USA/11.08/2]	AEP40432.1
V Protein	RecName: Full = Non-structural protein V	P26036.1
V Protein	V protein [Measles virus strain MVi/California.USA/16.03]	AEP40464.1
V Protein	V protein [Measles virus strain MVi/California.USA/8.04]	AEP40456.1
V Protein	V protein [Measles virus]	ABY21188.1
V Protein	V protein [Measles virus strain MVi/Washington.USA/18.08/1]	AEP40424.1
V Protein	V protein [Measles virus]	BAH96581.1
V Protein	V protein [Measles virus]	ABB71666.1
V Protein	RecName: Full = Non-structural protein V	P60168.1
V Protein	V protein [Measles virus]	BAH96589.1
V Protein	V protein [Measles virus]	ADU17954.1
V Protein	V protein [Measles virus strain MVi/New York.USA/26.09/3]	AEP40400.1
V Protein	V protein [Measles virus]	ABY21196.1
V Protein	virulence factor [Measles virus]	ABO69701.1
V Protein	V protein [Measles virus]	ABB71650.1
V Protein	V protein [Measles virus]	ACC86086.1
V Protein	V protein [Measles virus genotype D4]	AFY12702.1
V Protein	V protein [Measles virus strain MVi/New Jersey.USA/45.05]	AEP40448.1
V Protein	V protein [Measles virus]	BAE98295.1
V Protein	V protein [Measles virus]	ACC86083.1
V Protein	V protein [Measles virus]	ACU5139.1
V Protein	V protein [Measles virus]	ADO17334.1
V Protein	V protein [Measles virus]	ADU17930.1
V Protein	V protein [Measles virus genotype G3]	AFY12710.1
V Protein	V protein [Measles virus strain MVi/Pennsylvania.USA/20.09]	AEP40472.1
V Protein	phosphoprotein [Measles virus]	ADU17839.1
V Protein	V protein [Measles virus]	ADU17894.1
V Protein	V protein [Measles virus]	ACN50010.1
V Protein	V protein [Measles virus]	ADU17892.1
V Protein	unnamed protein product [Measles virus]	CAA34585.1
V Protein	V protein [Measles virus]	ABD33997.1

TABLE 16

Name	Sequence	SEQ ID NO:
Flagellin Nucleic Acid Sequences		
NT (5' UTR, ORF, 3' UTR)	<p>TCAAGCTTTTGGACCCCTCGTACAGAAGCTAATACGACTCACTAT AGGGAATAAGAGAGAAAAGAAGAGTAAGAAGAAATATAAG AGCCACCATGGCACAAGTCATTAATACAACAGCCTGTCTGCTG TTGACCCAGAATAACCTGAACAAATCCCAGTCCGCACTGGGCA CTGCTATCGAGCGTTTGTCTTCCGGTCTGCGTATCAACAGCGCG AAAGACGATGCGGCAGGACAGGCGATTGCTAACCGTTTACCG CGAACATCAAAGGTCTGACTCAGGCTTCCCGTAACGCTAACGA CGGTATCTCCATTGCGCAGACCCTGAAGGCGCGCTGAACGAA ATCAACAACAACCTGCAGCGTGTGCGTGAACCTGGCGGTTTCACT CTGCGAATGGTACTAATCCCAGTCTGACCTCGACTCCATCCAG GCTGAAATCACCCAGCGCCTGAACGAAATCGACCGTGATCCG GCCAGACTCAGTTCACCGCGTGAAAGTCTGGCGCAGGACAA CACCCCTGACCATCCAGGTTGGTGCCACGACGGTGAAATATC GATATTGATTTAAAAGAAATCAGCTCTAAAACTGGGACTTG ATAAGCTTAAATGTCCAAGATGCCTACACCCGAAAGAACTGC TGTAACCGTTGATAAACTACCTATAAAATGGTACAGATCCT ATTACAGCCAGAGCAATACTGATATCCAACTGCAATTGGCG GTGGTGCAACGGGGTTACTGGGGCTGATATCAAATTTAAAGA TGGTCAATACTATTTAGATGTTAAAGGCGGTGCTTCTGCTGGTG TTTATAAAGCCACTTATGATGAACTACAAGAAAGTAAATAT TGATACGACTGATAAACTCCGTTGGCACTGCGGAAGCTACA GCTATTTCGGGGAACGGCCACTATAACCCACAACCAATTTGCTG AAGTAACAAAAGAGGGTGTGATACGACCACAGTTGCGGCTCA ACTTGCTGCAGCAGGGTTACTGGCGCGGATAAGGACAATACT AGCCTTGTAATACTATCGTTTGGAGATAAAAACGGTAAGGTTA TTGATGGTGGCTATGCAGTGAAAAATGGGCGACGATTTCTATGC CGCTACATATGATGAGAAAACAGGTGCAATTACTGCTAAAACC ACTACTTATACAGATGGTACTGGCGTTGCTCAAACCTGGAGCTGT GAAATTTGGTGGCGCAAAATGGTAAATCTGAAGTTGTTACTGCT ACCGATGGTAAGACTTACTTAGCAAGCGACCTTGACAAACATA ACTTCAGAACAGGCGGTGAGCTTAAAGAGGTTAATACAGATAA GACTGAAAACCCACTGCAGAAAATGATGCTGCCTTGGCACAG GTTGATACACTTCGTCTGACCTGGGTGCGGTTGAGAACCGTTT CAACTCCGCTATCACCAACCTGGGCAATACCGTAAATAACCTG TCTTCTGCCCGTAGCCGTATCGAAGATTCCGACTACGCAACCGA AGTCTCCAACATGTCTCGCGCGCAGATTCTGCAGCAGGCGGT ACCTCCGTTCTGGCGCAGGCGAACCAGGTTCCGCAAAACGTCC TCTCTTTACTGCGTTGATAATAGGCTGGAGCCTCGGTGGCCATG CTTCTTGCCCTTGGGCTCCCCCAGCCCCCTCCTCCCCCTTCTG CACCCGTACCCCGTGCTCTTTGAATAAAGTCTGAGTGGGCGGC</p>	51
ORF Sequence, NT	<p>ATGGCACAAAGTCATTAATACAACAGCCTGTGCTGTTGACCC AGAATAACCTGAACAAATCCCAGTCCGCACTGGGCACTGCTAT CGAGCGTTTGTCTTCCGGTCTGCGTATCAACAGCGCGAAAGAC GATGCGGCAGGACAGGCGATTGCTAACCGTTTACCGCGAACA TCAAAGGTCTGACTCAGGCTTCCCGTAACGCTAACGACGGTAT CTCCATTGCGCAGACCCTGAAGGCGCGCTGAACGAAATCAAC AACAACCTGCAGCGTGTGCGTGAACCTGGCGGTTCACTGTCGA ATGGTACTAATCCCAGTCTGACCTCGACTCCATCCAGGCTGAA ATCACCCAGCGCCTGAACGAAATCGACCGTGATCCGGCCAGA CTCAGTTCAACGGCGTGAAAGTCTTGGCGCAGGACAACCCCT GACCATCCAGGTTGGTGCCAACGACGGTGAACTATCGATATT GATTTAAAAGAAATCAGCTCTAAAACACTGGGACTTGATAAGC TTAATGTCCAAGATGCCCTACCCCCGAAAGAACTGCTGTAAC CGTTGATAAACTACCTATAAAATGGTACAGATCCTATTACA GCCCAGAGCAATACTGATATCCAACTGCAATTGGCGGTGGTG CAACGGGGTTACTGGGCTGATATCAAATTTAAGATGGTCA ATACTATTAGATGTTAAAGGCGGTGCTTCTGCTGGTGTATTATA AAGCCACTTATGATGAACTACAAGAAAGTTAATATTGATAC GACTGATAAACTCCGTTGGCAACTGCGGAAGCTACAGCTATT CGGGGAACGGCCACTATAACCCACAACCAATTTGCTGAAGTAA CAAAAGAGGGTGTGATACGACCACAGTTGCGGCTCAACTTGC TGCAGCAGGGTTACTGGCGCGGATAAGGACAATACTAGCCTT GTAAAATATCGTTTGGAGATAAAAACGGTAAGGTTATTGATG GTGGCTATGCACTGAAAAATGGGCGACGATTTCTATGCCGCTAC ATATGATGAGAAAACAGGTGCAATTACTGCTAAAACCACTACT TATACAGATGGTACTGGCGTTGCTCAAACCTGGAGCTGTGAAAT TTGGTGGCGCAAAATGGTAAATCTGAAGTTGTTACTGCTACCGAT GGTAAGACTTACTTAGCAAGCGACCTTGACAAACATAACTTCA GAACAGGCGGTGAGCTTAAAGAGGTTAATACAGATAAGACTG AAAACCACTGCAGAAAATGATGCTGCCTGGCACAGGTTGA TACACTTCGTTCTGACCTGGGTGCGGTTGAGAACCGTTTCAACT</p>	52

TABLE 16-continued

Name	Sequence	SEQ ID NO:
	CCGCTATCACCAACCTGGGCAATACCGTAAATAACCTGTCTTCT GCCCCGTAGCCGTATCGAAGATTCCGACTACGCAACCGAAGTCT CCAACATGTCTCGCGCGCAGATTCTGCAGCAGGCCGGTACCTC CGTTCTGGCGCAGGCGAACAGGTTCCGCAAAACGTCTCTCTT TACTGCGT	
mRNA Sequence (assumes T100 tail)	G*GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAA GAGCCACCAUGGCACAAGUCAUUAUACAAACAGCCUGUCGC UGUUGACCAGAAUAACCUGAACAAAUCCAGUCCGCACUGG GCACUGCUAUCGAGCGUUUGUCUUCGGUCUGCGUAUCAACA GCGCGAAAGACGAUGCGGCAGGACAGGC GAUUGCUAACCGUU UUACCGCGAACAUCAAAGGUCUGACUCAGGCUUCGGUAACG CUAACGACGGUAUCUCCAUGCGCAGACCACUGAAGCGCGC UGAACGAAAUCAACAACACCUGCAGCGUGUGCGUAACUGG CGGUUCAGUCUGCGAAUGGUACUAACUCCAGUCUGACCUUG ACUCCAUCGAGGCGUAAAUCAACCAGCGCCUGAACGAAAUUG ACCGUGUAUCCGGCCAGACUCAGUUAACGCGGUGAAAGUCC UGGCGCAGGACAAACCCUGACCAUCCAGGUUGGUGCCAACG ACGGUGAAACUAUCGAUAUUGAUUUAAAAGAAAUCAGCUCU AAAAACACUGGGACUUGAUAGCUUAAUGUC CAAGAUGCCUAC ACCCCGAAAGAAACUGCUGUAACCGUUGAUAAAACUACCUAU AAAAAUGGUACAGAUCCUUAUACAGCCAGAGCAUAUCUGAU AUCCAAACUGCAAUUGGCGGUGGUGCAAACGGGGGUUACUGG GGCUGAUUAUAAAUAAGAUGGUCAUAUUAUUAUGAUG UUAAAGGCGGUGCUUCUGCUGGUGUUUAUAAAGCCACUUAU GAUGAAACUACAAAGAAAGUUAAUUAUGAUACGACUGAUAA AACUCCGUUGGCAACUGCGGAAGCUACGCUAUUCCGGGAAC GGCCACUAUAACCCACAACCAAUUGCUGAAGUAAACAAAGA GGGUGUUGAUACGACCACAGUUGCGGCUCAACUUGCUGCAGC AGGGGUUAUCUGGCGCCGAUAAGGACAAUACUAGCCUUGUA AACUAUCGUUUAGGAUAAAAACGGUAAGGUUAUUGAUGGU GGCUAUGCAGUAAAUUGGGCGACGAUUUCUAGCCGCUACA UAUGAUGAGAAAAAGGUGCAAUUCUGCUAAAACCAUAC UUUAACAGAUUGGUACUGGCGUUGCUCAACUGGAGCUGUGA AAUUUGGUGGCGCAAUUGGUAAAUCUGAAGUUGUUAUCUGCU ACCGAUGGUAAAGCUUAUCUAGCAAGCGACCUUGACAAACAU AACUUCAGAACAGGCGGUGAGCUUAAAGAGGUUAUAACAGA UAAGACUGAAAACCCACUGCAGAAAUAUGAUGCUGCCUUGGC ACAGGUUGAUACAUUCGUUCUGACCUUGGUGCGGUUCAGAA CCGUUUCAACUCCGCUAUCACCAACUGGGCAUAUCCGUAAA UAACCUUGCUUCUGCCCGUAGCCGUUUCGAAGAUUCCGACUA CGCAACCGAAGUCUCCAACAUUGUCUGCGCGCAGAUUCUGCA GCAGGCCGUAACCUUCGUUCUGGCGCAGGCGAACAGGUUCC GCAAAACGUCUCUUCUUAUCUGCGUUGAUAAUAGGCGUGAGC CUCGGUGGCAUGCUUCUUGCCCCUUGGGCCUCCCCCAGCC CCUCCUCCCCUUCUGCACCCGUACCCCGUGGUCUUUGAAU AAAGUCUGAGUGGGCGGCAAAAAAAAAAAAAAAAAAAAAA AA AAAUCUAG	53
Flagellin mRNA Sequences		
NT (5' UTR, ORF, 3' UTR)	UCAAGCUUUUGGACCCUCGUACAGAAGCUAAUACGACUCACU AUAGGGAUUAAGAGAGAAAAGAGAGUAAGAAGAAUAUA AGAGCCACCAUGGCACAAGUCAUUAUACAAACAGCCUGUCG CUGUUGACCAGAAUAACCUGAACAAUCCAGUCCGCACUG GGCACUGCUAUCGAGCGUUUGUCUUCGGUCUGCGUAUCAAC AGCGCGAAAGACGAUGCGGCAGGACAGGCGAUUGCUAACCGU UUUACCGCGAACAUCAAGGUUGACUCAGGCUUCCCGUAAC GCUAACGACGGUAUCUCCAUGCGCAGACCACUGAAGGCGCG CUGAACGAAAUCAACAACACUGCAGCGUGUGCGUGAACUG GCGGUUCAGUCUGCGAAUGGUACUAAUCCAGUCUGACCU GACUCCAUCCAGGCGUAAAUACCCAGCGCUGAACGAAAU GACCGUGUAUCGCGCCAGACUCAGUUAACGGCGUGAAGU CUGGCGCAGGACAAACACCUAGCCAUCCAGGUUGGUGCCAAC GACGGUGAAACUAUCGAUAUUGAUUUAAAAGAAUACGCU UAAAACACUGGGACUUGAUAGCUUAUUGUCCAAGAUGCCU ACACCCCGAAAGAAACUGCUGUAACCGUUGAUAAACUACCU AUAAAUAUGGUACAGAUCCUUAUACAGCCAGAGCAUAUCUG AUAUCCAACUGCAAUUGGCGGUGUGCAACGGGGGUUACU GGGGCUGAUUAUCAAUUUAAAAGUUGUCAAUAUUAUAGA UGUUAAGGCGGUGCUUCUGCUGGUGUUUAUAAAGCCACUU AUGAUGAAACUACAAAGAAAGUUAUUAUUGAUACGACUGAU AAAAUCUCCGUUGGCAACUGCGGAAGCUACGCUAUUCCGGGA ACGGCCACUAUAACCCACAACCAAUUGCUGAAGUAACAAA	81

TABLE 16-continued

Name	Sequence	SEQ ID NO :
	GAGGGUGUUGAUACGACCACAGUUGCGGCUCAACUUGCUGCA GCAGGGGUUACUGGCGCCGAUAAGGACAAUACUAGCCUUGUA AAACUUAUCGUUUGAGGAUAAAAACGGUAAGGUUAUUGAUGG UGGCUAUGCAGUGAAAAUUGGCGCAGAUUUUAUGCCGCUAC AUAUGAUGAGAAAACAGGUGCAAUUAUCGUUAAAAACCUA CUUAUACAGAUUGGUACUGGCGUUGCUAAACUGGAGCUGUG AAAUUUGGUGGCGCAAAUGGUAAAUCUGAAGUUGUUAUCUGC UACCGAUGGUAAGACUUAUCUAGCAAGCGACCUUGACAACAA UAAACUUCAGAAACAGGCGGUGAGCUUAAAGAGGUUAAUACAG AUAAGACUGAAAAACCACTUGCAGAAAAUUGAUGCGCCUUGG CACAGGUUGAUACACUUCGUUCUGACCUUGGUGCGGUUCAGA ACCGUUUAACUCCGCUAUACCAACCUUGGGCAUACCGUAA AUAACCUUGUCUUCUGCCCGUAGCCGUUACGAAGAUUCCGACU ACGCAACCGAAGUCUCCACAUGUCUCGCGCGCAGAUUCUGC AGCAGGCCCGUACUCCGUUCUGGCGCAGGCGAACCCAGGUUC CGCAAAACGUCCUUCUUAUACUGCGUUGAUAAUAGGCUGGAG CCUCGGUGGCCAUGCUUCUUGCCCUUGGGCCUCCCCCAGC CCCUCCUCCCCUCCUGCACCCCGUACCCCGUGGUCUUUGAA UAAAGUCUGAGUGGGCGGC	
ORF Sequence, NT	AUGGCACAAGUCAUUAUACAAACAGCCUGUCGUGUUGACC CAGAAUUAACCGAACAACUCCAGUCCGACUGGGCACUGCU AUCGAGCGUUUGUCUUCGCGUUCGCUAUAACAGCGCGAAA GACGAUGCGGCAGGACAGGCGAUUGCUAACCUGUUUACCGCG AACAUCAAAGGUCUGACUCAGGCUUCCCGUAACGCUAACGAC GGUUUCUCCAUUGCGCAGACCACUGAAGGCGCGUGAACGAA AUCAACAACAACUUGCAGCGUGUGCGUGAACUGGCGGUUCAG UCUGCGAAUGGUACUAACUCCAGUCUGACUCCGACUCCAUCC CAGGCUGAAAUACCCAGCGCGUGAACGAAUCCGACCGUGUA UCCGGCCAGACUCAGUUCACCGGCUGAAGUCCUGGCGCAG GACAAACACCCUGACCAUCCAGGUUGGUGCCAAACGACGGUGAA ACUAUCGAUUAUGAUUUAAGAAAUACGCUUAAACACU GGGACUUGAUUAGCUUAAUGUCCAAGAUGCCUACACCCCGAA AGAAACUGCGUUAACCGUUGAUAAACUACCUAUAUAAUUG GUACAGAUCCUAUUAACAGCCACAGAGCAUAUCGAUUAUCCAA CUGCAAUUGGCGGUGGUGCAACGGGGGUUACUGGGGCGUAGU AUCAAAUUUAAAGAUUGGUCAAUACUAUUAGAUGUUAAGG CGGUGCUUCUGCUGGUGUUUAUAAAGCCACUUAUGAUGAAA CUACAAAGAAAGUUAUUAUGAUACGACUGAUAAAACUCCG UUGGCAACUGCGGAAGCUACAGCUAUUCGGGAACGGCCACU AUAACCCACAACCAAUUGCUGAAGUAACAAAGAGGGUGU UGAUACGACCAACAGUUGCGGCUCAACUUGCUGCAGCAGGGGU UACUGGCGCCGAUAAGGACAAUACUAGCCUUGUAAAACUAUC GUUUGAGGAUAAAAACGGUAAGGUUAUUGAUGGUGGCUAUG CAGUGAAAUGGGCGACGAUUUCUUGCCGCUACAUUAGAU GAGAAAACAGGUGCAAUUACUGCUAAAACCAUACUUAUAC GAUGGUACUGGCGUUGCUCAAACUGGAGCUUGAUAUUGG UGGCGCAAUGGUAAAUCUGAAGUUGUUAUCUGCUACCGAUG GUAAAGCUUACUUAAGCAAGCGACCUUGACAAACUAUACUUA GAACAGGCGGUGAGCUUAAAGAGGUUAUAACAGAUAAAGACU GAAAAACCCACUGCAGAAAAUUGAUGCUGCCUUGGCACAGGUU GAUACACUUCGUUCUGACCUUGGUGCGGUUCAGAACCGUUC AACUCGCUUAUCACCAACCUUGGCAAUACCGUAAAUAACUG UCUCUGCCCGUAGCCGUUACGAAGAUUCCGACUACGCAACC GAAGUUCCAAUAUGUCUCGCGCGCAGAUUCUGCAGCAGGCC GGUACCUCCGUUCUGGCGCAGGCGAACAGGUUCCGCAAAAC GUCCUCUCUUACUGCGU	82
mRNA Sequence (assumes T100 tail)	G*GGGAAUUAAGAGAGAAAAGAGAGUUAAGAAGAAUUAUA GAGCCACCAUGGCACAAGUCAUUAUACAAACAGCCUGUCGC UGUUGACCCAGAAUAACTUGAACAAUCCAGUCCGCACUGG GCACUGCUAUCGAGCGUUUGUCUUCGCGUUCGCUAUAACA GCGCGAAAGACGAUGCGGCAGGACAGGCGAUUGCUAACCGUU UUAACCGCAACAUCAAAGGUCUGACUCAGGCUUCCGUAACG CUAACGACGGUAUCUCCAUUGCGCAGACCACUGAAGGCGCGC UGAACGAAAUCAAACAACUUGCAGCGUGUGCGUGAACUGG CGGUUCAGUCUGCGAAUGGUACUAACUCCAGUCUGACCUUG ACUCCAUCAGGCUGAAAUACCCAGCGCCUGAACGAAAUUG ACCGUGUAUCCGGCCAGACUCAGUUAACCGCGUGAAGUUC UGGCGCAGGACAAACCCUGACCAUCCAGGUUGGUGCAACG ACGGUGAAACUAUCGAUUAUGAUUAAAGAAAUACGUCU AAAACACUGGGACUUGAUUAGCUUAAUGUCCAAAGAUCCUAC ACCCGGAAAGAAACUGCUUUAACCGUUGAUAAAACUAACUAU AAAAUUGGUACAGAUCCUAUACAGCCACAGCAUACUGAU	83

TABLE 16-continued

Name	Sequence	SEQ ID NO:
	AUCCAAACUGCAAUUGGCGGUGGUGCAACGGGGGUUACUGG GGCUGAUUAUCAAUUUAAAAGUUGGUCUAUUAUUUAGAU UUAAGGCGGUGCUUCUGCUGGUGUUUUAUAAAGCCACUUU GAUGAAACUACAAAGAAAGUUAAUUAUGAUACGACUGAUAA AACUCGCUUGGCAACUGCGGAAGCUACAGCUAUUCGGGGAAC GGCCACUAUAACCCACAACCAAUUGCUGAAGUAACAAAGA GGGUGUUGAUACGACCACAGUUGCGGCUCAACUUGCUGCAGC AGGGGUUAUGGCGCGAUAAAGGACAAUACUAGCCUUGUAA AACUAUCGUUUGAGGAUAAAAACGGUAAGGUUAUUGAUGGU GGCUAUGCAGUGAAAUGGGCGACGAUUUCUAGCCGCUACA UAUGAUGAGAAAACAGGUGCAAUACUGCUAAAACCAUAC UUAUACAGAUGGUACUGGCGUUGCUCAACUGGAGCUGUGA AAUUUGGUGGCGCAAUUGGUAAAUCUGAAGUUGUUAUCUGCU ACCGAUGGUAAAGACUUAUACUAGCAAGCGACCUUGACAAACAU AACUUCAGAACAGGCGGUGAGCUUAAAGAGGUUAAUACAGA UAAGACUGAAAACCCACUGCAGAAAUAUGAUGCUGCCUUGGC ACAGGUUGAUACAUUCGUUCUGACCUUGGUGCGGUUCAGAA CCGUUUACAUCCGCUAUCACCAACUUGGGCAAUACCGUAAA UAACCUUGUCUUCUGCCGUAGCCGUUUCGAAUUCGACUA CGCAACCGAAGUCUCCAAUGUCUCGCGCGCAGAUUCUGCA GCAGGCCGGUACCUUCGUUCUGGCGCAGGCGAACAGGUUCC GCAAAACGUCCUCUUAUCUGCGUUGAUAAUAGGCUUGAGC CUCGGUGGCCAUGCUUCUUGCCCCUUGGGCCUCCCCCAGCC CCUCCUCCCCUUCUGCACCCGUACCCCGUGGUCUUUGAAU AAAGUCUGAGUGGGCGGCAAAAAAAAAAAAAAAAAAAAAA AA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAUUCUG	

TABLE 17

Flagellin Amino Acid Sequences		
Name	Sequence	SEQ ID NO:
ORF Sequence, AA	MAQVINTNSLSLLTQNNLNKSQSALGTAIERLSSGLRINSKDDAA GQAIANRFTANIKGLTQASRNANDGISIAQTTEGALNEINNLRV RELAVQSANGTNSQSDLDSIQAEITQRLNEIDRVSGQTQFNGVKVL AQDNTLTIQVGANDGETIDIDLKEISSKTLGLDKLNVQDAYTPKET AVTVDKTTYKNGTDPITAQSNTDIQTGIGGATGVTGADIKFKDG QYYLDVKGGASAGVYKATYDETTKKVNIIDTDKTPLATAEATAI RGTATI THNQIAEVTEKEGVDTTVAQAALAAAGVTGADKDNSTLV KLSFEDKNGKVIDGGYAVKMGGDFYAATYDEKTGAI TAKTTTYT DGTGVAQTGAVKFGGANGKSEVVATDGTLYLASDLDKHNFRT GGEKLEVNTDKTENPLQKIDAALAQVDTLRSDLGAVQNRFNSAIT NLGNTVNNLSARSRIEDSDYATEVSNMSRAQILQQAGTSVLAQA NQVPQNVLSLLR	54
Flagellin- GS linker- circumsporozoite protein (CSP)	MAQVINTNSLSLLTQNNLNKSQSALGTAIERLSSGLRINSKDDAA GQAIANRFTANIKGLTQASRNANDGISIAQTTEGALNEINNLRV RELAVQSANGTNSQSDLDSIQAEITQRLNEIDRVSGQTQFNGVKVL AQDNTLTIQVGANDGETIDIDLKQINSQTLGLDTLNVQQYKVS TAATVTGYADTTIALDNSTFKASATGLGGTDQKIDGDLKFDPTTG KYIAKVTVTGGTGKDGYYEVSVDKTNGEVTLAGGATSPLTGGLP ATATEDVKNVQVANADLTEAKAALTAAGVTGASVVKMSYTDN NGKTIDGGLAVKVGDDYYSATQNKDGSISINTTKYTADDGTSKTA LNKLGADGKTEVVSIGGKTYAASKAEGHNFKAPDLAEAAATT TENPLQKIDAALAQVDTLRSDLGAVQNRFNSAITNLGNTVNNLTS ARSRIEDSDYATEVSNMSRAQILQQAGTSVLAQANQVPQNVLSLL RGGGSGGGGSMMPDPNPANPNANPNANPNANPNANPNANPN <u>NPANPNANPNANPNANPNANPNANPNANPNANPNANPNANPN</u> <u>ANPNANPNKNNQNGQGHNMPNDPNRNVDENANANNNAVKNN</u> <u>NEEPSDKHIEQYLLKKIKNSISTEWSPCSVTCGNGIQVRIKPGSANKP</u> <u>KDELVDYENDIEKKICKMEKCSSVFNVVNS</u>	55
Flagellin- RPVT linker- circumsporozoite protein (CSP)	MMADPNANPNANPNANPNANPNANPNANPNANPNANPNANPN ANPNANPNANPNANPNANPNANPNANPNANPNANPNANPNKNN QNGQGHNMPNDPNRNVDENANANNNAVKNNNEEPSDKHIEQY LKKIKNSISTEWSPCSVTCGNGIQVRIKPGSANKPKDELVDYENDIEK KICKMEKCSSVFNVVNSRPVTMAQVINTNSLSLLTQNNLNKSQSA <u>LGTAIERLSSGLRINSKDDAAGQAIANRFTANIKGLTQASRNAND</u>	56

TABLE 17-continued

Flagellin Amino Acid Sequences		
Name	Sequence	SEQ ID NO:
	<u>GISIAQTTEGALNEINNLRVRELAVQSANSTNSQSDLDLSIQAEIT</u>	
	<u>QRLNEIDRVSGGTQFNGVKVLAQDNTLTIQVGANDGETIDIDLKQI</u>	
	<u>NSQTLGLDITLVQQKYKVSdTAAVTVTGYADTTIALDNSTFKASAT</u>	
	<u>GLGGTDQKIDGDLKFDDTTGKYYAKVTVTGGTGKDGYYEVSVD</u>	
	<u>KTNGEVTLAGGATSPLTGGLPATATEDVKNVQVANADLTEAKAA</u>	
	<u>LTAAGVTGTASVVKMSYTDNNGKTIIDGGLAVKVGDDYYSATQN</u>	
	<u>KDGSISINTTKYTADDGTSKTALNKLGGADGKTEVVSIGGKTYAA</u>	
	<u>SKAEGHNFKAQPDLAEEAAATTENPLQKIDAALAQVDTLRSDLG</u>	
	<u>AVQNRFNSAITNLGNTVNNLTSARSRIEDSDYATEVSNMSRAQILQ</u>	
	<u>QAGTSVLAQANQVPQNVLSLLR</u>	

TABLE 18

Human Metapneumovirus Mutant Amino Acid Sequences		
Strain	Sequence	SEQ ID NO:
HMPV_SC_DSCAVI_4MMV	MSWKVVIIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEVGDVENLTCSGSPSLIKTELDLTKSALRELKTVSADQLAREBQIENPGSGSFVLGAIALGVAAAAAVTAGVAICTIRLESEVTAINNALKKTNEAVSTLNGVVRVLATAVRELKDFVSKNLTRALNKNKCDIDDLKMAVSFSQFNRRFLNVVRQFS DNAGITPAISLDLMTDAELARAVPNMPTSAGQIKLMLENRAMVRRKGFILCGVYGSSVIYMQLP IFGV IDTPCWIVKAAPSCSEKKGNACLLREDQGWY CQNAGSTVYYPNEKDCETRGDHVFCDTAAGINVAEQSKECNINISTNYPCKVSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIIKQLNKGCSYITNQDADTVTIDNTVYQLSKVEGEQHVIGKRPVSSSFDPKFPEDQFNVALDQVFE NIENSQALVDQSNRILSSAEKGNTGFIIVILIAVLGSSMILVSIPIIKKTKK PTGAPPELSGVTNNGFIPHN	85
HMPV_SC_DSTRIC_4MMV	MSWKVVIIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEVGDVENLTCSGSPSLIKTELDLTKSALRELKTVSADQLAREBQIENPGSGSFVLGAIALGVAAAAAVTAGVAICTIRLESEVTAINNALKKTNEAVSTLNGVVRVLATAVRELKDFVSKNLTRALNKNKCDIDDLKMAVSFSQFNRRFLNVVRQFS DNAGITPAISLDLMTDAELARAVPNMPTSAGQIKLMLENRAMVRRKGFILCGVYGSSVIYMQLP IFGV IDTPCWIVKAAPSCSEKKGNACLLREDQGWY CQNAGSTVYYPNEKDCETRGDHVFCDTAAGINVAEQSKECNINISTNYPCKVSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIIKQLNKGCSYITNQDADTVTIDNTVYQLSKVEGEQHVIGKRPVSSSFDPKFPEDQFNVALDQVFE NIENSQALVDQSNRILSSAEKGNTGFIIVILIAVLGSSMILVSIPIIKKTKK PTGAPPELSGVTNNGFIPHN	86
HMPV_SC_DM_Krarup_T74LD185P	MSWKVVIIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEVGDVENLTCSGSPSLIKTELDLLKSALRELKTVSADQLAREBQIENPGSGSFVLGAIALGVAAAAAVTAGVAIAKTIRLESEVTAINNALKKTNEAVSTLNGVVRVLATAVRELKDFVSKNLTRALNKNKCDIDDLKMAVSFSQFNRRFLNVVRQFS DNAGITPAISLDLMTDAELARAVPNMPTSAGQIKLMLENRAMVRRKGFILIGVYGSSVIYMQLP IFGV IDTPCWIVKAAPSCSEKKGNACLLREDQGWYCQNAGSTVYYPNEKDCETRGDHVFCDTAAGINVAEQSKECNINISTNYPCKVSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIIKQLNKGCSYITNQDADTVTIDNTVYQLSKVEGEQHVIGKRPVSSSFDPKFPEDQFNVALDQVFE NIENSQALVDQSNRILSSAEKGNTGFIIVILIAVLGSSMILVSIPIIKKTKK PTGAPPELSGVTNNGFIPHN	87
HMPV_SC_TM_Krarup_T74LD185PD454N	MSWKVVIIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEVGDVENLTCSGSPSLIKTELDLLKSALRELKTVSADQLAREBQIENPGSGSFVLGAIALGVAAAAAVTAGVAIAKTIRLESEVTAINNALKKTNEAVSTLNGVVRVLATAVRELKDFVSKNLTRALNKNKCDIDDLKMAVSFSQFNRRFLNVVRQFS DNAGITPAISLDLMTDAELARAVPNMPTSAGQIKLMLENRAMVRRKGFILIGVYGSSVIYMQLP IFGV IDTPCWIVKAAPSCSEKKGNACLLREDQGWYCQNAGSTVYYPNEKDCETRGDHVFCDTAAGINVAEQSKECNINISTNYPCKVSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIIKQLNKGCSYITNQDADTVTIDNTVYQLSKVEGEQHVIGKRPVSSSFDPKFPEDQFNVALDQVFE NIENSQALVDQSNRILSSAEKGNTGFIIVILIAVLGSSMILVSIPIIKKTKK PTGAPPELSGVTNNGFIPHN	88

TABLE 18-continued

Human Metapneumovirus Mutant Amino Acid Sequences		
Strain	Sequence	SEQ ID NO:
HMPV_SC_4M_Krarup_T74LS170LD185P	MSWKVVIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEVGDVENLTCSDGPSLIKTELDLLKSALRELKTVSADQLAREEQIENPGSGSFVLGAIALGVAAAAAVTAGVAIAKTIRLESEVTAINNALKKTNEAVSTLNGNVRVLATAVRELKDFVLKNLTRAINKNKCDIPDLKMAVSFSQFNRRFLNVVRQFSDNAGITPAISLDLMTDAELARAVPNMPTSAGQIKLMLLENRAMVRRKGFGILIGVYGSSVIYMQLPPIFGVIDTPCWIVKAAPSCSEKKGNACLLREDQGWYCNAGSTVYYYPNEKDCETRGDHVPCDTAAGINVAEQSKECNINISTTNYPCKVSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIKQLNKGCSYITNQDADTVTIDNTVYQLSKVEGEQHVIGRPFVSSSFDPIKFPEDQFQVALDQVFENIENSQALVDQSNRILSSAEKGNTGFIIVIIILIAVLGSSMILVSIPIIIKTKKPTGAPPELSGVTNNGFIPHN	89
HMPV_SC_5M_Krarup_T74LS170LD185PD454N	MSWKVVIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEVGDVENLTCSDGPSLIKTELDLLKSALRELKTVSADQLAREEQIENPGSGSFVLGAIALGVAAAAAVTAGVAIAKTIRLESEVTAINNALKKTNEAVSTLNGNVRVLATAVRELKDFVLKNLTRAINKNKCDIPDLKMAVSFSQFNRRFLNVVRQFSDNAGITPAISLDLMTDAELARAVPNMPTSAGQIKLMLLENRAMVRRKGFGILIGVYGSSVIYMQLPPIFGVIDTPCWIVKAAPSCSEKKGNACLLREDQGWYCNAGSTVYYYPNEKDCETRGDHVPCDTAAGINVAEQSKECNINISTTNYPCKVSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIKQLNKGCSYITNQDADTVTIDNTVYQLSKVEGEQHVIGRPFVSSSFDPIKFPEDQFQVALDQVFENIENSQALVDQSNRILSSAEKGNTGFIIVIIILIAVLGSSMILVSIPIIIKTKKPTGAPPELSGVTNNGFIPHN	90
HMPV_SC_DM_Krarup_E51PT74L	MSWKVVIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEVGDVENLTCSDGPSLIKTELDLLKSALRELKTVSADQLAREEQIENPGSGSFVLGAIALGVAAAAAVTAGVAIAKTIRLESEVTAINNALKKTNEAVSTLNGNVRVLATAVRELKDFVSKNLTRAINKNKCDIDDLKMAVSFSQFNRRFLNVVRQFSDNAGITPAISLDLMTDAELARAVPNMPTSAGQIKLMLLENRAMVRRKGFGILIGVYGSSVIYMQLPPIFGVIDTPCWIVKAAPSCSEKKGNACLLREDQGWYCNAGSTVYYYPNEKDCETRGDHVPCDTAAGINVAEQSKECNINISTTNYPCKVSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIKQLNKGCSYITNQDADTVTIDNTVYQLSKVEGEQHVIGRPFVSSSFDPIKFPEDQFQVALDQVFENIENSQALVDQSNRILSSAEKGNTGFIIVIIILIAVLGSSMILVSIPIIIKTKKPTGAPPELSGVTNNGFIPHN	91
HMPV_SC_TM_Krarup_E51PT74LD454N	MSWKVVIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEVGDVENLTCSDGPSLIKTELDLLKSALRELKTVSADQLAREEQIENPGSGSFVLGAIALGVAAAAAVTAGVAIAKTIRLESEVTAINNALKKTNEAVSTLNGNVRVLATAVRELKDFVSKNLTRAINKNKCDIDDLKMAVSFSQFNRRFLNVVRQFSDNAGITPAISLDLMTDAELARAVPNMPTSAGQIKLMLLENRAMVRRKGFGILIGVYGSSVIYMQLPPIFGVIDTPCWIVKAAPSCSEKKGNACLLREDQGWYCNAGSTVYYYPNEKDCETRGDHVPCDTAAGINVAEQSKECNINISTTNYPCKVSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIKQLNKGCSYITNQDADTVTIDNTVYQLSKVEGEQHVIGRPFVSSSFDPIKFPEDQFQVALDQVFENIENSQALVDQSNRILSSAEKGNTGFIIVIIILIAVLGSSMILVSIPIIIKTKKPTGAPPELSGVTNNGFIPHN	92
HMPV_SC_StabilizeAlpha_T74L	MSWKVVIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEVGDVENLTCSDGPSLIKTELDLLKSALRELKTVSADQLAREEQIENPGSGSFVLGAIALGVAAAAAVTAGVAIAKTIRLESEVTAINNALKKTNEAVSTLNGNVRVLATAVRELKDFVSKNLTRAINKNKCDIDDLKMAVSFSQFNRRFLNVVRQFSDNAGITPAISLDLMTDAELARAVPNMPTSAGQIKLMLLENRAMVRRKGFGILIGVYGSSVIYMQLPPIFGVIDTPCWIVKAAPSCSEKKGNACLLREDQGWYCNAGSTVYYYPNEKDCETRGDHVPCDTAAGINVAEQSKECNINISTTNYPCKVSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIKQLNKGCSYITNQDADTVTIDNTVYQLSKVEGEQHVIGRPFVSSSFDPIKFPEDQFQVALDQVFENIENSQALVDQSNRILSSAEKGNTGFIIVIIILIAVLGSSMILVSIPIIIKTKKPTGAPPELSGVTNNGFIPHN	93
HMPV_SC_StabilizeAlpha_V55L	MSWKVVIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEVGDVENLTCSDGPSLIKTELDLLKSALRELKTVSADQLAREEQIENPGSGSFVLGAIALGVAAAAAVTAGVAIAKTIRLESEVTAINNALKKTNEAVSTLNGNVRVLATAVRELKDFVSKNLTRAINKNKCDIDDLKMAVSFSQFNRRFLNVVRQFSDNAGITPAISLDLMTDAELARAVPNMPTSAGQIKLMLLENRAMVRRKGFGILIGVYGSSVIYMQLPPIFGVIDTPCWIVKAAPSCSEKKGNACLLREDQGWYCNAGSTVYYYPNEKDCETRGDHVPCDTAAGINVAEQSKECNINISTTNYPCKVSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIKQLNKGCSYITNQDADTVTIDNTVYQLSKVEGEQHVIGRPFVSSSFDPIKFPEDQFQVALDQVFENIENSQALVDQSNRILSSAEKGNTGFIIVIIILIAVLGSSMILVSIPIIIKTKKPTGAPPELSGVTNNGFIPHN	94

TABLE 18-continued

Human Metapneumovirus Mutant Amino Acid Sequences		
Strain	Sequence	SEQ ID NO:
	ADTVTIDNTVYQLSKVEGEQHVIGKRPVSSSFDPIKFPEDQFQVALDQVFENI ENSQALVDQSNRILSSAEKGNTGFIIVIIILIAVLGSSMILVSIPIIIKTKKKP TGAPPELSGVTNNGFIPHN	
HMPV_SC_StabilizeAlpha_S170L	MSWKVVIIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEV DVENLTCSDGSPSLIKTELDLTKSALRELKTVSADQLAREEQIENPGSGSFVLG AIALGVAAAAAVTAGVAIAKTIRLESEVTAINNALKKTNEAVSTLGNQVRV LATAVRELKDFVLKNLTRAINKNKCDIDDLKMAVSFSQFNRRFLNVVRQFS DNAGITPAISLDLMTDAELARAVPNMPTSAGQIKMLLENRAMVRRKGFIL GVYGS SVI YMVQLPIFGVIDTPCWI VKAAPSCSEKKNYACLLREDQGWYC QNAGSTVYYPNEKDCETRGDHFVCDTAAGINVAEQSKECNINISTTNYPC VSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIKQLNKGCSYITNQD ADTVTIDNTVYQLSKVEGEQHVIGKRPVSSSFDPIKFPEDQFQVALDQVFENI ENSQALVDQSNRILSSAEKGNTGFIIVIIILIAVLGSSMILVSIPIIIKTKKKP TGAPPELSGVTNNGFIPHN	95
HMPV_SC_StabilizeAlpha_T174W	MSWKVVIIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEV DVENLTCSDGSPSLIKTELDLTKSALRELKTVSADQLAREEQIENPGSGSFVLG AIALGVAAAAAVTAGVAIAKTIRLESEVTAINNALKKTNEAVSTLGNQVRV LATAVRELKDFVSKNLTRAINKNKCDIDDLKMAVSFSQFNRRFLNVVRQFS DNAGITPAISLDLMTDAELARAVPNMPTSAGQIKMLLENRAMVRRKGFIL GVYGS SVI YMVQLPIFGVIDTPCWI VKAAPSCSEKKNYACLLREDQGWYC QNAGSTVYYPNEKDCETRGDHFVCDTAAGINVAEQSKECNINISTTNYPC VSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIKQLNKGCSYITNQD ADTVTIDNTVYQLSKVEGEQHVIGKRPVSSSFDPIKFPEDQFQVALDQVFENI ENSQALVDQSNRILSSAEKGNTGFIIVIIILIAVLGSSMILVSIPIIIKTKKKP TGAPPELSGVTNNGFIPHN	96
HMPV_SC_4M_StabilizeAlpha_V55LT74LS170LT174W	MSWKVVIIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEV DVENLTCSDGSPSLIKTELDLTKSALRELKTVSADQLAREEQIENPGSGSFVLG AIALGVAAAAAVTAGVAIAKTIRLESEVTAINNALKKTNEAVSTLGNQVRV LATAVRELKDFVLKNLTRAINKNKCDIDDLKMAVSFSQFNRRFLNVVRQFS DNAGITPAISLDLMTDAELARAVPNMPTSAGQIKMLLENRAMVRRKGFIL GVYGS SVI YMVQLPIFGVIDTPCWI VKAAPSCSEKKNYACLLREDQGWYC QNAGSTVYYPNEKDCETRGDHFVCDTAAGINVAEQSKECNINISTTNYPC VSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIKQLNKGCSYITNQD ADTVTIDNTVYQLSKVEGEQHVIGKRPVSSSFDPIKFPEDQFQVALDQVFENI ENSQALVDQSNRILSSAEKGNTGFIIVIIILIAVLGSSMILVSIPIIIKTKKKP TGAPPELSGVTNNGFIPHN	97
HMPV_ProlineStab_E51P	MSWKVVIIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEV DVENLTCSDGSPSLIKTELDLTKSALRELKTVSADQLAREEQIENPGSGSFVLG AIALGVAAAAAVTAGVAIAKTIRLESEVTAINNALKKTNEAVSTLGNQVRV LATAVRELKDFVSKNLTRAINKNKCDIDDLKMAVSFSQFNRRFLNVVRQFS DNAGITPAISLDLMTDAELARAVPNMPTSAGQIKMLLENRAMVRRKGFIL GVYGS SVI YMVQLPIFGVIDTPCWI VKAAPSCSEKKNYACLLREDQGWYC QNAGSTVYYPNEKDCETRGDHFVCDTAAGINVAEQSKECNINISTTNYPC VSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIKQLNKGCSYITNQD ADTVTIDNTVYQLSKVEGEQHVIGKRPVSSSFDPIKFPEDQFQVALDQVFENI ENSQALVDQSNRILSSAEKGNTGFIIVIIILIAVLGSSMILVSIPIIIKTKKKP TGAPPELSGVTNNGFIPHN	98
HMPV_ProlineStab_D185P	MSWKVVIIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEV DVENLTCSDGSPSLIKTELDLTKSALRELKTVSADQLAREEQIENPGSGSFVLG AIALGVAAAAAVTAGVAIAKTIRLESEVTAINNALKKTNEAVSTLGNQVRV LATAVRELKDFVSKNLTRAINKNKCDIDDLKMAVSFSQFNRRFLNVVRQFS DNAGITPAISLDLMTDAELARAVPNMPTSAGQIKMLLENRAMVRRKGFIL GVYGS SVI YMVQLPIFGVIDTPCWI VKAAPSCSEKKNYACLLREDQGWYC QNAGSTVYYPNEKDCETRGDHFVCDTAAGINVAEQSKECNINISTTNYPC VSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIKQLNKGCSYITNQD ADTVTIDNTVYQLSKVEGEQHVIGKRPVSSSFDPIKFPEDQFQVALDQVFENI ENSQALVDQSNRILSSAEKGNTGFIIVIIILIAVLGSSMILVSIPIIIKTKKKP TGAPPELSGVTNNGFIPHN	99
HMPV_ProlineStab_D183P	MSWKVVIIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEV DVENLTCSDGSPSLIKTELDLTKSALRELKTVSADQLAREEQIENPGSGSFVLG AIALGVAAAAAVTAGVAIAKTIRLESEVTAINNALKKTNEAVSTLGNQVRV LATAVRELKDFVSKNLTRAINKNKCDIDDLKMAVSFSQFNRRFLNVVRQFS DNAGITPAISLDLMTDAELARAVPNMPTSAGQIKMLLENRAMVRRKGFIL GVYGS SVI YMVQLPIFGVIDTPCWI VKAAPSCSEKKNYACLLREDQGWYC QNAGSTVYYPNEKDCETRGDHFVCDTAAGINVAEQSKECNINISTTNYPC VSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIKQLNKGCSYITNQD ADTVTIDNTVYQLSKVEGEQHVIGKRPVSSSFDPIKFPEDQFQVALDQVFENI ENSQALVDQSNRILSSAEKGNTGFIIVIIILIAVLGSSMILVSIPIIIKTKKKP TGAPPELSGVTNNGFIPHN	100

TABLE 18-continued

Human Metapneumovirus Mutant Amino Acid Sequences		
Strain	Sequence	SEQ ID NO:
	VSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIKQLNKGCSYITNQD ADTVTIDNTVYQLSKVEGEQHVIGKRPVSSSFDPKFPEDQFQVALDQVFENI ENSQALVDQSNRILSSAEKGNTGFIIVIIILIAVLGSSMILVSIPIIIKTKKP TGAPPELSGVTNNGFIPHN	
HMPV_ProlineStab_E131P	MSWKVVIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEV DVENLTCSDGPSLIKTELDTKSALRELKTVSADQLAREEQIENPGSGSFVLG AIALGVAAAAVATAGVAIAKTI RLPEVTAINNALKKTNEAVSTLNGVRV LATAVRELKDFVSKNLTRAINKNKCDIDDLKMAVSFSQFNRRFLNVVRQFS DNAGITPAISLDLMTDAELARAVPNMPTSAGQIKMLLENRAMVRRKGFIL GVYSSSVIYMQLPPIFGVIDTPCWIVKAAPSCSEKKGNACLLREDQGWYC QNAGSTVYYYPNEKDCETRGRDHVFCDTAAGINVAEQSKECNINISTTNYPC VSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIKQLNKGCSYITNQD ADTVTIDNTVYQLSKVEGEQHVIGKRPVSSSFDPKFPEDQFQVALDQVFENI ENSQALVDQSNRILSSAEKGNTGFIIVIIILIAVLGSSMILVSIPIIIKTKKP TGAPPELSGVTNNGFIPHN	101
HMPV_ProlineStab_D447P	MSWKVVIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEV DVENLTCSDGPSLIKTELDTKSALRELKTVSADQLAREEQIENPGSGSFVLG AIALGVAAAAVATAGVAIAKTI RLSEVTAINNALKKTNEAVSTLNGVRV LATAVRELKDFVSKNLTRAINKNKCDIDDLKMAVSFSQFNRRFLNVVRQFS DNAGITPAISLDLMTDAELARAVPNMPTSAGQIKMLLENRAMVRRKGFIL GVYSSSVIYMQLPPIFGVIDTPCWIVKAAPSCSEKKGNACLLREDQGWYC QNAGSTVYYYPNEKDCETRGRDHVFCDTAAGINVAEQSKECNINISTTNYPC VSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIKQLNKGCSYITNQD ADTVTIDNTVYQLSKVEGEQHVIGKRPVSSSFDPKFPEDQFQVALDQVFENI ENSQALVDQSNRILSSAEKGNTGFIIVIIILIAVLGSSMILVSIPIIIKTKKP TGAPPELSGVTNNGFIPHN	102
HMPV_TrimerRepulsionD454N	MSWKVVIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEV DVENLTCSDGPSLIKTELDTKSALRELKTVSADQLAREEQIENPGSGSFVLG AIALGVAAAAVATAGVAIAKTI RLSEVTAINNALKKTNEAVSTLNGVRV LATAVRELKDFVSKNLTRAINKNKCDIDDLKMAVSFSQFNRRFLNVVRQFS DNAGITPAISLDLMTDAELARAVPNMPTSAGQIKMLLENRAMVRRKGFIL GVYSSSVIYMQLPPIFGVIDTPCWIVKAAPSCSEKKGNACLLREDQGWYC QNAGSTVYYYPNEKDCETRGRDHVFCDTAAGINVAEQSKECNINISTTNYPC VSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIKQLNKGCSYITNQD ADTVTIDNTVYQLSKVEGEQHVIGKRPVSSSFDPKFPEDQFQVALDQVFENI ENSQALVDQSNRILSSAEKGNTGFIIVIIILIAVLGSSMILVSIPIIIKTKKP TGAPPELSGVTNNGFIPHN	103
HMPV_TrimerRepulsionE453N	MSWKVVIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEV DVENLTCSDGPSLIKTELDTKSALRELKTVSADQLAREEQIENPGSGSFVLG AIALGVAAAAVATAGVAIAKTI RLSEVTAINNALKKTNEAVSTLNGVRV LATAVRELKDFVSKNLTRAINKNKCDIDDLKMAVSFSQFNRRFLNVVRQFS DNAGITPAISLDLMTDAELARAVPNMPTSAGQIKMLLENRAMVRRKGFIL GVYSSSVIYMQLPPIFGVIDTPCWIVKAAPSCSEKKGNACLLREDQGWYC QNAGSTVYYYPNEKDCETRGRDHVFCDTAAGINVAEQSKECNINISTTNYPC VSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIKQLNKGCSYITNQD ADTVTIDNTVYQLSKVEGEQHVIGKRPVSSSFDPKFPEDQFQVALDQVFENI ENSQALVDQSNRILSSAEKGNTGFIIVIIILIAVLGSSMILVSIPIIIKTKKP TGAPPELSGVTNNGFIPHN	104
HMPV_StabilizeAlphaF196W	MSWKVVIIFSLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEV DVENLTCSDGPSLIKTELDTKSALRELKTVSADQLAREEQIENPGSGSFVLG AIALGVAAAAVATAGVAIAKTI RLSEVTAINNALKKTNEAVSTLNGVRV LATAVRELKDFVSKNLTRAINKNKCDIDDLKMAVSFSQFNRRFLNVVRQFS DNAGITPAISLDLMTDAELARAVPNMPTSAGQIKMLLENRAMVRRKGFIL GVYSSSVIYMQLPPIFGVIDTPCWIVKAAPSCSEKKGNACLLREDQGWYC QNAGSTVYYYPNEKDCETRGRDHVFCDTAAGINVAEQSKECNINISTTNYPC VSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIKQLNKGCSYITNQD ADTVTIDNTVYQLSKVEGEQHVIGKRPVSSSFDPKFPEDQFQVALDQVFENI ENSQALVDQSNRILSSAEKGNTGFIIVIIILIAVLGSSMILVSIPIIIKTKKP TGAPPELSGVTNNGFIPHN	105

TABLE 19

Strain	Nucleic Acid Sequence	SEQ ID NO:
Human Metapneumovirus Mutant Nucleic Acid Sequences		
HMPV_SC_DSCAV1_4MMV	ATGAGCTGGAAGGTGGTCATCATCTTCAGCCTGCTGATCA CACCTCAGCACGGCCTGAAAGAGAGCTACCTGGAAGAGT CCTGCAGCACCATCAGAGAGGGCTACCTGTCTGTGCTGAG AACCGGCTGGTACACCAACGTGTTACACTGGAAGTGGGC GACGTCGAGAATCTGACATGCTCTGATGGCCCTAGCCTGA TCAAGACCGAGCTGGATCTGACCAAGAGCGCCCTGAGAG AACTCAAGACCGTGTCTGCCGATCAGCTGGCCAGAGAGGA ACAGATCGAGAATCCTGGCAGCGGCAGCTTTGTGCTGGGA GCCATTGCTCTTGGAGTGGCTGCTGCTGCAGCTGTTACAG CAGGCGTGGCCATCTGCAAGACCATCAGACTGGAAAGCG AAGTGACCGCCATCAACAACGCCCTGAAGAAGACAAACG AGGCCGTCAGCACACTCGGCAATGGCGTTAGAGTGCTGGC CTTTGGCGTGCAGAGCTGAAGGACTTCGTGTCCAAGAAC CTGACACGGGCCCTGAACAAGAACAAGTGCGACATCGAC GACCTGAAGATGGCCGTGTCTTTAGCCAGTTCAACCGGC GGTTCCTGAACGTCGTGCGGCAGTTTAGCGACAACGCCGG AATCACACCAGCCATCAGCCTGGACCTGATGACAGATGCT GAGCTGGCTAGAGCCGTGCCTAACATGCCTACATCTGCCG GCCAGATCAAGCTGATGCTCGAGAATAGAGCCATGGTCCG ACGGAAAGGCTTCGGCATTCTGTGTGGCGTGTACGGCAGC AGCGTGATCTATATGGTGCAGCTGCCTATCTTCGGCGTGA TCGACACACCCCTGCTGGATTGTGAAGGCCGCTCCTAGCTG TAGCGAGAAGAAGGGCAATTACGCCTGCCCTGCTGAGAGA GGACCAAGGCTGGTATTGTGAGAACGCCCGCAGCACCGTG TACTACCCCTAACGAGAAGGACTGCGAGACAAGAGGCGAC CACGTGTTCTGTGATACCGCCGCTGGAATCAATGTGGCCG AGCAGAGCAAGAGTGCACATCAACATCAGCACCACCA ACTATCCCTGCAAGGTGTCCACCGGCAGGCACCCATTTC TATGGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGT ATAAGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGG GCATCATCAAGCAGCTGAACAAGGGCTGCAGCTACATCAC CAACCAGGACGCGGATACCGTGACCATCGACAACACCGTG TATCAGCTGAGCAAGGTGGAAGGCGAACAGCAGCTGATC AAGGGCAGACCTGTGTCCAGCAGCTTCGACCCATCAAGT TCCCTGAGGATCAGTTCAACGTGGCCCTGGACAGGTGTT CGAGAACATCGAGAATTCCAGGCTCTGGTGGACAGTCC AACAGAATCCTGTCTAGCGCCGAGAAGGGAAACACCGGC TTATCATCGTGATCATCTGATCGCCGTGCTGGGCAGCTC CATGATCCTGGTGCTCATCTTCATCATTATCAAGAAGACC AAGAAGCCACCGGCGCTCCTCCAGAATGAGCGGAGTG ACCAACAAATGGCTTCATCCCTCACAAC	106
HMPV_SC_DSTRIC_4MMV	ATGAGCTGGAAGGTGGTCATCATCTTCAGCCTGCTGATCA CACCTCAGCACGGCCTGAAAGAGAGCTACCTGGAAGAGT CCTGCAGCACCATCAGAGAGGGCTACCTGTCTGTGCTGAG AACCGGCTGGTACACCAACGTGTTACACTGGAAGTGGGC GACGTCGAGAATCTGACATGCTCTGATGGCCCTAGCCTGA TCAAGACCGAGCTGGATCTGACCAAGAGCGCCCTGAGAG AACTCAAGACCGTGTCTGCCGATCAGCTGGCCAGAGAGGA ACAGATCGAGAATCCTGGCAGCGGCAGCTTTGTGCTGGGA GCCATTGCTCTTGGAGTGGCTGCTGCTGCAGCTGTTACAG CAGGCGTGGCCATCTGCAAGACCATCAGACTGGAAAGCG AAGTGACCGCCATCAACAACGCCCTGAAGAAGACAAACG AGGCCGTCAGCACACTCGGCAATGGCGTTAGAGTGCTGGC CACAGCCGTGCGCGAGCTGAAGGACTTCGTGTCCAAGAAC CTGACACGGGCCATTAAACAAGAACAAGTGCGACATCGAC GACCTGAAGATGGCCGTGTCTTTAGCCAGTTCAACCGGC GGTTCCTGAACGTCGTGCGGCAGTTTAGCGACAACGCCGG AATCACACCAGCCATCAGCCTGGACCTGATGACAGATGCT GAGCTGGCTAGAGCCGTGCCTAACATGCCTACATCTGCCG GCCAGATCAAGCTGATGCTCGAGAATAGAGCCATGGTCCG ACGGAAAGGCTTCGGCATTCTGTGTGGCGTGTACGGCAGC AGCGTGATCTATATGGTGCAGCTGCCTATCTTCGGCGTGA TCGACACACCCCTGCTGGATTGTGAAGGCCGCTCCTAGCTG TAGCGAGAAGAAGGGCAATTACGCCTGCCCTGCTGAGAGA GGACCAAGGCTGGTATTGTGAGAACGCCCGCAGCACCGTG TACTACCCCTAACGAGAAGGACTGCGAGACAAGAGGCGAC CACGTGTTCTGTGATACCGCCGCTGGAATCAATGTGGCCG AGCAGAGCAAGAGTGCACATCAACATCAGCACCACCA ACTATCCCTGCAAGGTGTCCACCGGCAGGCACCCATTTC TATGGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGT ATAAGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGG	107

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
	GCATCATCAAGCAGCTGAACAAGGGCTGCAGCTACATCAC CAACCAGGACGCCGATACCGTGACCATCGACAACACCGTG TATCAGCTGAGCAAGGTGGAAGGCGAACAGCAGCTGATC AAGGGCAGACCTGTGTCCAGCAGCTTCGACCCATCAAGT TCCCTGAGCACCAGTGGCATGTGGCCCTGGACAGGTGTT CGAGAACATCGAGAATCCCAGGCTCTGGTGGACAGTCC AACAGAATCCTGTCTAGCGCCGAGAAGGGAAACACCGGC TTCATCATCGTGATCATCTGATCGCCGTGCTGGCAGCTC CATGATCCTGGTGTCCATCTTCATCATTATCAAGAAGACC AAGAAGCCACCGCGCTCCTCCAGAAGTGAAGCGGAGTG ACCAACAATGGCTTCATCCCTCACAAC	
HMPV_SC_DM_Krarup_T74LD185P	ATGAGCTGGAAGGTGGTCATCATCTTCAGCCTGCTGATCA CACCTCAGCACGGCTGAAAGAGAGCTACCTGGAAGAGT CCTGCAGCACCATCACAGAGGGCTACCTGTCTGTGCTGAG AACCGGCTGGTACACCAACGTGTTCACTGGAAGTGGGC GACGTGAGAAATCTGACATGCTCTGATGGCCCTAGCCTGA TCAAGACCGAGCTGGATCTGCTCAAGAGCGCCCTGAGAGA ACTCAAGACCGTGTCTGCCGATCAGCTGGCCAGAGAGGAA CAGATCGAGAATCCTGGCAGCGCAGCTTTGTGCTGGGAG CCATTGCTCTTGAGTGGCTGTGCTGCAGCTGTTACAGC AGGCGTGGCCATCGCTAAGACCATCAGACTGGAAGCGA AGTGACCGCCATCAACAACGCCCTGAAGAAGACAAACGA GGCCGTGAGCAGCTCGGCAATGGCGTTAGAGTGCTGGCC ACAGCCGTGCGGAGCTGAAGGACTTCGTGTCCAAGAACC TGACACGGGCCATTAAACAAGAACAGTGCGACATCCCTGA CCTGAAGATGGCCGTGTCTTTAGCCAGTTCAACCGGCGG TTTCTGAACGTGCTGCGGAGTTTACGACAAACGCCGAA TCACACCAGCCATCAGCCTGGACCTGATGACAGATGCTGA GCTGGCTAGAGCCGTGCCTAACATGCCTACATCTGCCGGC CAGATCAAGCTGATGCTCGAGAATAGAGCCATGGTCCGAC GGAAGGCTTCGGCATTCTGATTGGCGTGTACGGCAGCAG CGTGATCTATATGGTGCAGCTGCCTATCTTCGGCGTGATCG ACACACCTGTCTGGATTGTGAAGGCCGCTCCTAGCTGTAG CGAGAAGAAGGGCAATTACGCCTGCCTGCTGAGAGAGGA CCAAGGCTGGTATTGTGAGAACGCCGGCAGCACCGTGATC TACCTTAACGAGAAGGACTGCGAGACAAGAGGCGACCAC GTGTTCTGTGATACCGCGCTGGAATCAATGTGGCCGAGC AGAGCAAGAGTGAACATCAACATCAGCACCACCAACT ATCCCTGCAAGGTGTCCACCGGCGAGCACCTATTTCTAT GGTGGCTCTGTCTCTCTGGGAGCCCTGGTGGCTTGTATA AGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGGGCAT CATCAAGCAGCTGAACAAGGGCTGCAGCTACATCACCAAC CAGGACGCCGATACCGTGACCATCGACAACACCGTGATC AGCTGAGCAAGGTGGAAGGCGAACAGCAGCAGTGATCAAGG GCAGACCTGTGTCCAGCAGCTTCGACCCATCAAGTTCC TGAGGATCAGTTCCAGGTGGCCCTGGACAGGTGTTTCGAG AACATCGAGAATCCCAGGCTCTGGTGGACAGTCCAACA GAATCCTGTCTAGCGCCGAGAAGGGAAACACCGGCTTCAT CATCGTGATCATCTGATCGCCGTGCTGGGCGCTCCATG ATCCTGGTGTCCATCTTCATCATTATCAAGAAGACCAAGA AGCCACCGCGCTCCTCCAGAAGTGAAGCGAGTGACCAA CAATGGCTTCATCCCTCACAAC	108
HMPV_SC_TM_Krarup_T74LD185PD454N	ATGAGCTGGAAGGTGGTCATCATCTTCAGCCTGCTGATCA CACCTCAGCACGGCTGAAAGAGAGCTACCTGGAAGAGT CCTGCAGCACCATCACAGAGGGCTACCTGTCTGTGCTGAG AACCGGCTGGTACACCAACGTGTTCACTGGAAGTGGGC GACGTGAGAAATCTGACATGCTCTGATGGCCCTAGCCTGA TCAAGACCGAGCTGGATCTGCTCAAGAGCGCCCTGAGAGA ACTCAAGACCGTGTCTGCCGATCAGCTGGCCAGAGAGGAA CAGATCGAGAATCCTGGCAGCGCAGCTTTGTGCTGGGAG CCATTGCTCTTGAGTGGCTGTGCTGCAGCTGTTACAGC AGGCGTGGCCATCGCTAAGACCATCAGACTGGAAGCGA AGTGACCGCCATCAACAACGCCCTGAAGAAGACAAACGA GGCCGTGAGCAGCTCGGCAATGGCGTTAGAGTGCTGGCC ACAGCCGTGCGGAGCTGAAGGACTTCGTGTCCAAGAACC TGACACGGGCCATTAAACAAGAACAGTGCGACATCCCTGA CCTGAAGATGGCCGTGTCTTTAGCCAGTTCAACCGGCGG TTTCTGAACGTGCTGCGGAGTTTACGACAAACGCCGAA TCACACCAGCCATCAGCCTGGACCTGATGACAGATGCTGA GCTGGCTAGAGCCGTGCCTAACATGCCTACATCTGCCGGC CAGATCAAGCTGATGCTCGAGAATAGAGCCATGGTCCGAC GGAAGGCTTCGGCATTCTGATTGGCGTGTACGGCAGCAG	109

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
	CGTGATCTATATGGTGCAGCTGCCTATCTTCGGCGTGATCG ACACACCTGCTGGATTGTGAAGGCCGCTCCTAGCTGTAG CGAGAAGAAGGGCAATTACGCCCTGCTGTGAGAGAGGA CCAAGGCTGGTATGTGAGAACGCCGCGCAGCACCGTGATC TACCCTAACGAGAAGGACTGCGAGACAAGAGGCGACCAC GTGTTCTGTGATACCGCCGCTGGAATCAATGTGGCCGAGC AGAGCAAAGAGTGCAACATCAACATCAGCACCCCAACT ATCCCTGCAAGGTGTCCACCGCAGGCACCTATTTCTAT GGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGTATA AGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGGGCAT CATCAAGCAGCTGAACAAGGGCTGCAGCTACATCACCAC CAGGACGCCGATACCGTGACCATCGACAACACCGTGTATC AGCTGAGCAAGGTGGAAGGCGAACAGCAGCTGATCAAGG GCAGACCTGTGTCAGCAGCTTCGACCTATCAAGTTCCC TGAGAACCAAGTTCCAGGTGGCCCTGGACCAAGTGTTCGAG AACATCGAGAATTCCAGGCTCTGGTGGACCAAGTCCAACA GAATCCTGTCTAGCGCCGAGAAGGGAAACACCGGCTTCAT CATCGTGATCATCCTGATCGCCGCTGGGACAGCTCCATG ATCCTGGTGTCCATCTTCATCATTATCAAGAAGACCAAGA AGCCCAACCGGCGCTCTCCAGAACTGAGCGGAGTGACCAC CAATGGCTTCATCCCTCACAAAC	
HMPV_SC_4M_Krarup_T74LS170LD185P	ATGAGCTGGAAGGTGGTCATCATCTTCAGCCTGCTGATCA CACCTCAGCACGGCCGTAAGAGAGCTACCTGGAAGAGT CCTGCAGCACCATCAGAGGGCTACCTGTCTGTGCTGAG AACC GGCTGGTACACCAACGTGTTCACTGGAAGTGGGC GACGTCGAGAATCTGACATGCTCTGATGGCCCTAGCCTGA TCAAGACCGAGCTGGATCTGCTCAAGAGCGCCCTGAGAGA ACTCAAGACCGTGTCTGCCGATCAGCTGGCCAGAGAGGAA CAGATCGAGAATCCTGGCAGCGCAGCTTTGTGCTGGGAG CCATTGCTCTGGAGTGGCTGCTGCTGCAGCTGTTACAGC AGGCGTGGCCATCGCTAAGACCATCAGACTGGAAGCGA AGTGACCGCCATCAACAACGCCCTGAAGAAGACAAACGA GGCCGTCAGCACACTCGGCAATGGCGTTAGAGTGTGGCC ACAGCCGTGCGCAGCTGAAGGACTTCGTGCTTAAGAACC TGACACGGGCCATTAAACAAGAACAAGTGGACATCCCTGA CCTGAAGATGGCCGTGTCCTTAGCCAGTTCAACCGGCGG TTTCTGAACGTCTGCGGCAGTTTAGCGACAACGCCGGA TCACACCAGCCATCAGCCTGGACCTGATGACAGATGCTGA GCTGGCTAGAGCCGTGCCTAACATGCCTACATCTGCCGCG CAGATCAAGCTGATGCTCGAGAATAGAGCCATGGTCCGAC GGAAAGGCTTCGGCATTCTGATTGGCGGTGACGGCAGCAG CGTGATCTATATGGTGCAGCTGCCTATCTTCGGCGTGATCG ACACACCTGCTGGATTGTGAAGGCCGCTCCTAGCTGTAG CGAGAAGAAGGGCAATTACGCCCTGCTGTGAGAGAGGA CCAAGGCTGGTATGTGAGAACGCCGCGCAGCACCGTGATC TACCCTAACGAGAAGGACTGCGAGACAAGAGGCGACCAC GTGTTCTGTGATACCGCCGCTGGAATCAATGTGGCCGAGC AGAGCAAAGAGTGCAACATCAACATCAGCACCCCAACT ATCCCTGCAAGGTGTCCACCGCAGGCACCTATTTCTAT GGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGTATA AGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGGGCAT CATCAAGCAGCTGAACAAGGGCTGCAGCTACATCACCAC CAGGACGCCGATACCGTGACCATCGACAACACCGTGTATC AGCTGAGCAAGGTGGAAGGCGAACAGCAGCTGATCAAGG GCAGACCTGTGTCAGCAGCTTCGACCTATCAAGTTCCC TGAGGATCAGTTCCAGGTGGCCCTGGACCAAGTGTTCGAG AACATCGAGAATTCCAGGCTCTGGTGGACCAAGTCCAACA GAATCCTGTCTAGCGCCGAGAAGGGAAACACCGGCTTCAT CATCGTGATCATCCTGATCGCCGCTGGGACAGCTCCATG ATCCTGGTGTCCATCTTCATCATTATCAAGAAGACCAAGA AGCCCAACCGGCGCTCTCCAGAACTGAGCGGAGTGACCAC CAATGGCTTCATCCCTCACAAAC	110
HMPV_SC_5M_Krarup_T74LS170LD185PD454N	ATGAGCTGGAAGGTGGTCATCATCTTCAGCCTGCTGATCA CACCTCAGCACGGCCGTAAGAGAGCTACCTGGAAGAGT CCTGCAGCACCATCAGAGGGCTACCTGTCTGTGCTGAG AACC GGCTGGTACACCAACGTGTTCACTGGAAGTGGGC GACGTCGAGAATCTGACATGCTCTGATGGCCCTAGCCTGA TCAAGACCGAGCTGGATCTGCTCAAGAGCGCCCTGAGAGA ACTCAAGACCGTGTCTGCCGATCAGCTGGCCAGAGAGGAA CAGATCGAGAATCCTGGCAGCGCAGCTTTGTGCTGGGAG CCATTGCTCTGGAGTGGCTGCTGCTGCAGCTGTTACAGC AGGCGTGGCCATCGCTAAGACCATCAGACTGGAAGCGA AGTGACCGCCATCAACAACGCCCTGAAGAAGACAAACGA GGCCGTCAGCACACTCGGCAATGGCGTTAGAGTGTGGCC ACAGCCGTGCGCAGCTGAAGGACTTCGTGCTTAAGAACC TGACACGGGCCATTAAACAAGAACAAGTGGACATCCCTGA CCTGAAGATGGCCGTGTCCTTAGCCAGTTCAACCGGCGG TTTCTGAACGTCTGCGGCAGTTTAGCGACAACGCCGGA TCACACCAGCCATCAGCCTGGACCTGATGACAGATGCTGA GCTGGCTAGAGCCGTGCCTAACATGCCTACATCTGCCGCG CAGATCAAGCTGATGCTCGAGAATAGAGCCATGGTCCGAC GGAAAGGCTTCGGCATTCTGATTGGCGGTGACGGCAGCAG CGTGATCTATATGGTGCAGCTGCCTATCTTCGGCGTGATCG ACACACCTGCTGGATTGTGAAGGCCGCTCCTAGCTGTAG CGAGAAGAAGGGCAATTACGCCCTGCTGTGAGAGAGGA CCAAGGCTGGTATGTGAGAACGCCGCGCAGCACCGTGATC TACCCTAACGAGAAGGACTGCGAGACAAGAGGCGACCAC GTGTTCTGTGATACCGCCGCTGGAATCAATGTGGCCGAGC AGAGCAAAGAGTGCAACATCAACATCAGCACCCCAACT ATCCCTGCAAGGTGTCCACCGCAGGCACCTATTTCTAT GGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGTATA AGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGGGCAT CATCAAGCAGCTGAACAAGGGCTGCAGCTACATCACCAC CAGGACGCCGATACCGTGACCATCGACAACACCGTGTATC AGCTGAGCAAGGTGGAAGGCGAACAGCAGCTGATCAAGG GCAGACCTGTGTCAGCAGCTTCGACCTATCAAGTTCCC TGAGGATCAGTTCCAGGTGGCCCTGGACCAAGTGTTCGAG AACATCGAGAATTCCAGGCTCTGGTGGACCAAGTCCAACA GAATCCTGTCTAGCGCCGAGAAGGGAAACACCGGCTTCAT CATCGTGATCATCCTGATCGCCGCTGGGACAGCTCCATG ATCCTGGTGTCCATCTTCATCATTATCAAGAAGACCAAGA AGCCCAACCGGCGCTCTCCAGAACTGAGCGGAGTGACCAC CAATGGCTTCATCCCTCACAAAC	111

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
	AGTGACCGCCATCAACAACGCCCTGAAGAAGACAAACGA GGCCGTGAGCAGCACTCGGCAATGGCGTTAGAGTGCTGGCC ACAGCCGTGCGCGAGCTGAAGGACTTCGTGCTTAAGAACC TGACACGGGCCATTAAACAAGAACAAGTGCGACATCCCTGA CCTGAAGATGGCCGTGTCCTTTAGCCAGTTCAACCGCGG TTTCTGAACGTGCTGCGGCGAGTTTAGCGACAACGCCGGAA TCACACCAGCCATCAGCCTGGACCTGATGACAGATGCTGA GCTGGCTAGAGCCGTGCCTAACATGCCTACATCTGCCGGC CAGATCAAGCTGATGCTCGAGAATAGAGCCATGGTCCGAC GGAAAGGCTTCGGCATTCTGATTGGCGTGTACGGCAGCAG CGTGATCTATATGGTGCAGCTGCCTATCTTCGGCGTGATCG ACACACCCCTGCTGGATTGTGAAGGCCGCTCCTAGCTGTAG CGAGAAGAAGGGCAATTACGCCTGCCTGCTGAGAGAGGA CCAAGGCTGGTATTGTGAGAACGCCGGCAGCACCCTGTAC TACCCCTAACGAGAAGGACTGCGGAGACAAGAGCGACCCAC GTGTTCTGTGATACCGCCGCTGGAATCAATGTGGCCGAGC AGAGCAAAGAGTGCAACATCAACATCAGCACCACCAACT ATCCCTGCAAGGTGTCCACCGGCAGGCACCCCTATTCTAT GGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGTATA AGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGGGCAT CATCAAGCAGCTGAACAAGGGCTGCAGCTACATCACCAC CAGGACGCCGATACCGTGACCATCGACAACACCGTGTATC AGCTGAGCAAGGTGGAAGGCGAACAGCAGCAGTGATCAAGG GCAGACCTGTGTCCAGCAGCTTCGACCCCTATCAAGTTCCC TGAGAACCAGTTCCAGGTGGCCCTGGACAGGTGTTTCGAG AACATCGAGAATTCCAGGCTCTGGTGGACAGTCCAACA GAATCCTGTCTAGCGCCGAGAAGGGAAACACCGGCTTCAT CATCGTGATCATCCTGATCGCCGTGCTGGCAGCTCCATG ATCCTGGTGTCCATCTTCATCATTATCAAGAAGACCAAGA AGCCACCGGCGCTCCTCCAGAACTGAGCGGAGTGACCAA CAATGGCTTCATCCCTCACAAAC	
HMPV_SC_DM_Krarup_E51PT74L	ATGAGCTGGAAGGTGGTCATCATCTTCAGCCTGCTGATCA CACCTCAGCACCGCCCTGAAAAGAGAGTACCTGGAAGAGT CCTGCAGCACCATCAGAGAGGGCTACCTGTCTGTGCTGAG AACCGGCTGGTACACCAACGTGTTACACTGCCTGTGGGC GACGTCGAGAATCTGACATGCTCTGATGGCCCTAGCCTGA TCAAGACCGAGCTGGATCTGCTCAAGAGCGCCCTGAGAGA ACTCAAGACCGTGTCTGCCGATCAGCTGGCCAGAGAGGAA CAGATCGAGAATCCTGGCAGCGCAGCTTTGTGCTGGGAG CCATTGCTCTTGGAGTGGCTGTGCTGCAGCTGTTACAGC AGGCGTGCCCATCGCTAAGACCATCAGACTGGAAGCGA AGTGACCGCCATCAACAACGCCCTGAAGAAGACAAACGA GGCCGTGAGCAGCACTCGGCAATGGCGTTAGAGTGCTGGCC ACAGCCGTGCGCGAGCTGAAGGACTTCGTGTCCAAGAACC TGACACGGGCCATTAAACAAGAACAAGTGCGACATCGACG ACCTGAAGATGGCCGTGTCCTTTAGCCAGTTCAACCGGCG GTTTCTGAACGTGCTGCGGCGAGTTTAGCGACAACCGCCGA ATCACACCAGCCATCAGCCTGGACCTGATGACAGATGCTG AGCTGGCTAGAGCCGTGCCTAACATGCCTACATCTGCCGG CCAGATCAAGCTGATGCTCGAGAATAGAGCCATGGTCCGA CGAAAGGCTTCGGCATTCTGATTGGCGTGTACGGCAGCA GCGTGATCTATATGGTGCAGCTGCCTATCTTCGGCGTGATC GACACACCCCTGCTGGATTGTGAAGGCCGCTCCTAGCTGTA GCGAGAAGAAGGGCAATTACGCCTGCCTGCTGAGAGAGG ACCAAGGCTGGTATTGTGAGAACGCCGGCAGCACCCTGTA CTACCCCTAACGAGAAGGACTGCGAGACAAGAGCGACCA CGTGTTCTGTGATACCGCCGCTGGAATCAATGTGGCCGAG CAGAGCAAAGAGTGCAACATCAACATCAGCACCACCAAC TATCCCTGCAAGGTGTCCACCGGCAGGCACCCCTATTTCTAT GGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGTATA AGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGGGCAT CATCAAGCAGCTGAACAAGGGCTGCAGCTACATCACCAC CAGGACGCCGATACCGTGACCATCGACAACACCGTGTATC AGCTGAGCAAGGTGGAAGGCGAACAGCAGCAGTGATCAAGG GCAGACCTGTGTCCAGCAGCTTCGACCCCTATCAAGTTCCC TGAGGATCAGTTCCAGGTGGCCCTGGACAGGTGTTTCGAG AACATCGAGAATTCCAGGCTCTGGTGGACAGTCCAACA GAATCCTGTCTAGCGCCGAGAAGGGAAACACCGGCTTCAT CATCGTGATCATCCTGATCGCCGTGCTGGCAGCTCCATG ATCCTGGTGTCCATCTTCATCATTATCAAGAAGACCAAGA AGCCACCGGCGCTCCTCCAGAACTGAGCGGAGTGACCAA CAATGGCTTCATCCCTCACAAAC	112

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
HMPV_SC_TM_Krarup_E51PT74LD454N	ATGAGCTGGAAGGTGGTCATCATCTTCAGCCTGCTGATCA CACCTCAGCACGGCTGAAAGAGAGCTACCTGGAAGAGT CCTGCAGCACCATCACAGAGGGCTACCTGTCTGTGCTGAG AACCGGTGGTACACCAACGTGTTCACTGCTGTGGGC GACGTCGAGAATCTGACATGCTCTGATGGCCCTAGCCTGA TCAAGACCGAGCTGGATCTGCTCAAGAGCGCCCTGAGAGA ACTCAAGACCGTGTCTGCCGATCAGCTGGCCAGAGAGGAA CAGATCGAGAATCCTGGCAGCGCAGCTTTGTGCTGGGAG CCATTGCTCTTGAGTGGCTGTGCTGCAGCTGTTACAGC AGGCGTGGCCATCGCTAAGACCATCAGACTGGAAGCGA AGTGACCGCCATCAACAACGCCCTGAAGAAGACAAACGA GGCCGTGAGCAGCTCGGCAATGGCGTTAGAGTGCTGGCC ACAGCCGTGCGGAGCTGAAGGACTTCGTGTCCAAGAACC TGACACGGGCCATTAAACAAGAACAGTGCGACATCGACG ACCTGAAGATGGCCGTGTCCTTTAGCCAGTTCAACCGGCG GTTCTGAACGTGCTGCGGAGTTAGCGACAACGCCGGA ATCACACCGCCATCAGCCTGGACCTGATGACAGATGCTG AGCTGGCTAGAGCCGTGCCAATGCCTACATCTGCCGG CCAGATCAAGCTGATGCTCGAGAATAGAGCCATGGTCCGA CGGAAAGGCTTCGGCATTCTGATTGGCGTGTACGGCAGCA GCGTGATCTATATGGTGACGCTGCCTATCTTCGGCGTGATC GACACCCCTGCTGGATTGTGAAGGCCGCTCCTAGCTGTA GCGAGAAGAGGGCAATTACGCCCTGCCTGCTGAGAGAGG ACCAAGGCTGGTATTGTGAGAAGCGCCGAGCACCCTGTA CTACCTTAACGAGAAGGACTGCGAGACAAGAGGCGACCA CGTGTTCTGTGATACGCCCGCTGGAATCAATGTGGCCGAG CAGAGCAAGAGTGCAACATCAACATCAGCACCACCAAC TATCCCTGCAAGGTGTCCACCGCAGGCACCTTATTTCTAT GGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGTATA AGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGGGCAT CATCAAGCAGCTGAACAAGGGCTGCAGCTACATCACCAC CAGGACGCCGATACCGTGACCATCGACAACACCGTGTATC AGCTGAGCAAGGTGGAAGGCGAAGCAGCAGCTGATCAAGG GCAGACCTGTGTCCAGCAGCTTCGACCTTATCAAGTTCC TGAGAACCAGTTCCAGGTGGCCCTGGACCAAGTGTTCGAG AACATCGAGAATTTCCAGGCTCTGGTGGACAGTCCAACA GAATCCTGTCTAGCGCCGAGAAGGGAACACCGGCTTCAT CATCGTGATCATCTGATCGCCGTGCTGGCAGCTCCATG ATCCTGGTGTCATCTTCATCATTATCAAGAAGACCAAGA AGCCCCACCGCGCTCCTCCAGAATGAGCGGAGTGACCAA CAATGGCTTCATCCCTCACAA	113
HMPV_SC_StabilizeAlpha_T74L	ATGAGCTGGAAGGTGGTCATCATCTTCAGCCTGCTGATCA CACCTCAGCACGGCTGAAAGAGAGCTACCTGGAAGAGT CCTGCAGCACCATCACAGAGGGCTACCTGTCTGTGCTGAG AACCGGTGGTACACCAACGTGTTCACTGGAAGTGGGC GACGTCGAGAATCTGACATGCTCTGATGGCCCTAGCCTGA TCAAGACCGAGCTGGATCTGCTCAAGAGCGCCCTGAGAGA ACTCAAGACCGTGTCTGCCGATCAGCTGGCCAGAGAGGAA CAGATCGAGAATCCTGGCAGCGCAGCTTTGTGCTGGGAG CCATTGCTCTTGAGTGGCTGTGCTGCAGCTGTTACAGC AGGCGTGGCCATCGCTAAGACCATCAGACTGGAAGCGA AGTGACCGCCATCAACAACGCCCTGAAGAAGACAAACGA GGCCGTGAGCAGCTCGGCAATGGCGTTAGAGTGCTGGCC ACAGCCGTGCGGAGCTGAAGGACTTCGTGTCCAAGAACC TGACACGGGCCATTAAACAAGAACAGTGCGACATCGACG ACCTGAAGATGGCCGTGTCCTTTAGCCAGTTCAACCGGCG GTTCTGAACGTGCTGCGGAGTTAGCGACAACGCCGGA ATCACACCGCCATCAGCCTGGACCTGATGACAGATGCTG AGCTGGCTAGAGCCGTGCCAATGCCTACATCTGCCGG CCAGATCAAGCTGATGCTCGAGAATAGAGCCATGGTCCGA CGGAAAGGCTTCGGCATTCTGATTGGCGTGTACGGCAGCA GCGTGATCTATATGGTGACGCTGCCTATCTTCGGCGTGATC GACACCCCTGCTGGATTGTGAAGGCCGCTCCTAGCTGTA GCGAGAAGAGGGCAATTACGCCCTGCCTGCTGAGAGAGG ACCAAGGCTGGTATTGTGAGAAGCGCCGAGCACCCTGTA CTACCTTAACGAGAAGGACTGCGAGACAAGAGGCGACCA CGTGTTCTGTGATACGCCCGCTGGAATCAATGTGGCCGAG CAGAGCAAGAGTGCAACATCAACATCAGCACCACCAAC TATCCCTGCAAGGTGTCCACCGCAGGCACCTTATTTCTAT GGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGTATA AGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGGGCAT CATCAAGCAGCTGAACAAGGGCTGCAGCTACATCACCAC CAGGACGCCGATACCGTGACCATCGACAACACCGTGTATC	114

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
	AGCTGAGCAAGGTGGAAGGCGAACAGCACGTGATCAAGG GCAGACCTGTGTCCAGCAGCTTCGACCCATCAAGTTCCC TGAGGATCAGTTCCAGGTGGCCCTGGACCAAGTGTTCGAG AACATCGAGAATTCCAGGCTCTGGTGGACCAAGTCCAACA GAATCCTGTCTAGCGCCGAGAAGGGAACACCGGCTTCAT CATCGTGATCATCCTGATCGCCGTGCTGGGCAGCTCCATG ATCCTGGTGTCCATCTTCATCATTATCAAGAAGACCAAGA AGCCACCGGCGCTCCTCCAGAACTGAGCGGAGTGACCAA CAATGGCTTCATCCCTCACAAAC	
HMPV_SC_StabilizeAlpha_V55L	ATGAGCTGGAAGGTGGTCATCATCTTCAGCCTGCTGATCA CACCTCAGCACGGCCGAAAGAGAGCTACCTGGAAGAGT CCTGCAGCACCATCACAGAGGGCTACCTGTCTGTGCTGAG AACC GGCTGGTACACCAACGTGTTCACTGGAAGTGGGC GACCTCGAGAATCTGACATGCTCTGATGGCCCTAGCCTGA TCAAGACCGAGCTGGATCTGACCAAGAGCGCCCTGAGAG AACTCAAGACCGTGTCTGCCGATCAGCTGGCCAGAGAGGA ACAGATCGAGAATCCTGGCAGCGGCAGCTTTGTGCTGGGA GCCATTGCTCTTGGAGTGGCTGCTGCTGACGTGTTACAG CAGGCGTGGCCATCGCTAAGACCATCAGACTGGAAAGCG AAGTGACCGCCATCAACAACGCCCTGAAGAAGACAAACG AGGCCGTGACACACTCGGCAATGGCGT TAGAGTGCTGGC CACAGCCGTGCGGAGCTGAAGGACTTCGTGTCCAAGAAC CTGACACGGGCCATTAAACAAGAACAAGTGCACATCGAC GACCTGAAGATGGCCGTGCTCTTAGCCAGTTCAACCGGC GGTTTCTGAACGTCTGTCGGCAGTTTAGCGACAACGCCGG AATCACACCAGCCATCAGCCTGGACCTGATGACAGATGCT GAGCTGGCTAGAGCCGTGCCTAACATGCCCTACATCTGCCG GCCAGATCAAGCTGATGCTCGAATAGAGCCATGGTCCG ACGGAAGGCTTCGGCATTCTGATTGGCGTGTACGGCAGC AGCGTGATCTATATGGTGACGTGCCTATCTTCGGCGTGA TCGACACACCCCTGCTGGATTGTGAAGGCCGCTCCTAGCTG TAGCGAGAAGAAGGGCAATTACGCCCTGCCTGCTGAGAGA GGACCAAGGCTGGTATTGTGAGAAGCGCCGAGCACCGTG TACTACCTTAACGAGAAGGACTGCGAGACAAGAGGCGAC CACGTGTTCTGTGATACCGCCGTGGAATCAATGTGGCCG AGCAGAGCAAGAGTGCAACATCAACATCAGCACCA ACTATCCCTGCAAGGTGTCCACCGGAGGCACCTATTTCT TATGGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGTT ATAAGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGG GCATCATCAAGCAGCTGAACAAGGGCTGCAGCTACATCAC CAACCAGGACGCGGATACCGTGACCATCGACAACACCGTG TATCAGCTGAGCAAGGTGGAAGGCGAACAGCACGTGATC AAGGGCAGACCTGTGTCCAGCAGCTTCGACCTATCAAGT TCCCTGAGGATCAGTTCCAGGTGGCCCTGGACAGGTGTT CGAGAACATCGAGAATTCCAGGCTCTGGTGGACAGTCC AACAGAATCCTGTCTAGCGCCGAGAAGGGAACACCGGC TTCATCATCGTGATCATCCTGATCGCCGTGCTGGGCAGCTC CATGATCCTGGTGTCCATCTTCATCATTATCAAGAAGACC AAGAAGCCACCGGCGCTCCTCCAGAACTGAGCGGAGTG ACCAACAATGGCTTCATCCCTCACAAAC	115
HMPV_SC_StabilizeAlpha_S170L	ATGAGCTGGAAGGTGGTCATCATCTTCAGCCTGCTGATCA CACCTCAGCACGGCCGAAAGAGAGCTACCTGGAAGAGT CCTGCAGCACCATCACAGAGGGCTACCTGTCTGTGCTGAG AACC GGCTGGTACACCAACGTGTTCACTGGAAGTGGGC GACCTCGAGAATCTGACATGCTCTGATGGCCCTAGCCTGA TCAAGACCGAGCTGGATCTGACCAAGAGCGCCCTGAGAG AACTCAAGACCGTGTCTGCCGATCAGCTGGCCAGAGAGGA ACAGATCGAGAATCCTGGCAGCGGCAGCTTTGTGCTGGGA GCCATTGCTCTTGGAGTGGCTGCTGCTGACGTGTTACAG CAGGCGTGGCCATCGCTAAGACCATCAGACTGGAAAGCG AAGTGACCGCCATCAACAACGCCCTGAAGAAGACAAACG AGGCCGTGACACACTCGGCAATGGCGT TAGAGTGCTGGC CACAGCCGTGCGGAGCTGAAGGACTTCGTGCTTAAGAAC CTGACACGGGCCATTAAACAAGAACAAGTGCACATCGAC GACCTGAAGATGGCCGTGCTCTTAGCCAGTTCAACCGGC GGTTTCTGAACGTCTGTCGGCAGTTTAGCGACAACGCCGG AATCACACCAGCCATCAGCCTGGACCTGATGACAGATGCT GAGCTGGCTAGAGCCGTGCCTAACATGCCCTACATCTGCCG GCCAGATCAAGCTGATGCTCGAATAGAGCCATGGTCCG ACGGAAGGCTTCGGCATTCTGATTGGCGTGTACGGCAGC AGCGTGATCTATATGGTGACGTGCCTATCTTCGGCGTGA TCGACACACCCCTGCTGGATTGTGAAGGCCGCTCCTAGCTG	116

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
	TAGCGAGAAGAAGGGCAATTACGCCTGCCTGCTGAGAGA GGACCAAGGCTGGTATTGTGAGAACGCCGGCAGCACCCTG TACTACCCCTAACGAGAAGGACTGCGAGACAAGAGGCGAC CACGTGTTCTGTGATACCGCCGCTGGAATCAATGTGGCCG AGCAGAGCAAGAGGTGCAACATCAACATCAGCACCACCA ACTATCCCTGCAAGGTGTCCACCGGCAGGCACCCATTTC TATGGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGT ATAAGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGG GCATCATCAAGCAGCTGAACAAGGGCTGCAGCTACATCAC CAACCAGGACGCCGATACCGTGACCATCGACAACACCGTG TATCAGCTGAGCAAGGTGGAAGGCGAACAGCAGCTGATC AAGGGCAGACCTGTGTCCAGCAGCTTCGACCCATCAAGT TCCCTGAGGATCAGTTCAGGTGGCCCTGGACCAGGTGTT CGAGAACATCGAGAATTCCAGGCTCTGGTGGACCAGTCC AACAGAATCCTGTCTAGCGCCGAGAAGGAAACACCGGC TTCATCATCGTGATCATCTGATCGCCGTGCTGGGCAGCTC CATGATCCTGGTGTCCATCTTCATCATTATCAAGAAGACC AAGAAGCCACCGGCGCTCCTCCAGAAGTGAAGCGAGTG ACCAACATGGCTTCATCCCTCACAAC	
HMPV_SC_StabilizeAlpha_T174W	ATGAGCTGGAAGGTGGTCATCATCTTCAGCCTGCTGATCA CACCTCAGCACGGCCTGAAAGAGAGCTACCTGGAAGAGT CCTGCAGCACCATCAGAGAGGGCTACCTGTCTGTGCTGAG AACCGGCTGGTACACCAACGTGTTACACTGGAAGTGGGC GACGTCGAGAATCTGACATGCTCTGATGGCCCTAGCCTGA TCAAGACCGAGCTGGATCTGACCAAGAGCGCCCTGAGAG AACTCAAGACCGTGTCTGCCGATCAGCTGGCCAGAGAGGA ACAGATCGAGAATCCTGGCAGCGGCAGCTTGTGCTGGGA GCCATTGCTCTTGGAGTGGCTGCTGCTGACGTGTTACAG CAGGCGTGGCCATCGCTAAGACCATCAGACTGGAAGCG AAGTGACCGCCATCAACAACGCCCTGAAGAAGACAACG AGGCCGTGACACACTCGGCAATGGCGTTAGAGTGTGGC CACAGCCGTGCGCGAGCTGAAGGACTTCGTGTCCAAGAAC CTGTGGCGGGCATTAAACAAGAACAAGTGCGACATCGAC GACCTGAAGATGGCCGTGTCTTTAGCCAGTTCACACCGGC GGTTTCTGAACGTCGTGCGGCAGTTTAGCGACAACGCCGG AATCACACCAGCCATCAGCCTGGACCTGATGACAGATGCT GAGCTGGCTAGAGCCGTGCCTAACATGCCTACATCTGCCG GCCAGATCAAGCTGATGCTCGAGAATAGAGCCATGGTCCG ACGGAAGAGCTTCGGCATTCTGATTGGCGTGTACGGCAGC AGCGTGATCTATATGGTGCAGCTGCCTATCTTCGGCGTGA TCGACACACCCCTGCTGGATTGTGAAGGCCGCTCCTAGCTG TAGCGAGAAGAAGGGCAATTACGCCTGCCTGCTGAGAGA GGACCAAGGCTGGTATTGTGAGAACGCCGGCAGCACCCTG TACTACCCCTAACGAGAAGGACTGCGAGACAAGAGGCGAC CACGTGTTCTGTGATACCGCCGCTGGAATCAATGTGGCCG AGCAGAGCAAGAGGTGCAACATCAACATCAGCACCACCA ACTATCCCTGCAAGGTGTCCACCGGCAGGCACCCATTTC TATGGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGT ATAAGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGG GCATCATCAAGCAGCTGAACAAGGGCTGCAGCTACATCAC CAACCAGGACGCCGATACCGTGACCATCGACAACACCGTG TATCAGCTGAGCAAGGTGGAAGGCGAACAGCAGCTGATC AAGGGCAGACCTGTGTCCAGCAGCTTCGACCCATCAAGT TCCCTGAGGATCAGTTCAGGTGGCCCTGGACCAGGTGTT CGAGAACATCGAGAATTCCAGGCTCTGGTGGACCAGTCC AACAGAATCCTGTCTAGCGCCGAGAAGGAAACACCGGC TTCATCATCGTGATCATCTGATCGCCGTGCTGGGCAGCTC CATGATCCTGGTGTCCATCTTCATCATTATCAAGAAGACC AAGAAGCCACCGGCGCTCCTCCAGAAGTGAAGCGAGTG ACCAACATGGCTTCATCCCTCACAAC	117
HMPV_SC_4M_StabilizeAlpha_V55LT74LS170LT174W	ATGAGCTGGAAGGTGGTCATCATCTTCAGCCTGCTGATCA CACCTCAGCACGGCCTGAAAGAGAGCTACCTGGAAGAGT CCTGCAGCACCATCAGAGAGGGCTACCTGTCTGTGCTGAG AACCGGCTGGTACACCAACGTGTTACACTGGAAGTGGGC GACCTCGAGAATCTGACATGCTCTGATGGCCCTAGCCTGA TCAAGACCGAGCTGGATCTGCTCAAGAGCGCCCTGAGAGA ACTCAAGACCGTGTCTGCCGATCAGCTGGCCAGAGAGGAA CAGATCGAGAATCCTGGCAGCGGCAGCTTGTGCTGGGAG CCATTGCTCTTGGAGTGGCTGTGCTGACGTGTACAGC AGGCGTGGCCATCGCTAAGACCATCAGACTGGAAGCGA AGTGACCGCCATCAACAACGCCCTGAAGAAGACAACGA GGCCGTGAGCACACTCGGCAATGGCGTTAGAGTGTGGCC	118

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
	ACAGCCGTGCGGAGCTGAAGGACTTCGTGCTTAAGAACC TGTGGCGGGCCATTAAACAAGAACAGTGCGACATCGACG ACCTGAAGATGGCCGTGTCCTTTAGCCAGTTC AACCGGCG GTTTCTGAACGTCGTGCGGCAGTTTAGCGACAACGCCGGA ATCACACCAGCCATCAGCCTGGACCTGATGACAGATGCTG AGCTGGCTAGAGCCGTGCCTAACATGCCTACATCTGCCGG CCAGATCAAGCTGATGCTCGAGAATAGAGCCATGGTCCGA CGGAAAGGCTTCGGCATTCTGATTGGCGTGACGGCAGCA GCGTGATCTATATGGTGACGCTGCCTATCTTCGGCGTGATC GACACACCCTGCTGGATTGTGAAGGCCGCTCCTAGCTGTA GCGAGAAGAAGGGCAATTACGCCTGCCTGCTGAGAGAGG ACCAAGGCTGGTATTGTGAGAAGCCGGCAGCACCCTGTA CTACCCTAACGAGAAGGACTGCGAGACAAGAGGCGACCA CGTGTTCTGTGATACGCCCGCTGGAATCAATGTGGCCGAG CAGAGCAAGAGTGCAACATCAACATCAGCACCACCAAC TATCCCTGCAAGGTGTCCACCGCAGGCACCCATTCTCTAT GGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGTATA AGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGGGCAT CATCAAGCAGCTGAACAAGGGCTGCAGCTACATCACCAC CAGGACGCCGATACCGTGACCATCGACAACACCGTGATC AGCTGAGCAAGGTGGAAGGCGAAGCAGCAGTGATCAAGG GCAGACCTGTGTCCAGCAGCTTCGACCCTATCAAGTTCC TGAGGATCAGTTCAGGTGGCCCTGGACCAGGTGTTTCGAG AACATCGAGAATTCACAGGCTCTGGTGGACAGTCCAACA GAATCCTGTCTAGCGCCGAGAAGGGAACACCGGCTTCAT CATCGTGATCATCTGATCGCCGTGCTGGGCAGCTCCATG ATCCTGGTGTCCATCTTCATCATTATCAAGAAGACCAAGA AGCCCCACCGCGCTCCTCCAGAACTGAGCGGAGTGACCAA CAATGGCTTCATCCCTCACAAAC	
HMPV_ProlineStab_E51P	ATGAGCTGGAAGGTGGTCATCATCTTCAGCCTGCTGATCA CACCTCAGCACGGCCTGAAAGAGAGCTACCTGGAAGAGT CCTGCAGCACCATCACAGAGGGCTACCTGTCTGTGCTGAG AACC GGCTGGTACACCAACGTGTTCACTGCGCTGTGGGC GACGTCGAGAATCTGACATGCTCTGATGGCCCTAGCCTGA TCAAGACCGAGCTGGATCTGACCAAGAGCGCCCTGAGAG AACTCAAGACCGTGTCTGCCGATCAGCTGGCCAGAGAGGA ACAGATCGAGAATCCTGGCAGCGCAGCTTTGTGCTGGGA GCCATTGCTCTTGGAGTGGCTGCTGCTGACGCTGTTACAG CAGGCGTGGCCATCGCTAAGACCATCAGACTGGAAAGCG AAGTGACCGCCATCAACAACGCCCTGAAGAAGACAAACG AGGCCGTAGCACACTCGGCAATGGCGTTAGAGTGCTGGC CACAGCCGTGCGCGAGCTGAAGGACTTCGTGTCCAAGAAC CTGACACGGGCATTAAACAAGAACAAGTGCACATCGAC GACCTGAAGATGGCCGTGCTTTAGCCAGTTCAACCGGC GGTTTCTGAACGTCGTGCGGCAGTTTAGCGACAACGCCGG AATCACACCAGCCATCAGCCTGGACCTGATGACAGATGCT GAGCTGGCTAGAGCCGTGCCTAACATGCCCTACATCTGCCG GCCAGATCAAGCTGATGCTCGAGAATAGAGCCATGGTCCG ACGGAAAGGCTTCGGCATTCTGATTGGCGTGACGGCAGC AGCGTGATCTATATGGTGACGCTGCCTATCTTCGGCGTGA TCGACACACCCTGCTGGATTGTGAAGGCCGCTCCTAGCTG TAGCGAGAAGAAGGGCAATTACGCTGCTGCTGAGAGA GGACCAAGGCTGGTATTGTGAGAAGCCCGCAGCACCGTG TACTACCTTAACGAGAAGGACTGCGAGACAAGAGGCGAC CAGTGTTCTGTGATACCGCCGCTGGAATCAATGTGGCGG AGCAGAGCAAGAGTGCAACATCAACATCAGCACCACCA ACTATCCCTGCAAGGTGTCCACCGGCAGGCACCCATTTC TATGGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGT ATAAGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGG GCATCATCAAGCAGCTGAACAAGGGCTGCAGCTACATCAC CAACCAGGACGCCGATACCGTGACCATCGACAACACCGTG TATCAGCTGAGCAAGGTGGAAGGCGAACAGCACGTGATC AAGGGCAGACCTGTGTCCAGCAGCTTCGACCCTATCAAGT TCCTTGAGGATCAGTTCCAGGTGGCCCTGGACAGGTGTT CGAGAACATCGAGAATTCAGGCTCTGGTGGACAGTCC AACAGAATCCTGTCTAGCGCCGAGAAGGGAAACACCGGC TTCATCATCGTGATCATCTGATCGCCGTGCTGGGCAGCTC CATGATCCTGGTGTCCATCTTCATCATTATCAAGAAGACC AAGAAGCCACCGCGCTCCTCCAGAACTGAGCGGAGTG ACCAACAATGGCTTCATCCCTCACAAAC	119

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
HMPV_ProlineStab_D185P	ATGAGCTGGAAGGTGGTCATCATCTTCAGCCTGCTGATCA CACCTCAGCACGGCCTGAAAGAGAGCTACCTGGAAGAGT CCTGCAGCACCATCACAGAGGGCTACCTGTCTGTGCTGAG AACCGGCTGGTACACCAACGTGTTACACTGGAAGTGGGC GACGTCGAGAATCTGACATGCTCTGATGGCCCTAGCCTGA TCAAGACCGAGCTGGATCTGACCAAGAGCGCCCTGAGAG AACTCAAGACCGTGTCTGCCGATCAGCTGGCCAGAGAGGA ACAGATCGAGAATCCTGGCAGCGGCAGCTTTGTGCTGGGA GCCATTGCTCTTGGAGTGGCTGCTGCTGCAGCTGTTACAG CAGGCGTGGCCATCGCTAAGACCATCAGACTGGAAAGCG AAGTGACCGCCATCAACAACGCCCTGAAGAAGACAAACG AGGCCGTCAGCACACTCGGCAATGGCGTTAGAGTGCTGGC CACAGCCGTGCGCGAGCTGAAGGACTTCGTGTCCAAGAAC CTGACACGGGCCATTAAACAAGAACAAGTGCAGACATCCCTG ACCTGAAGATGGCCGTGTCCTTTAGCCAGTTCAACCGGCG GTTCTGAACGTGCTGCGGCAGTTTAGCGACAACGCCGGA ATCACACCGCCATCAGCCTGGACCTGATGACAGATGCTG AGCTGGCTAGAGCCGTGCCAATACATGCCCTACATCTGCCGG CCAGATCAAGCTGATGCTCAGAAATAGAGCCATGGTCCGA CGGAAAGGCTTCGGCATTCTGATTGGCGTGTACGGCAGCA GCGTGATCTATATGGTGCAGCTGCCTATCTTCGGCGTGATC GACACACCTGCTGGATTGTGAAGGCCGCTCCTAGCTGTA GCGAGAAGAAGGGCAATTACGCCCTGCCTGCTGAGAGAGG ACCAAGGCTGGTATTGTGAGAAGCGCCGCGAGCACCGTGTA CTACCCCTAACGAGAAGGACTGCGAGACAAGAGGCGACCA CGTGTTCTGTGATACCGCCGCTGGAATCAATGTGGCCGAG CAGAGCAAGAGTGCAACATCAACATCAGCACCACCAAC TATCCCTGCAAGGTGTCCACCGGCAGGCACCTATTCTTAT GGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGTATATA AGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGGGCAT CATCAAGCAGCTGAACAAGGGCTGCAGCTACATCACCAAC CAGGACGCCGATACCGTGACCATCGACAACACCGTGTATC AGCTGAGCAAGGTGGAAGGCGAACAGCAGCTGATCAAGG GCAGACCTGTGTCCAGCAGCTTCGACCCCTATCAAGTTCCC TGAGGATCAGTTCCAGGTGGCCCTGGACAGGTGTTCCGAG AACATCGAGAATTCCAGGCTCTGGTGGACAGTCCAACA GAATCCTGTCTAGCGCCGAGAAGGGAAACACCGGCTTCAT CATCGTGATCATCCTGATCGCCGTGCTGGGCAGCTCCATG ATCCTGGTGTCCATCTTCATCATTATCAAGAAGACCAAGA AGCCACCGGCGCTCCTCCAGAACTGAGCGGAGTGACCAA CAATGGCTTCATCCCTCACAAAC	120
HMPV_ProlineStab_D183P	ATGAGCTGGAAGGTGGTCATCATCTTCAGCCTGCTGATCA CACCTCAGCACGGCCTGAAAGAGAGCTACCTGGAAGAGT CCTGCAGCACCATCACAGAGGGCTACCTGTCTGTGCTGAG AACCGGCTGGTACACCAACGTGTTACACTGGAAGTGGGC GACGTCGAGAATCTGACATGCTCTGATGGCCCTAGCCTGA TCAAGACCGAGCTGGATCTGACCAAGAGCGCCCTGAGAG AACTCAAGACCGTGTCTGCCGATCAGCTGGCCAGAGAGGA ACAGATCGAGAATCCTGGCAGCGGCAGCTTTGTGCTGGGA GCCATTGCTCTTGGAGTGGCTGCTGCTGCAGCTGTTACAG CAGGCGTGGCCATCGCTAAGACCATCAGACTGGAAAGCG AAGTGACCGCCATCAACAACGCCCTGAAGAAGACAAACG AGGCCGTCAGCACACTCGGCAATGGCGTTAGAGTGCTGGC CACAGCCGTGCGCGAGCTGAAGGACTTCGTGTCCAAGAAC CTGACACGGGCCATTAAACAAGAACAAGTGCCCTATCGAGC ACCTGAAGATGGCCGTGTCCTTTAGCCAGTTCAACCGGCG GTTCTGAACGTGCTGCGGCAGTTTAGCGACAACGCCGGA ATCACACCGCCATCAGCCTGGACCTGATGACAGATGCTG AGCTGGCTAGAGCCGTGCCAATACATGCCCTACATCTGCCGG CCAGATCAAGCTGATGCTCAGAAATAGAGCCATGGTCCGA CGGAAAGGCTTCGGCATTCTGATTGGCGTGTACGGCAGCA GCGTGATCTATATGGTGCAGCTGCCTATCTTCGGCGTGATC GACACACCTGCTGGATTGTGAAGGCCGCTCCTAGCTGTA GCGAGAAGAAGGGCAATTACGCCCTGCCTGCTGAGAGAGG ACCAAGGCTGGTATTGTGAGAAGCGCCGCGAGCACCGTGTA CTACCCCTAACGAGAAGGACTGCGAGACAAGAGGCGACCA CGTGTTCTGTGATACCGCCGCTGGAATCAATGTGGCCGAG CAGAGCAAGAGTGCAACATCAACATCAGCACCACCAAC TATCCCTGCAAGGTGTCCACCGGCAGGCACCTATTCTTAT GGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGTATATA AGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGGGCAT CATCAAGCAGCTGAACAAGGGCTGCAGCTACATCACCAAC	121

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
	CAGGACGCCGATACCGTGACCATCGACAACACCGTGTATC AGCTGAGCAAGGTGGAAGGCGAACAGCACGTGATCAAGG GCAGACCTGTGTCCAGCAGCTTCGACCCCTATCAAGTTCCC TGAGGATCAGTTCCAGGTGGCCCTGGACCAGGTGTTTCGAG AACATCGAGAATTCCAGGCTCTGGTGGACCAGTCCAACA GAATCCTGTCTAGCGCCGAGAAGGGAACACCGGCTTCAT CATCGTGATCATCCTGATCGCCGTGCTGGCAGCTCCATG ATCCTGGTGTCCATCTTCATCATTATCAAGAAGACCAAGA AGCCCACCGGCGCTCCTCCAGAACTGAGCGGAGTGACCAA CAATGGCTTCATCCCTCACAA	
HMPV_ProlineStab_E131P	ATGAGCTGGAAGGTGGTCATCATCTTCAGCCTGCTGATCA CACCTCAGCACGGCCCTGAAAGAGAGCTACCTGGAAGAGT CCTGCAGCACCATCAGAGAGGGCTACCTGTCTGTGCTGAG AACCGGCTGGTACACCAACGTGTTACACTGGAAGTGGGC GACGTCGAGAATCTGACATGCTCTGATGGCCCTAGCCTGA TCAAGACCGAGCTGGATCTGACCAAGAGCGCCCTGAGAG AACTCAAGACCGTGTCTGCCGATCAGCTGGCCAGAGAGGA ACAGATCGAGAATCCTGGCAGCGGCAGCTTTGTGCTGGGA GCCATTGCTCTTGGAGTGGCTGCTGCTGACGTGTTACAG CAGGCGTGGCCATCGCTAAGACCATCAGACTGCCTAGCGA AGTGACCGCCATCAACAACGCCCTGAAGAAGACAAACGA GGCCGTGAGCACACTCGGCAATGGCGTTAGAGTGCTGGCC ACAGCCGTGCGCGAGCTGAAGGACTTCGTGTCCAAGAACC TGACACGGGCCATTAAACAAGAACAAGTGCGACATCGACG ACCTGAAGATGGCCGTGCTCTTTAGCCAGTTCAACCGGCG GTTCTGAACGTGTCGCGCAGTTTAGCGACAACGCCCGGA ATCACACCGCCATCAGCCTGGACCTGATGACAGATGCTG AGCTGGCTAGAGCCGTGCCTAACATGCCTACATCTGCCGG CCAGATCAAGCTGATGCTCGAGAATAGAGCCATGGTCCGA CGGAAAGGCTTCGGCATTCTGATTGGCGTGTACGGCAGCA GCGTGATCTATATGGTGCAGCTGCCTATCTTCGGCGTGATC GACACACCCCTGCTGGATTGTGAAGGCCGCTCCTAGCTGTA GCGAGAAGAAGGGCAATTACGCTGCTGCTGCTGAGAGAGG ACCAAGGCTGGTATTGTGAGAACGCCGGCAGCACCGTGTA CTACCCTAACGAGAAGGACTGCGAGACAAGAGCGGACCA CGTGTTCTGTGATACCGCCGTGGAATCAATGTGGCCGAG CAGAGCAAGAGTGCAACATCAACATCAGCACCAACCAAC TATCCCTGCAAGGTGTCCACCGGCGAGCACCCATTTCTAT GGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGTATA AGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGGGCAT CATCAAGCAGCTGAACAAGGGCTGCAGCTACATCACCAAC CAGGACGCCGATACCGTGACCATCGACAACACCGTGATC AGCTGAGCAAGGTGGAAGGCGAACAGCACGTGATCAAGG GCAGACCTGTGTCCAGCAGCTTCGACCCCTATCAAGTTCCC TGAGGATCAGTTCCAGGTGGCCCTGGACCAGGTGTTTCGAG AACATCGAGAATTCCAGGCTCTGGTGGACCAGTCCAACA GAATCCTGTCTAGCGCCGAGAAGGGAACACCGGCTTCAT CATCGTGATCATCCTGATCGCCGTGCTGGCAGCTCCATG ATCCTGGTGTCCATCTTCATCATTATCAAGAAGACCAAGA AGCCCACCGGCGCTCCTCCAGAACTGAGCGGAGTGACCAA CAATGGCTTCATCCCTCACAA	122
HMPV_ProlineStab_D447P	ATGAGCTGGAAGGTGGTCATCATCTTCAGCCTGCTGATCA CACCTCAGCACGGCCCTGAAAGAGAGCTACCTGGAAGAGT CCTGCAGCACCATCAGAGAGGGCTACCTGTCTGTGCTGAG AACCGGCTGGTACACCAACGTGTTACACTGGAAGTGGGC GACGTCGAGAATCTGACATGCTCTGATGGCCCTAGCCTGA TCAAGACCGAGCTGGATCTGACCAAGAGCGCCCTGAGAG AACTCAAGACCGTGTCTGCCGATCAGCTGGCCAGAGAGGA ACAGATCGAGAATCCTGGCAGCGGCAGCTTTGTGCTGGGA GCCATTGCTCTTGGAGTGGCTGCTGCTGACGTGTTACAG CAGGCGTGGCCATCGCTAAGACCATCAGACTGGAAGCG AAGTGACCGCCATCAACAACGCCCTGAAGAAGACAAACG AGGCCGTGAGCACACTCGGCAATGGCGTTAGAGTGCTGGC CACAGCCGTGCGCGAGCTGAAGGACTTCGTGTCCAAGAAC CTGACACGGGCCATTAAACAAGAACAAGTGCGACATCGAC GACCTGAAGATGGCCGTGCTCTTTAGCCAGTTCAACCGGC GGTTCTGAACGTGTCGCGGCAGTTTAGCGACAACGCCGG AATCACACCGCCATCAGCCTGGACCTGATGACAGATGCT GAGCTGGCTAGAGCCGTGCCTAACATGCCTACATCTGCCG GCCAGATCAAGCTGATGCTCGAGAATAGAGCCATGGTCCG ACGGAAGGCTTCGGCATTCTGATTGGCGTGTACGGCAGC AGCGTGATCTATATGGTGCAGCTGCCTATCTTCGGCGTGA	123

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
	TCACACACCCCTGCTGGATTGTGAAGGCCGCTCCTAGCTG TAGCGAGAAGAAGGGCAATTACGCCTGCTGCTGAGAGA GGACCAAGGCTGGTATTGTGAGAACGCCGGCAGCACCCTG TACTACCTTAACGAGAAGGACTGCGAGACAAGAGGCGAC CACGTGTTCTGTGATACCGCCGCTGGAATCAATGTGGCCG AGCAGAGCAAGAGTGCAACATCAACATCAGCACCACCA ACTATCCCTGCAAGGTGTCCACGGCAGGCACCCTATTTT TATGGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGT ATAAGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGG GCATCATCAAGCAGCTGAACAAGGGCTGCAGCTACATCAC CAACCAGGACGCCGATACCGTGACCATCGACAACACCGTG TATCAGCTGAGCAAGGTGGAAGGCCAACAGCAGCTGATC AAGGGCAGACCTGTGTCCAGCAGCTTCCACCTATCAAGT TCCCTGAGGATCAGTTCAGGTGGCCCTGGACCAGGTGTT CGAGAACATCGAGAATTCCAGGCTCTGGTGGACAGTCC AACAGAATCCTGTCTAGCGCCGAGAAGGGAAACACCGGC TTCATCATCGTGATCATCTGATCGCCGTGCTGGGCAGCTC CATGATCCTGGTGTCCATCTTCATCATTATCAAGAAGACC AAGAAGCCACCGCGCTCCTCCAGAAGTGAGCGGAGTG ACCAACATGGCTTCATCCCTCACAAC	
HMPV_TrimmerRepulsionD454N	ATGAGCTGGAAGGTGGTCATCATCTTCAGCCTGCTGATCA CACCTCAGCACGGCCTGAAAGAGAGCTACCTGGAAGAGT CCTGCAGCACCATCAGAGGGCTACCTGTCTGTGCTGAG AACCGGCTGGTACACCAACGTGTTCACTGGAAGTGGGC GACGTCGAGAATCTGACATGCTCTGATGGCCCTAGCCTGA TCAAGACCGAGCTGGATCTGACCAAGAGCGCCCTGAGAG AACTCAAGACCGTGTCTGCCGATCAGCTGGCCAGAGAGGA ACAGATCGAGAATCTGGCAGCGGCAGCTTTGTGCTGGGA GCCATTGCTCTTGGAGTGGCTGCTGCTGCAGCTGTTACAG CAGGCGTGGCCATCGCTAAGACCATCAGACTGGAAAGCG AAGTGACCGCCATCAACAACGCCCTGAAGAAGACAAACG AGGCCGTCAGCACACTCGGCAATGGCGTTAGAGTGTGGC CACAGCCGTGCGGAGCTGAAGGACTTCGTGTCCAAGAAC CTGACACGGGCATTAAACAAGAACAAGTGCACATCGAC GACCTGAAGATGGCCGTGTCTTTAGCCAGTTCAACCGGC GGTTCGTAACGTCGTGCGCAGTTTAGCGACACGCCCGG AATCACACCAGCCATCAGCCTGGACCTGATGACAGATGCT GAGCTGGCTAGAGCCGTGCCTAACATGCCTACATCTGCCG GCCAGATCAAGCTGATGCTCGAGAATAGAGCCATGGTCCG ACGGAAAGGCTTCGGCATTCTGATTGGCGTGTACGGCAGC AGCGTGATCTATATGGTGCAGCTGCCTATCTTCGGCGTGA TCGACACACCCCTGCTGGATTGTGAAGGCCGCTCCTAGCTG TAGCGAGAAGAAGGGCAATTACGCCTGCTGCTGAGAGA GGACCAAGGCTGGTATTGTGAGAACGCCGGCAGCACCCTG TACTACCTTAACGAGAAGGACTGCGAGACAAGAGGCGAC CACGTGTTCTGTGATACCGCCGCTGGAATCAATGTGGCCG AGCAGAGCAAGAGTGCAACATCAACATCAGCACCACCA ACTATCCCTGCAAGGTGTCCACGGCAGGCACCCTATTTT TATGGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGT ATAAGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGG GCATCATCAAGCAGCTGAACAAGGGCTGCAGCTACATCAC CAACCAGGACGCCGATACCGTGACCATCGACAACACCGTG TATCAGCTGAGCAAGGTGGAAGGCCAACAGCAGCTGATC AAGGGCAGACCTGTGTCCAGCAGCTTCGACCTTATCAAGT TCCCTGAGAACCAGTTCAGGTGGCCCTGGACCAGGTGTT CGAGAACATCGAGAATTCCAGGCTCTGGTGGACAGTCC AACAGAATCCTGTCTAGCGCCGAGAAGGGAAACACCGGC TTCATCATCGTGATCATCTGATCGCCGTGCTGGGCAGCTC CATGATCCTGGTGTCCATCTTCATCATTATCAAGAAGACC AAGAAGCCACCGCGCTCCTCCAGAAGTGAGCGGAGTG ACCAACATGGCTTCATCCCTCACAAC	124
HMPV_TrimmerRepulsionE453N	ATGAGCTGGAAGGTGGTCATCATCTTCAGCCTGCTGATCA CACCTCAGCACGGCCTGAAAGAGAGCTACCTGGAAGAGT CCTGCAGCACCATCAGAGGGCTACCTGTCTGTGCTGAG AACCGGCTGGTACACCAACGTGTTCACTGGAAGTGGGC GACGTCGAGAATCTGACATGCTCTGATGGCCCTAGCCTGA TCAAGACCGAGCTGGATCTGACCAAGAGCGCCCTGAGAG AACTCAAGACCGTGTCTGCCGATCAGCTGGCCAGAGAGGA ACAGATCGAGAATCTGGCAGCGGCAGCTTTGTGCTGGGA GCCATTGCTCTTGGAGTGGCTGCTGCTGCAGCTGTTACAG CAGGCGTGGCCATCGCTAAGACCATCAGACTGGAAAGCG AAGTGACCGCCATCAACAACGCCCTGAAGAAGACAAACG AGGCCGTCAGCACACTCGGCAATGGCGTTAGAGTGTGGC CACAGCCGTGCGGAGCTGAAGGACTTCGTGTCCAAGAAC CTGACACGGGCATTAAACAAGAACAAGTGCACATCGAC GACCTGAAGATGGCCGTGTCTTTAGCCAGTTCAACCGGC GGTTCGTAACGTCGTGCGCAGTTTAGCGACACGCCCGG AATCACACCAGCCATCAGCCTGGACCTGATGACAGATGCT GAGCTGGCTAGAGCCGTGCCTAACATGCCTACATCTGCCG GCCAGATCAAGCTGATGCTCGAGAATAGAGCCATGGTCCG ACGGAAAGGCTTCGGCATTCTGATTGGCGTGTACGGCAGC AGCGTGATCTATATGGTGCAGCTGCCTATCTTCGGCGTGA TCGACACACCCCTGCTGGATTGTGAAGGCCGCTCCTAGCTG TAGCGAGAAGAAGGGCAATTACGCCTGCTGCTGAGAGA GGACCAAGGCTGGTATTGTGAGAACGCCGGCAGCACCCTG TACTACCTTAACGAGAAGGACTGCGAGACAAGAGGCGAC CACGTGTTCTGTGATACCGCCGCTGGAATCAATGTGGCCG AGCAGAGCAAGAGTGCAACATCAACATCAGCACCACCA ACTATCCCTGCAAGGTGTCCACGGCAGGCACCCTATTTT TATGGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGT ATAAGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGG GCATCATCAAGCAGCTGAACAAGGGCTGCAGCTACATCAC CAACCAGGACGCCGATACCGTGACCATCGACAACACCGTG TATCAGCTGAGCAAGGTGGAAGGCCAACAGCAGCTGATC AAGGGCAGACCTGTGTCCAGCAGCTTCGACCTTATCAAGT TCCCTGAGAACCAGTTCAGGTGGCCCTGGACCAGGTGTT CGAGAACATCGAGAATTCCAGGCTCTGGTGGACAGTCC AACAGAATCCTGTCTAGCGCCGAGAAGGGAAACACCGGC TTCATCATCGTGATCATCTGATCGCCGTGCTGGGCAGCTC CATGATCCTGGTGTCCATCTTCATCATTATCAAGAAGACC AAGAAGCCACCGCGCTCCTCCAGAAGTGAGCGGAGTG ACCAACATGGCTTCATCCCTCACAAC	125

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
	AGGCCGTCAGCACACTCGGCAATGGCGTTAGAGTGCTGGC CACAGCCGTGCGCGAGCTGAAGGACTTCGTGTCCAAGAAC CTGACACGGGCCATTAAACAAGAACAAGTGCACATCGAC GACCTGAAGATGGCCGTGTCTTTAGCCAGTTCAACCGGC GGTTTCTGAACGTCGTGCGGCAGTTTAGCGACACACGCCGG AATCACACCAGCCATCAGCCTGGACCTGATGACAGATGCT GAGCTGGCTAGAGCCGTGCCTAACATGCCATACATCTGCCG GCCAGATCAAGCTGATGCTCGAGAATAGAGCCATGGTCCG ACGGAAGGCTTCGGCATTCTGATTGGCGTGTACGGCAGC AGCGTGATCTATATGGTGCAGCTGCCTATCTTCGGCGTGA TCGACACACCCCTGCTGGATTGTGAAGGCCGCTCCTAGCTG TAGCGAGAAGAAGGGCAATTACGCCCTGCCTGCTGAGAGA GGACCAAGGCTGGTATTGTGAGAAGCCCGGCAGCACCGTG TACTACCCCTAACGAGAAGGACTGCGAGACAAGAGGCGAC CACGTGTTCTGTGATACCGCCGTGGAATCAATGTGGCCG AGCAGAGCAAAGAGTGCAACATCAACATCAGCACCA ACTATCCCTGCAAGGTGTCCACCGGCAGGCACCCCTATTT TATGGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGTT ATAAGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGG GCATCATCAAGCAGCTGAACAAGGGCTGCAGCTACATCAC CAACCAGGACGCCGATACCGTGACCATCGACAACACCGTG TATCAGCTGAGCAAGGTGGAAGGCGAACAGCACGTGATC AAGGGCAGACCTGTGTCCAGCAGCTTCGACCCCTATCAAGT TCCCTCAGGATCAGTTCAGGTGGCCCTGGACAGGTGTT CGAGAACATCGAGAATCCAGGCTCTGGTGGACAGTCC AACAGAATCCTGTCTAGCGCCGAGAAGGGAAACACCGGC TTCATCATCGTGATCATCTGATCGCCGTGCTGGGCAGCTC CATGATCCTGGTGTCCATCTTCATCATTATCAAGAAGACC AAGAAGCCACCGCGCTCCTCCAGAAGTGAAGCGAGTG ACCAACAATGGCTTCATCCCTCACAAC	
HMPV_StabilizeAlphaF196W	ATGAGCTGGAAGGTGGTCATCATCTTCAGCCTGCTGATCA CACCTCAGCACGGCCGTAAGAGAGCTACCTGGAAGAGT CCTGCAGCACCATCAAGAGGGCTACCTGTCTGTGCTGAG AACCAGCTGGTACACCAACGTGTTCACACTGGAAGTGGGC GACGTGAGAAATCTGACATGCTCTGATGGCCCTAGCCTGA TCAAGACCGAGCTGGATCTGACCAAGAGCGCCCTGAGAG AACTCAAGACCGTGTCTGCCGATCAGCTGGCCAGAGAGGA ACAGATCGAGAATCCTGGCAGCGCAGCTTTGTGCTGGGA GCCATTGCTCTTGGAGTGGCTGCTGCTGAGCTGTTACAG CAGGCGTGGCCATCGCTAAGACCATCAGACTGGAAAGCG AAGTGACCGCCATCAACAACGCCCTGAAGAAGACAACG AGGCCGTAGCACACTCGGCAATGGCGTTAGAGTGCTGGC CACAGCCGTGCGCGAGCTGAAGGACTTCGTGTCCAAGAAC CTGACACGGGCCATTAAACAAGAACAAGTGCACATCGAC GACCTGAAGATGGCCGTGTCTTTAGCCAGTGAACCGGC GGTTTCTGAACGTCGTGCGGCAGTTTAGCGACAACGCCGG AATCACACCAGCCATCAGCCTGGACCTGATGACAGATGCT GAGCTGGCTAGAGCCGTGCCTAACATGCCATACATCTGCCG GCCAGATCAAGCTGATGCTCGAGAATAGAGCCATGGTCCG ACGGAAGGCTTCGGCATTCTGATTGGCGTGTACGGCAGC AGCGTGATCTATATGGTGCAGCTGCCTATCTTCGGCGTGA TCGACACACCCCTGCTGGATTGTGAAGGCCGCTCCTAGCTG TAGCGAGAAGAAGGGCAATTACGCCCTGCCTGCTGAGAGA GGACCAAGGCTGGTATTGTGAGAAGCCCGGCAGCACCGTG TACTACCCCTAACGAGAAGGACTGCGAGACAAGAGGCGAC CACGTGTTCTGTGATACCGCCGTGGAATCAATGTGGCCG AGCAGAGCAAAGAGTGCAACATCAACATCAGCACCA ACTATCCCTGCAAGGTGTCCACCGGCAGGCACCCCTATTT TATGGTGGCTCTGTCTCCTCTGGGAGCCCTGGTGGCTTGTT ATAAGGGCGTGTCTGTAGCATCGGCAGCAACAGAGTGG GCATCATCAAGCAGCTGAACAAGGGCTGCAGCTACATCAC CAACCAGGACGCCGATACCGTGACCATCGACAACACCGTG TATCAGCTGAGCAAGGTGGAAGGCGAACAGCACGTGATC AAGGGCAGACCTGTGTCCAGCAGCTTCGACCCCTATCAAGT TCCCTGAGGATCAGTTCAGGTGGCCCTGGACAGGTGTT CGAGAACATCGAGAATCCAGGCTCTGGTGGACAGTCC AACAGAATCCTGTCTAGCGCCGAGAAGGGAAACACCGGC TTCATCATCGTGATCATCTGATCGCCGTGCTGGGCAGCTC CATGATCCTGGTGTCCATCTTCATCATTATCAAGAAGACC AAGAAGCCACCGCGCTCCTCCAGAAGTGAAGCGAGTG ACCAACAATGGCTTCATCCCTCACAAC	126

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
Human Metapneumovirus mRNA Sequences		
HMPV_SC_DSCAV1_4MMV	AUGAGCUGGAAGGUGGUCAUCAUCUUCAGCCUGCUGAU CACACUCAGCACGGCCUGAAAGAGAGCUACCUUGGAAGA GUCCUGCAGCACCAUCACAGAGGGCUACCUUGUCUGUGCU GAGAACC CGCUGGUACACCAACGUGUUCACACUGGAAGU GGGCGACGUCGAGAAUCUGACAUGCUUGAUUGGCCCUAG CCUGAUCAGACCGAGCUGGAUCUGACCAAGAGCGCCCU GAGAGAAUCUAGACCGUGUCUGCCGAUCAGCUGGCCAG AGAGGAACAGAUCCGAGAAUCCUGGCAGCGGCAGCUUUG UGCUGGGAGCCAUUGUCUUGGAGUGGCUGCUGCUGCA GCUGUUCAGCAGGCGUGGCCAUUCUGCAAGACCAUCAGA CUGGAAGCGAAGUGACCGCCAUCAACAACGCCUGAAG AAGACAAACGAGGCCGUCAGCACUCUGGCAUUGGCGUU AGAGUGCUGGCCUUUGCCGUGCGCAGCUGAAGGACUUC GUGUCCAAGAACUGACACGGGCCUGAACAAAGAACAG UGCGACAUCCAGACCUAGAAGUGGCCGUGUCUUUAGC CAGUUCACCGCGGCUUUGAACGUCGUGCGGCAGUUU AGCGACAACGCGGAUACACACAGCUCAGCUGGCCUGGAC CUGAUGACAGAUCCUGAGCUGGCUAGAGCCGUGCCUAC AUGCCUACAUCCGCGGCCAGAUCAAGCUGAUGCUCGAG AAUAGAGCCAUUGGUCCGACGGAAGGCUUCGGCAUUCU GUGUGCGUGUACGGCAGCAGCUGAUUAUUGGUGC AGCUGCCUACUUCGGCGUGAUCGACACACCCUGCUGGA UUUGAAGGCCCGUCCUAGCUGUAGCGAGAAGAGGGC AAUUCAGCCUGCCUGUGAGAGAGGACCAGGCUUGUA UUUGCAGAACCGCGCAGCACCGUGUACUACCUAACGA GAAGGACUGCGAGACAGAGGCGACACGUGUUCUGUG AUACCGCCCGUGGAUCAAUGUGGCCGAGCAGAGCAAAG AGUGCAACAUCAACUAGCACCACCAACUACUCCUGCA AGGUGUCCACCGCGAGGCACCUUAUUUCUAGGUGGCUC UGUCUCUCUGGGAGCCUGGUGGCUUGUUAUAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUAC AAGCAGCUGAACAGGGCUGCAGCUACAUCAACCAACAG GACGCCGAUACCGUGACCAUCGACCAACCCGUGUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCAGCUGAUCAGGG CAGACCUGUCCAGCAGCUUCGACCCUACUAGUUCUCC UGAGGAUCAGUCAAAGUGGCCUGGACAGGUGUUCG AGAACAUCCGAGAAUCCAGGCUCUGGUGGACAGUCCA ACAGAAUCUGUCUAGCGCCGAGAAGGGAACACCGGCU UCAUCAUCUGAUAUCUGAUCGCGUGCUGGGCAGCU CCAUGAUCCUGGUGUCCAUUUCAUCAUAUACAAGAAGA CCAAGAAGCCACCGCGCUCUCCAGAACUGAGCGGAG UGACCAACAAGGCUUCAUCCUACAAAC	127
HMPV_SC_DSURIC_4MMV	AUGAGCUGGAAGGUGGUCAUCAUCUUCAGCCUGCUGAU CACACUCAGCACGGCCUGAAAGAGAGCUACCUUGGAAGA GUCCUGCAGCACCAUCACAGAGGGCUACCUUGUCUGUGCU GAGAACC CGCUGGUACACCAACGUGUUCACACUGGAAGU GGGCGACGUCGAGAAUCUGACAUGCUUGAUUGGCCCUAG CCUGAUCAGACCGAGCUGGAUCUGACCAAGAGCGCCCU GAGAGAAUCUAGACCGUGUCUGCCGAUCAGCUGGCCAG AGAGGAACAGAUCCGAGAAUCCUGGCAGCGGCAGCUUUG UGCUGGGAGCCAUUGUCUUGGAGUGGCUGCUGCUGCA GCUGUUCAGCAGGCGUGGCCAUUCUGCAAGACCAUCAGA CUGGAAGCGAAGUGACCGCCAUCAACAACGCCUGAAG AAGACAAACGAGGCCGUCAGCACUCUGGCAUUGGCGUU AGAGUGCUGGCCACAGCCGUGCGCAGCUGAAGGACUUC GUGUCCAAGAACUGACACGGGCCAUUAACAAGAACAAAG UGCGACAUCGACGACUGAAGUGGCCGUGUCUUUAGC CAGUUCACCGCGGCUUUCUGAACGUCGCGGCAGUUU AGCGACAACGCGGAUACACACAGCUCAGCUGGCCUGGAC CUGAUGACAGAUCCUGAGCUGGCUAGAGCCGUGCCUAC AUGCCUACAUCCGCGGCCAGAUCAAGCUGAUGCUCGAG AAUAGAGCCAUUGGUCCGACGGAAGGCUUCGGCAUUCU GUGUGCGUGUACGGCAGCAGCUGAUCUAUUGGUGC AGCUGCCUACUUCGGCGUGAUCGACACACCCUGCUGGA UUUGAAGGCCCGUCCUAGCUGUAGCGAGAAGAGGGC AAUUCAGCCUGCCUGUGAGAGAGGACCAGGCUUGUA UUUGCAGAACCGCGCAGCACCGUGUACUACCUAACGA GAAGGACUGCGAGACAGAGGCGACCAAGUUCUGUG AUACCGCCCGUGAAUCAAUGUGGCCGAGCAGAGCAAAG AGUGCAACAUCAACUAGCACCACCAACUACUCCUGCA AGGUGUCCACCGCGAGGCACCUUAUUUCUAGGUGGCUC	128

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
	UGUCUCCUCUGGGAGCCCUUGGUGGCUUGUUAUAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUCAUC AAGCAGCUGAACAGGGCUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACAACACCGUGUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCAGUGAUCAGGG CAGACCUUGUUCAGCAGCUUCGACCCUAUCAAGUUC UGAGCAACAGUGGCAUGUGGCCUGGACAGGUGUUCGA GAACAUCGAGAAUUCACAGGCUUCUGGUGGACAGUCCAA CAGAAUCCUGUUCAGCGCCGAGAAGGGAACACCGGCUU CAUCAUCGUAUCAUCUGAUCGCGUGUGGCGAGCUC CAUGAUCUGGUGUCCAUUCUAUCAUUAUCAAGAAGAC CAAGAAGCCACCGGCGCUCCUCCAGAACUGAGCGGAGU GACCAACAAGGCUUCAUCCUCACAAAC	
HMPV_SC_DM_Krarup_U74LD185P	AUGAGCUGGAAGGUGGUCAUCAUCUUCAGCCUGCUGAU CACACCUAGCAGCGCCUGAAAGAGAGCUACCUUGGAAGA GUCCUGCAGCACCAUACAGAGGGCUACUGUCUGUGCU GAGAACCAGGUGUACCAACGUGUUCACACUGGAAGU GGGCGACGUCGAGAAUCUGACAUGCUUGAUGGCCUAG CCUGAUCAGACCGAGCUGGAUCUGUCUAGAGCGCCU GAGAGAACUCAAGACCGUGUCUGCCGAUCAGCUGGCCAG AGAGGAACAGAUCAAGAAUCCUGGCGAGCGGACGUUUG UGCUUGGAGCCAUUGCUUUGGAGUGGCUUGCUGUGCA GCUGUACAGCAGGCGUGGCCAUCGCUAAGACCAUCAGA CUGGAAGCGAAGUGACCGCCAUACAACGCGCCUGAAG AAGACAAACGAGGCCGUCAGCACACUCGGCAUUGGCGUU AGAGUGCUGGCCACAGCCGUGCGGAGCUGAAGGACUUC GUGUCCAAGAACUGACACGGGCCAUUAACAAGAACAG UGCGACAUCUCCUGACUGAAGAUGGCGUGUCUUUAGC CAGUUCACCGGCGGUUUCUGAACGUCGUGCGGCGAUUU AGCGACAACGCGGAAUACACAGCACAUCAGCCUGGAC CUGAUGACAGAUUGCUGAGCUGGCUAGAGCCGUGCCUAC AUGCCUACAUCUGCCGGCCAGAUCAAGCUGAUGCUGGAG AAUAGAGCCAUUGGUCGAGCGAAAGGCUUCGGCAUUCU GAUUGGCGUGUACGGCAGCAGCUGAUCUAUUGGUGC AGCUGCCUAUCUUCGGCGUGAUCGACACACCCUGCUGGA UUGUGAAGGCCGCUCCUAGCUGUAGCGAGAAGAAGGC AAUUAACGCCUGCCUGUGAGAGAGGACCAGGCGUGUA UUGUCAGAACGCCGCGCAGCACCGUGUACUACCUAACGA GAAGGACUGCGAGACAGAGGCGACACGUGUUCUGUG AUACCGCCCGUGGAUUCUUGUGGCGAGCAGAGCAAAG AGUGCAACAUAACAUCAGCACCAACUAUCCUGCA AGGUGUCCACCGCAGGCACCUAUUUCUAUGGUGGCU UGUCUCUUCUGGAGGCCUGGUGGCUUGUUAAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUAC AAGCAGCUGAACAGGGCUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACAACACCGUGUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCAGCUGAUCAGGG CAGACCUUGUCCAGCAGCUUCGACCCUAUCAAGUUC UGAGGAUCAGUUCAGGUGGCCUGGACAGGUGUUCG AGAAACAUCGAGAAUCCAGGCUUCUGGUGACAGUCCA ACAGAAUCUGUCUAGCGCCGAGAAGGGAACACCGGCU UCAUCAUCUGAUCAUUCUGAUCGCGUGCUGGGCAGCU CCAUGAUCUGGUGUCCAUUCUAUCAUUAUCAAGAAGA CCAAGAAGCCACCGGCGUCCUCCAGAACUGAGCGGAG UGACCAACAAGGCUUCAUCCUCACAAAC	129
HMPV_SC_UM_Krarup_U74LD185PD454N	AUGAGCUGGAAGGUGGUCAUCAUCUUCAGCCUGCUGAU CACACCUAGCAGCGCCUGAAAGAGAGCUACCUUGGAAGA GUCCUGCAGCACCAUACAGAGGGCUACUGUCUGUGCU GAGAACCAGGUGGUACCAACGUGUUCACACUGGAAGU GGGCGACGUCGAGAAUCUGACAUGCUUGAUGGCCUAG CCUGAUCAGACCGAGCUGGAUCUGCUAAGAGCGCCU GAGAGAACUCAAGACCGUGUCUGCCGAUCAGCUGGCCAG AGAGGAACAGAUCAAGAAUCCUGGCGAGCGGACGUUUG UGCUUGGAGCCAUUGCUUUGGAGUGGCUUGCUGUGCA GCUGUACAGCAGGCGUGGCCAUCGCUAAGACCAUCAGA CUGGAAGCGAAGUGACCGCCAUACAACGCGCCUGAAG AAGACAAACGAGGCCGUCAGCACACUCGGCAUUGGCGUU AGAGUGCUGGCCACAGCCGUGCGGAGCUGAAGGACUUC GUGUCCAAGAACUGACACGGGCCAUUAACAAGAACAG UGCGACAUCUCCUGACCGGCGAAGUGGCGUGUCUUUAGC CAGUUCACCGGCGGUUUCUGAACGUCGUGCGGCGAUUU AGCGACAACGCGGAAUACACAGCACAUCAGCCUGGAC	130

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
	CUGAUGACAGAUGCUGAGCUGGCUAGAGCCGUGCCUAAC AUGCCUACAUCUGCCGGCCAGAUCAAGCUGAUGCUCGAG AAUAGAGCCAUUGGUCCGACGGAAGGCUUCGGCAUUCU GAUUGGCGUGUACGGCAGCAGCGUAUCUAUAUGGUGC AGCUGCCUAUCUUCGGCGUGAUCGACACCCUGCUGGA UUGUGAAGGCCGUCUAGCUGUAGCGAGAAGAAGGGC AAUUACGCCUGCCUGCUGAGAGAGGACCAAGGCUUGUA UUGUCAGAACGCCGGCAGCACCUGUACUACCCUAACGA GAAGGACUGCGAGACAAGAGGCGACCCAGUGUUCUGUG AUACCGCCGCGUGGAUCAAUGUGGCCGAGCAGAGCAAAG AGUGCAACAUCACAUCAGCACCAACAACUAUCCUGCA AGGUGUCCACCGGCAGGCACCUAUUUCUAUGGUGGCUC UGUCUCUCUGGGAGCCUGGUGGCUUGUUAUAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUCAUC AAGCAGCUGAACAGGGCUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACAAACCCUGUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCAGUGAUCAGGG CAGACCUGUGUCAGCAGCUUCGACCCUAUCAAGUCC UGAGAACCAUUCAGGUGGCCUGGACCAAGGUGUUCGA GAACAUCGAGAAUUCAGGCUUCUGUGGACCAAGUCCAA CAGAAUCCUGUCUAGCGCCGAGAAGGGAACACCGGCUU CAUCAUCGUAUCAUCCUGAUCGCGUGCUGGGCAGCUC CAUGAUCUGGUGUCAUCUUAUCAUUAACAAGAGAC CAAGAAGCCACCGGCGCUCCUCCAGAACUGAGCGGAGU GACCAACAAGGCUUCAUCCUCACAAAC	
HMPV_SC_4M_Krarup_U74LS170LD185P	AUGAGCUGGAAGGUGGUCAUCAUCUUCAGCCUGCUGAU CACACCUCAGCACGGCCUGAAAGAGAGCUACCCUGGAAGA GUCCUGCAGCACCAUACAGAGGGCUACUGUCUGUGCU GAGAACC GGCUAGUACCAACGUGUACACUUGGAAGU GGGCGACGUCGAGAAUCUGACAUGCUUGAUGGCCUAG CCUGAUCAGAACCGAGCUGGAUCUGUCUAGAGCGCCU GAGAGAACUCAAGACCGUGUCUGCCGUAUCAGCUGGCCAG AGAGGAACAGAUCAAGAAUCCUGGCAGCGGCAGCUUUG UGCUUGGAGCCAUUGUCUUGGAGUGGCUGCUGUGCA GCUGUACAGCAGGCGUGGCCAUCCGUAAGACCAUCAGA CUGGAAGCGAAGUGACCGCCAUAACAACGCCUUGAAG AAGACAAACGAGGCCGUCAGCACACUCGGCAUUGGCGUU AGAGUGCUGGCCACAGCCGUGCGGAGCUGAAGGACUUC GUGCUUAAGAACUGACACGGGCCAUUAACAAGAACAA GUGCGACAUCUCCUGACCUAGAAGUGGCCUGUCCUUUAG CCAGUUAACCGCGGCUUUCUGAACGUCUGCGGCAGUU UAGCGACAACCGCGGAUACACACAGCCAUACGCCUGGA CCUGAUGACAGAUGCUGAGCUGGCUAGAGCCUGGCCUAA CAUGCCUACAUCUGCCGGCCAGAUCAAGCUGAUGCUCGA GAAUAGAGCCAUUGUCCGACGGAAGGCUUCGGCAUUC UGAUUGGCGUGUACGGCAGCAGCGUGAUCUAUAUGGUG CAGCUGCCUAUCUUCGGCGUGAUCGACACCCUGCUGG AUUGUGAAGGCCGCUCCUAGCUGUAGCGAGAAAGGG CAAUUAACGCCUGCUGUGAGAGAGGACCAGGCUUGUA UUGUCAGAACGCCGGCAGCACCGUACUACCCUAACGA GAAGGACUGCGAGACAAGAGGCGACACGUGUUCUGUG AUACCGCCGCGUGGAUCAAUGUGGCCGAGCAGAGCAAAG AGUGCAACAUAACAUCAGCACCAACAACUAUCCUGCA AGGUGUCCACCGCAGGCACCUAUUUCUAUGGUGGCUC UGUCUCUCUGGGAGCCUGGUGGCUUGUUAUAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUCAUC AAGCAGCUGAACAGGGCUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACAAACCGUGUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCACGUGAUCAGGG CAGACCUGUUCAGCAGCUUCGACCCUAUCAAGUCC UGAGGAUCAGUUCAGGUGGCCUGGACCAAGGUGUUCG AGAACAUCAAGAAUUCAGGCUUCUGGUGACCAAGUCCA ACAGAAUCUGUCUAGCGCCGAGAAGGGAACACCGGCU UCAUCAUCGUAUCAUCUGAUCGCGUGCUGGGCAGCU CCAUGAUCCUGGUGUCCAUCUUAUCAUUAACAAGAAGA CCAAGAAGCCACCGGCGCUCCUCCAGAACUGAGCGGAG UGACCAACAAGGCUUCAUCCUCACAAAC	131
HMPV_SC_5M_Krarup_U74LS170LD185PD454N	AUGAGCUGGAAGGUGGUCAUCAUCUUCAGCCUGCUGAU CACACCUCAGCACGGCCUGAAAGAGAGCUACCCUGGAAGA GUCCUGCAGCACCAUACAGAGGGCUACUGUCUGUGCU GAGAACC GGCUAGUACCAACGUGUACACUUGGAAGU GGGCGACGUCGAGAAUCUGACAUGCUUGAUGGCCUAG CCUGAUCAGAACCGAGCUGGAUCUGUCUAGAGCGCCU GAGAGAACUCAAGACCGUGUCUGCCGUAUCAGCUGGCCAG AGAGGAACAGAUCAAGAAUCCUGGCAGCGGCAGCUUUG UGCUUGGAGCCAUUGUCUUGGAGUGGCUGCUGUGCA GCUGUACAGCAGGCGUGGCCAUCCGUAAGACCAUCAGA CUGGAAGCGAAGUGACCGCCAUAACAACGCCUUGAAG AAGACAAACGAGGCCGUCAGCACACUCGGCAUUGGCGUU AGAGUGCUGGCCACAGCCGUGCGGAGCUGAAGGACUUC GUGCUUAAGAACUGACACGGGCCAUUAACAAGAACAA GUGCGACAUCUCCUGACCUAGAAGUGGCCUGUCCUUUAG CCAGUUAACCGCGGCUUUCUGAACGUCUGCGGCAGUU UAGCGACAACCGCGGAUACACACAGCCAUACGCCUGGA CCUGAUGACAGAUGCUGAGCUGGCUAGAGCCUGGCCUAA CAUGCCUACAUCUGCCGGCCAGAUCAAGCUGAUGCUCGA GAAUAGAGCCAUUGUCCGACGGAAGGCUUCGGCAUUC UGAUUGGCGUGUACGGCAGCAGCGUGAUCUAUAUGGUG CAGCUGCCUAUCUUCGGCGUGAUCGACACCCUGCUGG AUUGUGAAGGCCGCUCCUAGCUGUAGCGAGAAAGGG CAAUUAACGCCUGCUGUGAGAGAGGACCAGGCUUGUA UUGUCAGAACGCCGGCAGCACCGUACUACCCUAACGA GAAGGACUGCGAGACAAGAGGCGACACGUGUUCUGUG AUACCGCCGCGUGGAUCAAUGUGGCCGAGCAGAGCAAAG AGUGCAACAUAACAUCAGCACCAACAACUAUCCUGCA AGGUGUCCACCGCAGGCACCUAUUUCUAUGGUGGCUC UGUCUCUCUGGGAGCCUGGUGGCUUGUUAUAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUCAUC AAGCAGCUGAACAGGGCUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACAAACCGUGUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCACGUGAUCAGGG CAGACCUGUUCAGCAGCUUCGACCCUAUCAAGUCC UGAGGAUCAGUUCAGGUGGCCUGGACCAAGGUGUUCG AGAACAUCAAGAAUUCAGGCUUCUGGUGACCAAGUCCA ACAGAAUCUGUCUAGCGCCGAGAAGGGAACACCGGCU UCAUCAUCGUAUCAUCUGAUCGCGUGCUGGGCAGCU CCAUGAUCCUGGUGUCCAUCUUAUCAUUAACAAGAAGA CCAAGAAGCCACCGGCGCUCCUCCAGAACUGAGCGGAG UGACCAACAAGGCUUCAUCCUCACAAAC	132

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
	CCUGAUC AAGACCGAGCUGGAUCUGCUCAAGAGCGCCU GAGAGAACUCAAGACCGUGUCUGCCGAUCAGCUGGCCAG AGAGGAACAGAUCCGAGAAUCCUGGCAGCGGCAGCUUUG UGCUGGGAGCCAUUGCUCUUGGAGUGGCUGCUGCUGCA GCUGUACAGCAGGCGUGGCCAUCGCUAAGACCAUCAGA CUGGAAAGCGAAGUGACCGCCAUCAACAACGCCCCUGAAG AAGACAAACGAGGCCGUCAGCACACUCGGCAAUGGCGUU AGAGUGCUGGCCACAGCCGUGCGCAGCUGAAGGACUUC GUGCUUAAGAACCUGACACGGGCCAUUAACAAGAACAA GUGCGACAUC CUGACCUAGAAGUGGCCGUGUCCUUUAG CCAGUUCACACCGCGGCUUUCUGAACGUCGUGCGCAGUU UAGCGACAACCGCGGAUACACCCAGCCAUACGCUGGA CCUGAUGACAGAUCCUGAGCUGGCUGAGCCGUGCCUAA CAUGCCUACAU CUGCCGGCCAGAUCAAGCUGAUGCUGA GAAUAGAGCCAUUGGUCGACGGAAGGCUUCGGCAUUC UGAUUGGCGUGUACGGCAGCAGCGUGAUCUAUUGGUG CAGCUGCCUAUCUUCGGCGUGAUCGACACCCUGCUGG AUUGUGAAGGCCGCUCCUAGCUGUAGCGAGAAGAAGGG CAAUUAACGCCUGCUGCUGAGAGAGGACCAAGGCUUGUA UUGUCAGAACGCGGCAGCACCGUGUACUACCUAACGA GAAGGACUGCGAGACAAGAGGCGACCGUGUUCUGUG AUACCGCCGUGGAAUCAUUGGCGGAGCAGAGCAAAG AGUGCAACAUACAUCAGCACCAACCAUUAUCCUGCA AGGUGUCCACCGGCAGGCACCUAUUUCUAUGGUGGCUC UGUCUCUCUGGGAGCCUGGUGGCUUGUUAUAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUCAUC AAGCAGCUGAACCAAGGGCUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACAAACCGUGUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCAGUGAUC AAGGG CAGACCUUGUUCAGCAGCUUCGACCCUAUCAAGUCC UGAGAACCAUUC CAGGUGGCCUGGACCAAGGUGUUCGA GAACAUCGAGAAUUC CAGGCUUCUGUGGACCAAGUCCAA CAGAAUCCUGUUCUAGCGCCGAGAAGGGAACACCGGCUC CAUCAUCGUGAUCAUCCUGAUCGCGUGCUGGGCAGCUC CAUGAUCCUGGUGUCUUCUACAUAUUAACAAGAGAC CAAGAAGCCACCGGCGCUCCUCCAGAACUGAGCGGAGU GACCAACAAGGCUUCAUCCUACAAAC	
HMPV_SC_DM_Krarup_E51PU74L	AUGAGCUGGAAGGUGGUCAUCAUCUUCAGCCUGCUGAU CACACCUAGCACCGCCUGAAAGAGAGCUACCUAGGAAGA GUCCUGCAGCACCAUACAGAGGGCUACUGUCUGUGCU GAGAACC GGCUAGUACCAACCGUUCACACUGCCUGU GGGCGACGUCGAGAAUCUGACAUUCUGAUGGCCUAG CCUGAUCAAGACCGAGCUGGAUCUGCUAAGAGCGCCU GAGAGAACUCAAGACCGUGUCUGCCGAUCAGCUGGCCAG AGAGGAACAGAUCCGAGAAUCCUGGCAGCGGCAGCUUUG UGCUGGGAGCCAUUGCUCUUGGAGUGGCUGCUGCUGCA GCUGUACAGCAGGCGUGGCCAUUCGCUAAGACCAUCAGA CUGGAAAGCGAAGUGACCGCCAUCAACAACGCCCUAGAAG AAGACAAACGAGGCCGUCAGCACACUCGGCAAUGGCGUU AGAGUGCUGGCCACAGCCGUGCGCAGCUGAAGGACUUC GUGUCCAAGAACCUAGACACGGGCCAUUAACAAGAACAG UGCAGCAUCGACGACUGAAGAUGGCCGUGUCCUUUAGC CAGUUCACCGCGGCUUUCUGAACGUCGUGCGCAGUUU AGCGACAACCGCGGAUACACCCAGCCAUACAGCCUGGAC CUGAUGACAGAUCCUGAGCUGGCUAGAGCCGUGCCUAAC AUGCCUACAUCUGCCGGCCGAUCAAGCUGAUGCUCGAG AAUAGAGCCAUUGGUCGACGGAAGGCUUCGGCAUUCU GAUUGGCGUGUACGGCAGCAGCGUGAUCUAUUGGUGC AGCUGCCUAUCUUCGGCGUGAUCGACACACCCUGCUGGA UUUGAAGGCCGCUUCUAGCUGUAGCGAGAAGAAGGGC AAUUAACGCCUGCCUGUGAGAGAGGACCAAGGCUUGUA UUUGCAGAACGCGGCAGCACCGUGUACUACCUAACGA GAAGGACUGCGAGACAAAGAGCGACCAAGUUCUGUG AUACCGCCGUGGAAUCAUUGGCGGAGCAGAGCAAAG AGUGCAACAUAACAUCAGCACCAACUAUCCUGCA AGGUGUCCACCGGCAGGCACCUAUUUCUAUGGUGGCUC UGUCUCUCUGGGAGCCUGGUGGCUUGUUAUAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUCAUC AAGCAGCUGAACCAAGGGCUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACAAACCGUGUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCAGCUGAUC AAGGG CAGACCUUGUCCAGCAGCUUCGACCCUAUCAAGUCC UGAGGAUCAGUUC CAGGUGGCCUGGACCAAGGUGUUCG	133

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
	AGAACAUCGAGAAUCCAGGCUCUGGUGGACCAGUCCA ACAGAAUCCUGUCUAGCGCCGAGAAGGGAACACCGGCU UCAUCAUCGUGAUCAUCCUGAUCGCCGUGCUGGGCAGCU CCAUGAUCCUGGUGUCCAUUCUCAUAUAUCAAGAAGA CCAAGAAGCCACCGCGCUCUCCAGAACUGAGCGGAG UGACCAACAUGGCUUCAUCCUCACAAAC	
HMPV_SC_UM_Krarup_E51PU74LD454N	AUGAGCUGGAAGGUGGUCAUCAUUCAGCCUGCUGAU CACACCUCAGCACGGCCUGAAAGAGAGCUACCUGGAAGA GUCCUGCAGCACCAUCACAGAGGGCUACCUGUCUGUGCU GAGAACC GGCUUGUACACCAACGUGUUCACACUGCCUGU GGGCGACGUCGAGAAUCUGACAUGCUCUGAGGCCCUAG CCUGAUCAAGACCGAGCUGGAUCUGCUCAAGAGCGCCCU GAGAGAACUCAAGACCGUGUCUGCCGAUACGUGGCCAG AGAGGAACAGAUCCGAGAAUCCUGGCAGCGGCAGCUUUG UGCUGGGAGCCAUUGCUCUUGGAGUGGCUGCUGCUGCA GCUGUUCACAGCAGGCGUGGCCAUCGCUAAGACCAUCAGA CUGGAAAGCGAAGUGACCGCCAUAACAACGCCCUAGAAG AAGACAAACGAGGCCGUCAGCACACUCGGCAAUGGCGUU AGAGUGCUGGCCACAGCCGUGCGCAGCUGAAGGACUUC GUGUCCAAGAACCUGACACGGGCCAUUAACAAGAACAAG UGCGACAUCGACGACCUGAAGAUGGCCGUGUCCUUUAGC CAGUUCACCGCGCGUUUCUGAACGUCUGCGCAGUUU AGCGACAACCGCCGGAUUCACACAGCCAUACAGCCUGGAC CUGAUGACAGAUGCUGAGCUGGCUAGAGCCGUGCCUAAC AUGCCUACAUUCGCCGCCAGAUCAAGCUGAUGCUCGAG AAUAGAGCCAUUGGUCGACGGAAGGCUUCGGCAUUCU GAUUGGCGUUAACGGCAGCAGCGUAUCUAUAUGGUGC AGCUGCCUAUCUUCGGCGUGAUCGACACACCCUGCUGGA UUGUGAAGGCCGUCUCUAGCUGUAGCGAGAAGAAGGGC AAUUAACGCCUGCCUGCUGAGAGAGGACCAAGGCUUGUA UUGUCAGAACGCGCGCAGCACCGUGUACUACCUAACGA GAAGGACUGCGAGACAAGAGGCCAGCCAGUGUUCUGUG AUACCGCCGCUUGAAUCAAUUGGCCGAGCAGAGCAAAG AGUGCAACAUCAUCAAGCACCAACCAUUAUCCUGCA AGGUGUCCACCGCGAGGCCCUAUUUCUAUGGUGGCUC UGUCUCUCUGGGAGCCUGGUGGCUUGUUAUAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUCAUC AAGCAGCUGAACCAAGGGCUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACAACACCGUGUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCAGUGAUCAAAGGG CAGACCUGUGUCCAGCAGCUUCGACCCUAUCAAGUCC UGAGAACCAUUCAGGUGGCCUGGACCAAGGUGUUCGA GAACAUCGAGAAUUCACAGGCUUGGUGGACCAUUCCAA CAGAAUCCUGUCUAGCGCCGAGAAGGGAACACCGGCUU CAUCAUCGUAUCAUCCUGAUCGCGUGCUGGGCAGCUC CAUGAUCCUGGUGUCAUCUUAUCAUUAUCAAGAAGAC CAAGAAGCCACCGCGCUCUCCAGAACUGAGCGGAGU GACCAACAAGGCUUCAUCCUCACAAAC	134
HMPV_SC_SUabilizeAlpha_U74L	AUGAGCUGGAAGGUGGUCAUCAUUCAGCCUGCUGAU CACACCUCAGCACGGCCUGAAAGAGAGCUACCUGGAAGA GUCCUGCAGCACCAUCACAGAGGGCUACCUGUCUGUGCU GAGAACC GGCUUGUACACCAACGUGUUCACACUGGAAGU GGGCGACGUCGAGAAUCUGACAUGCUCUGAUGGCCCUAG CCUGAUCAAGACCGAGCUGGAUCUGCUCAAGAGCGCCCU GAGAGAACUCAAGACCGUGUCUGCCGAUCAGCUGGCCAG AGAGGAACAGAUCCGAGAAUCCUGGCAGCGGCAGCUUUG UGCUGGGAGCCAUUGCUCUUGGAGUGGCUGCUGCUGCA GCUGUUCACAGCAGGCGUGGCCAUCGCUAAGACCAUCAGA CUGGAAAGCGAAGUGACCGCCAUAACAACGCCCUAGAAG AAGACAAACGAGGCCGUCAGCACACUCGGCAAUGGCGUU AGAGUGCUGGCCACAGCCGUGCGCGAGCUGAAGGACUUC GUGUCCAAGAACCUGACACGGGCCAUUAACAAGAACAAG UGCGACAUCGACGACCUGAAGAUGGCCGUGUCCUUUAGC CAGUUCACCGCGCGUUUCUGAACGUCGUGCGCAGUUU AGCGACAACCGCGGAUUCACACAGCCAUACAGCCUGGAC CUGAUGACAGAUGCUGAGCUGGCUAGAGCCGUGCCUAAC AUGCCUACAUCUGCCGGCCAGAUCAAGCUGAUGCUCGAG AAUAGAGCCAUUGGUCGACGGAAGGCUUCGGCAUUCU GAUUGGCGUUAACGGCAGCAGCGUAUCUAUAUGGUGC AGCUGCCUAUCUUCGGCGUGAUCGACACACCCUGCUGGA UUGUGAAGGCCGUCUCUAGCUGAAGCGAGAAGAAGGGC AAUUAACGCCUGCCUGCUGAGAGAGGACCAAGGCUUGUA	135

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
	UUGUCAGAACGCCGGCAGCACCGUGUACUACCCUAACGA GAAGGACUGCGAGACAGAGGCGACACGUGUUCUGUG AUACCGCCGUGGAAUCAUUGUGGCGAGCAGAGCAAAG AGUGCAACAUCAACAUCAGCACCACCACTAUCCUGCA AGGUGUCCACCGGCAGGCACCCUAUUUCUAUGGUGGCUC UGUCUCCUCUGGGAGCCUGGUGGCUGUUAUAAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUCAUC AAGCAGCUGAACAGGGCUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACAACACCGUUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCAGUGAUCAAGGG CAGACCUUGUGUCCAGCAGCUUCGACCCUAUCAAGUCCC UGAGGAUCAGUUCAGGUGGCCUGGACAGGUGUUCG AGAACAUCCAGAAUCCAGGCUCUGGUGGACAGUCCA ACAGAAUCUGUCUAGCGCCGAGAAGGGAACACCGGCU UCAUCAUCGUGAUCAUCUGAUCGCCGUGUGGGCAGCU CCAUGAUCCUGGUGUCCAUUCUCAUAUAUCAAGAAGA CCAAGAAGCCACCGGCGCUCUCCAGAACUGAGCGGAG UGACCAACAAGGCUUCAUCCUCACAAAC	
HMPV_SC_SUabilizeAlpha_V55L	AUGAGCUGGAAGGUGGUCAUCAUCUUCAGCCUGCUGAU CACACCUCAGCACGGCCUGAAAGAGAGCUACCGUGAAGA GUCCUGCAGCACCAUCAAGAGGGCUACCGUCUGUGCU GAGAACC GGCGUGUACACCAACGUGUUCACACUGGAAGU GGGCGACCCUGGAAUUCAGCAUGCUCUGAUGGCCUAG CCUGAUCAAGACCGAGCUGGAUCUGACCAAGAGCGCCU GAGAGAACUCAAGACCGUGUCUGCCGAUACGUGGCCAG AGAGGAACAGAUCCGAGAAUCCUGGCAGCGGCAGCUUUG UGCUGGGAGCCAUUGCUUUGGAGUGGCUGCUGCUGCA GCUGUACAGCAGGCGUGGCCAUCCGUAAGACCAUCAGA CUGGAAAGCGAAGUGACCGCCAUAACAACGCCUUGAAG AAGACAAACGAGGCCGUCAGCACACUCGGCAAUGGCGUU AGAGUGCUGGCCACAGCCGUGCGCAGCUGAAGGACUUC GUGUCCAAGAACCUGACACGGGCCAUUAACAAGAACAAG UGCGACAUCGACGACCGUAAGAUGGCCGUGUCCUUUAGC CAGUUAACCGGCGGUUUCUGAACGUCUGCGGCGAUUU AGCGACAACCGCCGGAUUCACACAGCCAUACAGCCUGGAC CUGAUGACAGAUCCUGAGCUGGCUAGAGCCGUGCCUAAC AUGCCUACAUUGCCGGCCAGAUCAAGCUGAUGCUCGAG AAUAGAGCCAUUGGUCGACGGAAGGCUUCGGCAUUCU GAUUGGCGUUAACGGCAGCAGCGUAUCUAUUGGUGC AGCUGCCUAUCUUCGGCGUGAUCGACACACCCUGCUGGA UUGUGAAGGCCGCUCCUAGCUGUAGCGAGAAGAAGGGC AAUUAAGCCUGCCUGCUGAGAGAGGACCAAGGCUUGUA UUGUCAGAACGCCGGCAGCACCGUGUACUACCCUAACGA GAAGGACUGCGAGACAAGAGGCGACACGUGUUCUGUG AUACCGCCGUGGAAUCAUUGUGGCGGAGCAGAGCAAAG AGUGCAACAUCAACAUCAGCACCAACCAUAUCCUGCA AGGUGUCCACCGGCAGGCACCCUAUUUCUAUGGUGGCUC UGUCUCCUCUGGGAGCCUGGUGGCUGUUAUAAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUCAUC AAGCAGCUGAACAGGGCUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACAACACCGUGUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCAGUGAUCAAGGG CAGACCUUGUCCAGCAGCUUCGACCCUAUCAAGUCCC UGAGGAUCAGUUCAGGUGGCCUGGACAGGUGUUCG AGAACAUCCAGAAUCCAGGCUCUGGUGGACAGUCCA ACAGAAUCCUGUCUAGCGCCGAGAAGGGAACACCGGCU UCAUCAUCGUGAUCAUCCUGAUCGCCGUGCUGGGCAGCU CCAUGAUCCUGGUGUCCAUUCUCAUAUAUCAAGAAGA CCAAGAAGCCACCGGCGCUCUCCAGAACUGAGCGGAG UGACCAACAAGGCUUCAUCCUCACAAAC	136
HMPV_SC_SUabilizeAlpha_S170L	AUGAGCUGGAAGGUGGUCAUCAUCUUCAGCCUGCUGAU CACACCUCAGCACGGCCUGAAAGAGAGCUACCGUGAAGA GUCCUGCAGCACCAUCAAGAGGGCUACCGUCUGUGCU GAGAACC GGCGUGUACACCAACGUGUUCACACUGGAAGU GGGCGACGUCGAGAAUCUGACAUGCUCUGAUGGCCUAG CCUGAUCAAGACCGAGCUGGAUCUGACCAAGAGCGCCU GAGAGAACUCAAGACCGUGUCUGCCGAUCAGCUGGCCAG AGAGGAACAGAUCCGAGAAUCCUGGCAGCGGCAGCUUUG UGCUGGGAGCCAUUGCUUUGGAGUGGCUGCUGCUGCA GCUGUACAGCAGGCGUGGCCAUCCGUAAGACCAUCAGA CUGGAAAGCGAAGUGACCGCCAUAACAACGCCUUGAAG AAGACAAACGAGGCCGUCAGCACACUCGGCAAUGGCGUU AGAGUGCUGGCCACAGCCGUGCGCAGCUGAAGGACUUC GUGUCCAAGAACCUGACACGGGCCAUUAACAAGAACAAG UGCGACAUCGACGACCGUAAGAUGGCCGUGUCCUUUAGC CAGUUAACCGGCGGUUUCUGAACGUCUGCGGCGAUUU AGCGACAACCGCCGGAUUCACACAGCCAUACAGCCUGGAC CUGAUGACAGAUCCUGAGCUGGCUAGAGCCGUGCCUAAC AUGCCUACAUUGCCGGCCAGAUCAAGCUGAUGCUCGAG AAUAGAGCCAUUGGUCGACGGAAGGCUUCGGCAUUCU GAUUGGCGUUAACGGCAGCAGCGUAUCUAUUGGUGC AGCUGCCUAUCUUCGGCGUGAUCGACACACCCUGCUGGA UUGUGAAGGCCGCUCCUAGCUGUAGCGAGAAGAAGGGC AAUUAAGCCUGCCUGCUGAGAGAGGACCAAGGCUUGUA UUGUCAGAACGCCGGCAGCACCGUGUACUACCCUAACGA GAAGGACUGCGAGACAAGAGGCGACACGUGUUCUGUG AUACCGCCGUGGAAUCAUUGUGGCGGAGCAGAGCAAAG AGUGCAACAUCAACAUCAGCACCAACCAUAUCCUGCA AGGUGUCCACCGGCAGGCACCCUAUUUCUAUGGUGGCUC UGUCUCCUCUGGGAGCCUGGUGGCUGUUAUAAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUCAUC AAGCAGCUGAACAGGGCUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACAACACCGUGUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCAGUGAUCAAGGG CAGACCUUGUCCAGCAGCUUCGACCCUAUCAAGUCCC UGAGGAUCAGUUCAGGUGGCCUGGACAGGUGUUCG AGAACAUCCAGAAUCCAGGCUCUGGUGGACAGUCCA ACAGAAUCCUGUCUAGCGCCGAGAAGGGAACACCGGCU UCAUCAUCGUGAUCAUCCUGAUCGCCGUGCUGGGCAGCU CCAUGAUCCUGGUGUCCAUUCUCAUAUAUCAAGAAGA CCAAGAAGCCACCGGCGCUCUCCAGAACUGAGCGGAG UGACCAACAAGGCUUCAUCCUCACAAAC	137

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
	AGAGUGCUGGCCACAGCCGUGCGCGAGCUGAAGGACUUC GUGCUUAAGAACCGUGACACGGGCCAUUAACAAGAACAA GUGCGCAUCGACGACCCUGAAGAUGGCCGUGUCCUUUAG CCAGUUAACCGCGGUGUUCUGAACGUCGUGCGGCAGUU UAGCGACAACGCGGAUACACCCAGCCAUAGCCUGGA CCUGAUGACAGAUGCUGAGCUGGCUAGAGCCGUGCCUAA CAUGCCUACAUCUGCCGGCCAGAUCAAGCUGAUGCUCGA GAAUAGAGCCAUUGGUCCGACGGAAGGCUUCGGCAUUC UGAUUGGCGUGUACGGCAGCAGCGUGAUCUAUAUGGUG CAGCUGCCUAUCUUCGGCGUGAUCGACACACCCUGCUGG AUUGUGAAGGCCGCUCCUAGCUGUAGCGAGAAGAAGGG CAAUUAACGCCUGCCUGCUGAGAGAGGACCAAGGCUGGUA UUGUCAGAACGCGGCAGCACCGUGUACUACCCUAACGA GAAGGACUGCGAGACAAGAGGCGACACGUGUUCUGUG AUACCGCCGUGGAAUCAUUGGGCCGAGCAGAGCAAAG AGUGCAACAUAACAUCAGCACCACCACTUAUCCUGCA AGGUGUCCACCGGCAGGCACCCUAUUUCUAUGGUGGCUC UGUCUCUCUGGGAGCCUGGUGGCUGUUAUAAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUCAUC AAGCAGCUGAACAGGGCUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACAAACCCGUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCAGUGAUCAAGGG CAGACCUUGUGUCAGCAGCUUCGACCCUAUCAAGUCCC UGAGGAUACAGUUCAGGUGGCCUGGACCAAGGUGUUCG AGAACAUCGAGAAUUCACAGGCUCUGGUGGACAGUCCA ACAGAAUCUGUCUAGCGCCGAGAAGGGAAACACCGGCU UCAUCAUCGUGAUCUCCUGAUCGCCGUGCUGGGCAGCU CCAUGAUCUGGUGUCCAUUCUAUCAUAUUAAGAAGA CCAAGAAGCCCACCGGCGUCCUCCAGAACUGAGCGGAG UGACCAACAAGGCUUCAUCCUCACAAAC	
HMPV_SC_SUabilizeAlpha_U174W	AUGAGCUGGAAGGUGGUCAUCAUCUUCAGCCUGCUGAU CACACCUCAGCACGGCCUGAAAGAGAGCUACCCUGGAAGA GUCCUGCAGCACCAUCAACAGAGGGCUACCCUGUCUGUGCU GAGAACCGGCUUGUACACCAACGUGUUCACACUGGAAGU GGGCGACGUCGAGAAUCUGACAUGCUCUGAUGGCCUAG CCUGAUAAGACCGAGCUGGAUCUGACCAAGAGCGCCCU GAGAGAACUCAAGACCGUGUCUGCCGAUCAGCUGGCCAG AGAGGAACAGAUCCGAGAAUCCUGGCAGCGGCAGCUUUG UGCUGGGAGCCAUUGCUUCUGGAGUGGCUGCUGCUGCA GCUGUUAACAGCAGGCUGGCCAUUCGUAAGACCAUCAGA CUGGAAAGCGAAGUGACCGCCAUAACAACGCCCUUGAAG AAGACAAACGAGGCCGUCAGCACACUCGGCAAUGGCGUU AGAGUGCUGGCCACAGCCGUGCGCGAGCUGAAGGACUUC GUGUCCAAGAACCUUGUGCGGGCCAUUAACAAGAACA GUGCGCAUCGACGACCCUGAAGAUGGCCGUGUCCUUUAG CCAGUUAACCGCGGUGUUCUGAACGUCGUGCGGCAGUU UAGCGACAACCGCGGAUACACCCAGCCAUAGCCUGGA CCUGAUGACAGAUGCUGAGCUGGCUAGAGCCGUGCCUAA CAUGCCUACAUCUGCCGGCCAGAUCAAGCUGAUGCUCGA GAAUAGAGCCAUUGGUCCGACGGAAGGCUUCGGCAUUC UGAUUGGCGUGUACGGCAGCAGCGUGAUCUAUAUGGUG CAGCUGCCUAUCUUCGGCGUGAUCGACACCCUGCUGG AUUGUGAAGGCCGCUCCUAGCUGUAGCGAGAAGAAGGG CAAUUAACGCCUGCCUGCUGAGAGAGGACCAAGGCUGGUA UUGUCAGAACGCGGCAGCACCGUGUACUACCCUAACGA GAAGGACUGCGAGACAAGAGGCGACACGUGUUCUGUG AUACCGCCGUGGAAUCAUUGGGCCGAGCAGAGCAAAG AGUGCAACAUAACAUCAGCACCAACCAUAUCCUGCA AGGUGUCCACCGGCAGGCACCCUAUUUCUAUGGUGGCUC UGUCUCUCUGGGAGCCUGGUGGCUGUUAUAAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUCAUC AAGCAGCUGAACAGGGCUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACAAACCGUGUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCAGUGAUCAGGG CAGACCUUGUCCAGCAGCUUCGACCCUAUCAAGUCCC UGAGGAUACAGUUCAGGUGGCCUGGACCAAGGUGUUCG AGAACAUCGAGAAUUCACAGGCUCUGGUGGACCAUCCA ACAGAAUCCUGUCUAGCGCCGAGAAGGGAACACCGGCU UCAUCAUCGUGAUCUCCUGAUCGCCGUGCUGGGCAGCU CCAUGAUCUGGUGUCCAUUCUAUCAUAUUAAGAAGA CCAAGAAGCCCACCGGCGUCCUCCAGAACUGAGCGGAG UGACCAACAAGGCUUCAUCCUCACAAAC	138

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
HMPV_SC_4M_SUabilizeAlpha_V55LU74LS170LU174W	AUGAGCUGGAAGGUGGUCAUCAUCUUCAGCCUGCUGAU CACACCUCAGCACGGCCUGAAAGAGAGCUACCUGGAAGA GUCCUGCAGCACCAUCACAGAGGGCUACCUGUCUGUGCU GAGAACC GGCGUGGUACCAACGUGUUCACACUGGAAGU GGGCGACCU CGAGAAUCUGACAUGCUCUGAUGGCCCUAG CCUGAUCAAGACCGAGCUGGAUCUGCUC AAGAGCGCCCU GAGAGAACUCAAGACCGUGUCGCGAUCAGCUGGCCAG AGAGGAACAGAU CGAGAAUCCUGGCAGCGGCAGCUUUG UGCUGGGAGCCAUGUCUUGGAGUGGCUGCUGCUGCA GCUGUACAGCAGGCGUGGCCAUCGCUAAGACCAUCAGA CUGGAAAGCGAAGUGACCGCCAUCACCAACGCCCUAAG AAGACAAACGAGGCCGUCAGCACACUCGGCAAUGGCGUU AGAGUGCUGGCCACAGCCGUGCGGAGCUGAAGGACUUC GUGCUUAAGAACUGUGGCCGGGCCAUUAACAAGAACAA GUGCGACAUCGACGACCUAGAAGUGGCCGUGUCCUUUAG CCAGUUAACCGGCGGUUUCUGAACGUCGUGCGGCAGUU UAGCGACAACGCGGAAUCACACAGCCAU CAGCCUGGA CCUGAUGACAGAU CUGAGCUGGCUAGAGCCGUGCCUAA CAUGCCUACAUCUGCCGGCCAGAUCAAGCUGAUGCUCGA GAAUAGAGCCAUUGGUCCGACGGAAGGCUUCGGCAUUC UGAUUGGCGUGUACGGCAGCAGCUGAUUAU AUGGUG CAGCUGCCUAUCUUCGGCGUGAUCGACACACCCUGCUGG AUUGUGAAGGCCGUCUCCUAGCUGUAGCGAGAAGAGGG CAAUUAACGCCUGCCUGCUGAGAGAGGACCAAGGCUGGUA UUGUCAGAACGCGGCAGCACCGUGUACUACCUAACGA GAAGGACUGCGAGACAAGAGGCAGCACGUGUUCUGUG AUACCGCCGUGGAAUCAUUGUGGCCGAGCAGAGCAAAG AGUGCAACAUCAACAUCAGCACCAACUAUCCUGCA AGGUGUCCACCGGCAGGCACCCUAUUAUCUAGGUGGCUC UGUCUCCUCUGGGAGCCUGGUGGCUGUUAUAAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUCAUC AAGCAGCUGAAC AAGGCGUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACAACACCGUUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCACGUGAUCAAGGG CAGACCUGUGUCCAGCAGCUUCGACCCUAUCAAGUCCC UGAGGAUCAGUUC CAGGUGGCCUGGAC CAGGUGUUCG AGAACAUCGAGAAUUC CAGGCUCUGGUGGAC CAGUCCA ACAGAAUCUGUCUAGCGCCGAGAAGGGAACACCGGCU UCAUCAUCGUGAUCAUCUGAUCGCGGUGCUGGGCAGCU CCAUGAUCCUGGUGUCCAUCUUAUCAUAUUAAGAAGA CCAAGAAGCCCACCGGCGCUCUCCAGAACUGAGCGGAG UGACCAACA AUGGCUUCAUCCUCACAAAC	139
HMPV_ProlineSUab_E51P	AUGAGCUGGAAGGUGGUCAUCAUCUUCAGCCUGCUGAU CACACCUCAGCACGGCCUGAAAGAGAGCUACCUGGAAGA GUCCUGCAGCACCAUCACAGAGGGCUACCUGUCUGUGCU GAGAACCGGCGUGUACCAACGUGUUCACACUGCCUGU GGGCGACGUCGAGAAUCUGACAUGCUCUGAUGGCCCUAG CCUGAUCAAGACCGAGCUGGAUCUGACCAAGAGCGCCCU GAGAGAACUCAAGACCGUGUCGCGAUCAGCUGGCCAG AGAGGAACAGAU CGAGAAUCCUGGCAGCGGCAGCUUUG UGCUGGGAGCCAUGUCUUGGAGUGGCUGCUGCUGCA GCUGUACAGCAGGCGUGGCCAUCGCUAAGACCAUCAGA CUGGAAAGCGAAGUGACCGCCAUCACCAACGCCCUAAG AAGACAAACGAGGCCGUCAGCACACUCGGCAAUGGCGUU AGAGUGCUGGCCACAGCCGUGCGGAGCUGAAGGACUUC GUGUCCAAGAACCUGACACGGGCCAUUAACAAGAACAAG UGCACAUCGACGACCUGAAGAUGGCCGUGUCCUUUAGC CAGUUCAACCGGCGGUUUCUGAACGUCGUGCGGAGUUU AGCGACAACGCGGAUUCACACAGCCAU CAGCCUGGAC CUGAUGACAGAU CUGAGCUGGCUAGAGCCGUGCCUAAC AUGCCUACAUCUGCCGGCCAGAUCAAGCUGAUGCUCGAG AAUAGAGCCAUUGUCCGACGGAAGGCUUCGGCAUUCU GAUUGGCGUGUACGGCAGCAGCGUAUCUAUAUGGUGC AGCUGCCUAUCUUCGGCGUGAUCGACACACCCUGCUGGA UUUGAAGGCCGCUCCUAGCUGUAGCGAGAAGAAGGGC AAUUAACGCCUGCCUGCUGAGAGAGGACCAAGGCUGGUA UUGUCAGAACGCGGCAGCACCGUGUACUACCUAACGA GAAGGACUGCGAGACAAGAGGCAGCACGUGUUCUGUG AUACCGCCGUGGAAUCAUUGUGGCCGAGCAGAGCAAAG AGUGCAACAUCAACAUCAGCACCAACUAUCCUGCA AGGUGUCCACCGGCAGGCACCCUAUUAUCUAGGUGGCUC UGUCUCCUCUGGGAGCCUGGUGGCUGUUAUAAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUCAUC	140

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
	AAGCAGCUGAACCAAGGGCUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACCAACCCGUGUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCAGCUGAUCAAGGG CAGACCUUGUCCAGCAGCUUCGACCCUAUCAAGUCC UGAGGAUCAGUCCAGGUGGCCUGGACAGGUGUUCG AGAACAUCCGAGAAUCCAGGCUCUGGUGGACAGUCCA ACAGAAUCCUGUCUAGCGCCGAGAAGGGAACACCGGCU UCAUCAUCGUGAUCAUCUGAUCGCCGUGCUGGGCAGCU CCAUGAUCCUGGUGCCAUCUUAUCAUUAUCAAGAAGA CCAAGAAGCCACCGCGCUCUCAGAACUGAGCGGAG UGACCAACAAGGCUUCAUCCUCACAAC	
HMPV_ProlineSUab_D185P	AUGAGCUGGAAGGUGGUCAUCAUUCAGCCUGCUGAU CACACCUCAGCACGGCCUGAAAGAGAGCUACCGUGAAGA GUCCUGCAGCACCAUACAGAGGGCUACCGUCUGUGCU GAGAACCGGCGUGUACACCAACGUGUUCACACUGGAAGU GGCGACGUCGAGAAUCUGACAUGCUCUGAUGGCCUAG CCUGAUCAAGACCGAGCUGGAUCUGACCAAGAGCGCCCU GAGAGAACUCAAGACCGUGUCUGCCGAUCAGCUGGCCAG AGAGGAACAGAUCCGAGAAUCCUGGCAGCGGACGUUUG UGCUGGGAGCCAUGUCUUGGAGUGGCUGCUGUGCA GCUGUACAGCAGGCGUGGCCAUCGCUAAGACCAUCAGA CUGGAAAGCGAAGUGACCGCCAUCACAACGCCCUAGAAG AAGACAAACGAGGCCGUCAGCACACUCGGCAAUGGCGUU AGAGUGCUGGCCACAGCCGUGCGGAGCUGAAGGACUUC GUGUCCAAGAACUGACACGGGCCAUUAACAAGAACAAAG UGCGACAUCGCCUGACUGAAGAUGGCCGUGUCUUUAGC CAGUUCACACGGCGGUUUCUGAACGUCUGCGGCGAGUUU AGCGACAACGCCGGAUACACACAGCCAUCAGCCUGGAC CUGAUGACAGAUCCUGAGCUGGCUAGAGCCGUGCCUAAC AUGCCUACAUCUGCCGCCAGAUCAAGCUGAUGCUCGAG AAUAGAGCCAUUGUCCGACGGAAGGCUUCGGAUUCU GAUUGGCGUGUACGGCAGCAGCGUAUCUAUAGGUGC AGCUGCCUAUCUUCGGCGUGAUCGACACACCCUGCUGGA UUGUGAAGGCCGCUCCUAGCUGUAGCGAGAAGAGGGC AAUUAACGCCUGCCUGCUGAGAGAGGACCAAGGCUUGUA UUGUCAGAACGCCGCGCAGCACCGUGUACUACCUAACGA GAAGGACUGCGAGACAGAGGGCAGCACGUGUUCUGUG AUACCGCCGUGGAUCAUUGUGGCCGAGCAGAGCAAAG AGUGCAACAUCAACUACAGCACCAACCAUCCUGCA AGGUGUCCACCGGCAGGCACCUAUUUCUAUGGUGGCU UGUCUCCUCUGGGAGCCUGGUGGCUUGUUAUAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUCAUC AAGCAGCUGAACAGGGCUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACAAACCCGUGUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCAGUGAUCAAGGG CAGACCUUGUCCAGCAGCUUCGACCCUAUCAAGUCC UGAGGAUCAGUCCAGGUGGCCUGGACAGGUGUUCG AGAACAUCCGAGAAUCCAGGCUCUGGUGGACAGUCCA ACAGAAUCCUGUCUAGCGCCGAGAAGGGAACACCGGCU UCAUCAUCGUGAUCAUCUGAUCGCCGUGCUGGGCAGCU CCAUGAUCCUGGUGCCAUCUUAUCAUUAUCAAGAAGA CCAAGAAGCCACCGCGCUCUCAGAACUGAGCGGAG UGACCAACAAGGCUUCAUCCUCACAAC	141
HMPV_ProlineSUab_D183P	AUGAGCUGGAAGGUGGUCAUCAUUCAGCCUGCUGAU CACACCUCAGCACGGCCUGAAAGAGAGCUACCGUGAAGA GUCCUGCAGCACCAUACAGAGGGCUACCGUCUGUGCU GAGAACCGGCGUGUACACCAACGUGUUCACACUGGAAGU GGCGACGUCGAGAAUCUGACAUGCUCUGAUGGCCUAG CCUGAUCAAGACCGAGCUGGAUCUGACCAAGAGCGCCCU GAGAGAACUCAAGACCGUGUCUGCCGAUCAGCUGGCCAG AGAGGAACAGAUCCGAGAAUCCUGGCAGCGGACGUUUG UGCUGGGAGCCAUGUCUUGGAGUGGCUGCUGUGCA GCUGUACAGCAGGCGUGGCCAUCGCUAAGACCAUCAGA CUGGAAAGCGAAGUGACCGCCAUCACAACGCCCUAGAAG AAGACAAACGAGGCCGUCAGCACACUCGGCAAUGGCGUU AGAGUGCUGGCCACAGCCGUGCGGAGCUGAAGGACUUC GUGUCCAAGAACCUGACACGGGCCAUUAACAAGAACAAG UGCCCUAUCGACGACCUGAAGAUGGCCGUGUCUUUAGC CAGUUCACACGGCGGUUUCUGAACGUCUGCGGCGAGUUU AGCGACAACGCCGGAUACACACAGCCAUCAGCCUGGAC CUGAUGACAGAUCCUGAGCUGGCUAGAGCCGUGCCUAAC AUGCCUACAUCUGCCGCCAGAUCAAGCUGAUGCUCGAG AAUAGAGCCAUUGUCCGACGGAAGGCUUCGGAUUCU GAUUGGCGUGUACGGCAGCAGCGUAUCUAUAGGUGC AGCUGCCUAUCUUCGGCGUGAUCGACACACCCUGCUGGA UUGUGAAGGCCGCUCCUAGCUGUAGCGAGAAGAGGGC AAUUAACGCCUGCCUGCUGAGAGAGGACCAAGGCUUGUA UUGUCAGAACGCCGCGCAGCACCGUGUACUACCUAACGA GAAGGACUGCGAGACAGAGGGCAGCACGUGUUCUGUG AUACCGCCGUGGAUCAUUGUGGCCGAGCAGAGCAAAG AGUGCAACAUCAACUACAGCACCAACCAUCCUGCA AGGUGUCCACCGGCAGGCACCUAUUUCUAUGGUGGCU UGUCUCCUCUGGGAGCCUGGUGGCUUGUUAUAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUCAUC AAGCAGCUGAACAGGGCUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACAAACCCGUGUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCAGUGAUCAAGGG CAGACCUUGUCCAGCAGCUUCGACCCUAUCAAGUCC UGAGGAUCAGUCCAGGUGGCCUGGACAGGUGUUCG AGAACAUCCGAGAAUCCAGGCUCUGGUGGACAGUCCA ACAGAAUCCUGUCUAGCGCCGAGAAGGGAACACCGGCU UCAUCAUCGUGAUCAUCUGAUCGCCGUGCUGGGCAGCU CCAUGAUCCUGGUGCCAUCUUAUCAUUAUCAAGAAGA CCAAGAAGCCACCGCGCUCUCAGAACUGAGCGGAG UGACCAACAAGGCUUCAUCCUCACAAC	142

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
	AAUAGAGCCAUGGUCCGACGGAAAGGCUUCGGCAUUCU GAUUGGCGUGUACGGCAGCAGCGUGAUCUAUAUGGUGC AGCUGCCUAUCUUCGGCGUGAUCGACACACCCUGCUGGA UUGUGAAGGCCCGCUCUAGCUGUAGCGAGAAGAAGGGC AAUUACGCCUGCCUGUGAGAGAGGACCAGGCUGGUA UUGUCAGAACGCCGGCAGCACCGUGUACUACCCUAACGA GAAGGACUGCGAGACAAGAGGCGACCAGUGUUCUGUG AUACCGCCCGUGGAUCAAUGUGGCCGAGCAGAGCAAAG AGUGCAACAUCAACUAGCACCACCAACUAUCCUGCA AGGUGUCCACCGGCAGGCACCCUAUUUCUAUGGUGGCUC UGUCUCUCUGGGAGCCUGGUGGCUGUUUAUAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUACU AAGCAGCUGAACAAAGGCGUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACCAACCCGUGUAUCAG CUGAGCAAGUGGAAGGCGAACAGCAGCUGAUCAAGGG CAGACCUGUUCAGCAGCUUCGACCCUAUCAAGUUCCTC UGAGGAUCAGUUCAGGUGGCCUGGACAGGUGUUCG AGAACAUCCAGAAUCCAGGCUCUGGUGGACAGUCCA ACAGAAUCUGUCUAGCGCCGAGAAGGGAACACCGGCU UCAUCAUCGUGAUCUCCUGAUCGCCGUGCUGGGCAGCU CCAUGAUCUGGUGUCCAUCUUAUCAUUAUCAAGAAGA CCAAGAAGCCACCGCGCUCUCCAGAACUGAGCGGAG UGACCAACAAGGCUUCAUCCUCCACAAC	
HMPV_ProlineSUab_E131P	AUGAGCUGGAAGGUGGUCAUCAUCUUCAGCCUGCUGAU CACACCUCAGCACGGCCUGAAAGAGAGCUACCCUGGAAGA GUCCUGCAGCACCAUCACAGAGGGCUACCGUCUGUGCU GAGAACC GGCGUGGUACACCAACGUGUUCACACUGGAAGU GGCGACCGUCGAGAAUCUGACAUUCUGAUGGCCUAG CCUGAUCAAGACCGAGCUGGAUCUGACCAAGAGCGCCCU GAGAGAACUCAAGACCGUGUCUGCCGAUCAGCUGGCCAG AGAGGAACAGAUUCGAGAAUCCUGGCAGCGGCAGCUUUG UGCUGGGAGCCAUGUCUUCUGGAGUGGCUGCUGUGCA GCUGUUAACAGCAGGCGUGGCCAUCCGCUAAGACCAUCAGA CUGCCUAGCGAAGUGACCGCCAUCAACAACGCCUUGAAG AAGACAAACGAGGCCUGCAGCACACUCGGCAAUGGCGUU AGAGUGCUGGCCACAGCCGUGCGCAGCUGAAGGACUUC GUGUCCAAGAACUGACACGGGCCAUUAACAAGAAACAG UGCGACAUCGACGACUGAAGAUGGCCGUGUCUUUAGC CAGUUCAACCGCGGUUUCUGAACGUCUGCGCGAGUUU AGCGACAACGCCGGAUUCACACAGCCAUCAAGCCUGGAC CUGAUGACAGAUCUGAGCUGGCUAGAGCCGUGCCUAAC AUGCCUACAUCUGCCGGCCAGAUAAGCUGAUGCUCGAG AAUAGAGC CAUGGUCGACGGAAGGCUUCGGCAUUCU GAUUGGCGUGUACGGCAGCAGCGUGAUCUAUAUGGUGC AGCUGCCUAUCUUCGGCGUGAUCGACACACCCUGCUGGA UUGUGAAGGCCCGCUCUAGCUGUAGCGAGAAGAAGGGC AAUUACGCCUGCCUGUGAGAGAGGACCAGGCUGGUA UUGUCAGAACGCCGGCAGCACCGUGUACUACCCUAACGA GAAGGACUGCGAGACAAGAGGCGACCAGUGUUCUGUG AUACCGCCCGUGAAUCAUUGUGGCCGAGCAGAGCAAAG AGUGCAACAUCAACAUCAGCACCACCAACUAUCCUGCA AGGUGUCCACCGGCAGGCACCCUAUUUCUAUGGUGGCUC UGUCUCCUCUGGGAGCCUGGUGGCUGUUUAUAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUCAUC AAGCAGCUGAACAAAGGCGUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACAAACCCGUGUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCAGUGAUCAAGGG CAGACCUGUGUCCAGCAGCUUCGACCCUAUCAAGUUCCTC UGAGGAUCAGUUCAGGUGGCCUGGACAGGUGUUCG AGAACAUCCAGAAUCCAGGCUCUGGUGGACAGUCCA ACAGAAUCUGUCUAGCGCCGAGAAGGGAACACCGGCU UCAUCAUCGUGAUCUCCUGAUCGCCGUGCUGGGCAGCU CCAUGAUCUGGUGUCCAUCUUAUCAUUAUCAAGAAGA CCAAGAAGCCACCGCGCUCUCCAGAACUGAGCGGAG UGACCAACAAGGCUUCAUCCUCCACAAC	143
HMPV_ProlineSUab_D447P	AUGAGCUGGAAGGUGGUCAUCAUCUUCAGCCUGCUGAU CACACCUCAGCACGGCCUGAAAGAGAGCUACCCUGGAAGA GUCCUGCAGCACCAUCACAGAGGGCUACCGUCUGUGCU GAGAACC GGCGUGGUACACCAACGUGUUCACACUGGAAGU GGCGACCGUCGAGAAUCUGACAUUCUGAUGGCCUAG CCUGAUCAAGACCGAGCUGGAUCUGACCAAGAGCGCCCU GAGAGAACUCAAGACCGUGUCUGCCGAUCAGCUGGCCAG AGAGGAACAGAUUCGAGAAUCCUGGCAGCGGCAGCUUUG UGCUGGGAGCCAUGUCUUCUGGAGUGGCUGCUGUGCA GCUGUUAACAGCAGGCGUGGCCAUCCGCUAAGACCAUCAGA CUGCCUAGCGAAGUGACCGCCAUCAACAACGCCUUGAAG AAGACAAACGAGGCCUGCAGCACACUCGGCAAUGGCGUU AGAGUGCUGGCCACAGCCGUGCGCAGCUGAAGGACUUC GUGUCCAAGAACUGACACGGGCCAUUAACAAGAAACAG UGCGACAUCGACGACUGAAGAUGGCCGUGUCUUUAGC CAGUUCAACCGCGGUUUCUGAACGUCUGCGCGAGUUU AGCGACAACGCCGGAUUCACACAGCCAUCAAGCCUGGAC CUGAUGACAGAUCUGAGCUGGCUAGAGCCGUGCCUAAC AUGCCUACAUCUGCCGGCCAGAUAAGCUGAUGCUCGAG AAUAGAGC CAUGGUCGACGGAAGGCUUCGGCAUUCU GAUUGGCGUGUACGGCAGCAGCGUGAUCUAUAUGGUGC AGCUGCCUAUCUUCGGCGUGAUCGACACACCCUGCUGGA UUGUGAAGGCCCGCUCUAGCUGUAGCGAGAAGAAGGGC AAUUACGCCUGCCUGUGAGAGAGGACCAGGCUGGUA UUGUCAGAACGCCGGCAGCACCGUGUACUACCCUAACGA GAAGGACUGCGAGACAAGAGGCGACCAGUGUUCUGUG AUACCGCCCGUGAAUCAUUGUGGCCGAGCAGAGCAAAG AGUGCAACAUCAACAUCAGCACCACCAACUAUCCUGCA AGGUGUCCACCGGCAGGCACCCUAUUUCUAUGGUGGCUC UGUCUCCUCUGGGAGCCUGGUGGCUGUUUAUAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUCAUC AAGCAGCUGAACAAAGGCGUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACAAACCCGUGUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCAGUGAUCAAGGG CAGACCUGUGUCCAGCAGCUUCGACCCUAUCAAGUUCCTC UGAGGAUCAGUUCAGGUGGCCUGGACAGGUGUUCG AGAACAUCCAGAAUCCAGGCUCUGGUGGACAGUCCA ACAGAAUCUGUCUAGCGCCGAGAAGGGAACACCGGCU UCAUCAUCGUGAUCUCCUGAUCGCCGUGCUGGGCAGCU CCAUGAUCUGGUGUCCAUCUUAUCAUUAUCAAGAAGA CCAAGAAGCCACCGCGCUCUCCAGAACUGAGCGGAG UGACCAACAAGGCUUCAUCCUCCACAAC	144

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
	AGAGGAACAGAU CGAGAAUCCUGGCAGCGGCAGCUUUG UGCUGGAGCCAUUGUCUUGGAGUGGCUGCUGUGCA GCUGUUACAGCAGGCGUGGCCAUUCGUAAGACCAUCAGA CUGGAAAGCGAAGUGACCGCCAUAACAACGCCUGAAG AAGACAAACGAGGCCGUCAGCACUCGCGCAUUGCGUU AGAGUGCUGGCCACAGCCGUGCGCGAGCUGAAGGACUUC GUGUCCAAGAACCUGACACGGGCCAUUAACAAGACAAG UGCGACAU CGACACCU GAAGAUGGCCGUGUCUUUAGC CAGUUC AACCGGCGUUUCUGAACGUCGUGCGCAGUUU AGCGACAACGCGGAUACACACAGCAUCAGCCUGGAC CUGAUGACAGAU CGUGAGCUGGCUAGAGCCGUGCCU AAC AUGCCUACAUCUGCCGGCCAGAUCAAGCUGAUGCUCGAG AAUAGAGCCAUUGGUCCGACGGAAGGCCUUCGGCAUUCU GAUUGGCGUGUACGGCAGCAGCGUGAUCUAUUGGUGC AGCUGCCUAUCUUCGGCGUGAUCGACACACCCUGCUGGA UUUGAAGGCCCGUCCUAGCUGUAGCGAGAAGAGGGC AAUUACGCCUGCCUGUGAGAGAGGACCAGGCUUGUA UUUGCAGAACGCCGGCAGCACCGUGUACUACCUAACGA GAAGGACUGCGAGACAAGAGGCGACCGUGUUCUGUG AUACCGCCCGUGGAUCAAUGUGGCCGAGCAGAGCAAAG AGUGCAACAUAACAUCAGCACCAACUAUCCUGCA AGGUGUCCACCGGCAGGCACCUAUUUUAUGGUGGCUC UGUCUCUCUGGAGGCCUGGUGGCUUGUUUAAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUAC AAGCAGCUGAACAGGGCUGCAGCUACAUCACCAACAG GACGCCGAUACCGUGACCAUCGACAACCCGUGUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCACGUGAUCAGGG CAGACCUUGUCCAGCAGCUUCCACCUACAAGUUC UGAGGAUCAGUCCAGGUGGCCUGGACAGGUGUUCG AGAACAU CGAGAAUCCAGGCUUGGUGGACAGUCCA ACAGAAUCUGUCUAGCGCCGAGAAGGGAACACCGGCU UCAUCAUCGUGAUCUCCUGAUCGCGUGUGGCGAGCU CCAUGAUCUGGUGUCCAUUUCAUCAUAACAAGAAGA CCAAGAAGCCACCGGCGUCCUCCAGAACUGAGCGGAG UGACCAACAAGGCUUCAUCCUCACAAC	
HMPV_UrimerRepulsionD454N	AUGAGCUGGAAGGUGGUAUCAUCUUCAGCCUGCUGAU CACACCUCAGCAGCGCCUGAAAAGAGAGCUACCGUGAAGA GUCCUGCAGCACCAUCACAGAGGGCUACCGUCUGUGCU GAGAACC GGCGUGUACACCAACGUGUUCACACUGGAAGU GGGCGACGUCGAGAAUCUGACAUGCUCUGAUGGCCUAG CCUGAUCAAGACCGAGCUGGAUCUGACCAAGAGCGCCCU GAGAGAACUCAAGACCGUGUCUGCCGAUCAGCUGGCCAG AGAGGAACAGAU CGAGAAUCCUGGCAGCGGCAGCUUUG UGCUGGGAGCCAUUGUCUUGGAGUGGCUGCUGUGCA GCUGUACAGCAGGCGUGGCCAUUCGCUAAGACCAUCAGA CUGGAAAGCGAAGUGACCGCCAUAACAACGCCUGAAG AAGACAAACGAGGCCGUCAGCACUCGCGCAUUGCGUU AGAGUGCUGGCCACAGCCGUGCGGAGCUGAAGGACUUC GUGUCCAAGAACUGACACGGGCCAUUAACAAGACAAG UGCGACAUCGACGACUGAAGAUGGCCGUGUCUUUAGC CAGUUCAACCGGCGUUUCUGAACGUCGUGCGCAGUUU AGCGACAACGCGGAUACACACAGCCAUCAGCCUGGAC CUGAUGACAGAU CGUGAGCUGGCUAGAGCCGUGCCU AAC AUGCCUACAUCUGCCGGCCAGAUCAAGCUGAUGCUCGAG AAUAGAGCCAUUGGUCCGACGGAAGGCCUUCGGCAUUCU GAUUGGCGUGUACGGCAGCAGCGUGAUCUAUUGGUGC AGCUGCCUAUCUUCGGCGUGAUCGACACACCCUGCUGGA UUUGAAGGCCCGUCCUAGCUGUAGCGAGAAGAGGGC AAUUACGCCUGCCUGUGAGAGAGGACCAGGCUUGUA UUUGCAGAACGCCGGCAGCACCGUGUACUACCUAACGA GAAGGACUGCGAGACAAGAGGCGACCAAGUGUUCUGUG AUACCGCCCGUGAAUCAUUGUGGCCGAGCAGAGCAAAG AGUGCAACAUAACAUCAGCACCAACUAUCCUGCA AGGUGUCCACCGGCAGGCACCUAUUUUAUGGUGGCUC UGUCUCUCUGGAGGCCUGGUGGCUUGUUUAAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUCAUC AAGCAGCUGAACAGGGCUGCAGCUACAUCACCAACAG GACGCCGAUACCGUGACCAUCGACAACCCGUGUAUCAG CUGAGCAAGGUGGAAGGCGAACAGCACGUGAUCAGGG CAGACCUUGUCCAGCAGCUUCGACCCUAUCAAGUUC UGAGAACCAGUUC CAGGUGGCCUGGAC CAGGUGUUCGA GAACAUCGAGAAUCCAGGCUUGGUGGAC CAGUCCAA CAGAAUCCUGUCUAGCGCCGAGAAGGGAACACCGGCU	145

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
	CAUCAUCGUGAUCAUCCUGAUCGCGUGCUGGGCAGCUC CAUGAUCCUGGUGUCCAUCUUAUCAUUAUCAAGAAGAC CAAGAAGCCACCGGCGUCUCCUCCAGAACUGAGCGGAGU GACCAACAUGGCUUCAUCCUCACAAAC	
HMPV_UrimerRepulsionE453N	AUGAGCUGGAAGGUGGUCAUCAUCUUCAGCCUGCUGAU CACACCUCAGCACGGCCUGAAAGAGAGCUACCUGGAAGA GUCCUGCAGCACCAUCACAGAGGGCUACUGUCUGUGCU GAGAACC GGUGUACCAACGUGUUCACACUGGAAGU GGGCGACGUCGAGAAUCUGACAUGCUCUGAUGGCCUAG CCUGAUCAAGACCGAGCUGGAUCUGACCAAGAGCGCCU GAGAGAACUCAAGACCGUGUCUGCGAUCAGCUGGCCAG AGAGGAACAGAUCAAGAAUCCUGGACGCGGACGCUUUG UGCUGGGAGCCAUUGCUCUUGGAGUGGCGUCGUCUGCA GCUGUACAGCAGGCGUGGCCAUUCGUAAGACCAUCAGA CUGGAAGCGAAGUGACCGCCAUCAACAACGCCCUAGAAG AAGACAAACGAGGCCGUCAGCACACUCGGCAAUGGCGUU AGAGUGCUGGCCACAGCCGUGCGGAGCUGAAGGACUUC GUGUCCAAGAACCUGACACGGGCCAUUAAACAAGACAAG UGCGACAUCGACGACUGAAGAUGGCCGUGUCUUUAGC CAGUUCACCGGCGUUUCUGAACGUCGUGCGGAGUUU AGCGACAACGCGGAUACACACGACCAUCAGCCUGGAC CUGAUGACAGAUUGCUGAGCUGGCUAGAGCCGUGCCUAC AUGCCUACAUCUGCCGGCCAGAUCAGCUGAUGCUCGAG AAUAGAGCCAUUGGUCCGACGGAAGGCUUCGGCAUUCU GAUUGGCGUGUACGGCAGCAGCGUGAUCUAUUGGUGC AGCUGCCUAUCUUCGGCGUGAUCGACACACCCUGCUGGA UUUGAAGGCCGCUCCUAGCUGUAGCGAGAAGAAGGC AAUUAAGCCUGCCUGUGAGAGAGGACCAAGGCUUGUA UUUGCAGAACGCCGGCAGCACCGUGUACUACCUAACGA GAAGGACUGCGAGACAGAGGCGACCAAGUUCUGUG AUACCGCCCGUGGAUUCUAUGUGGCCGAGCAGAGCAAAG AGUGCAACAUCACAUCAGCACCAACUUAUCCUGCA AGGUGUCCACCGGCGAGCACCUUAUUUCUAUGGUGGUC UGUCUCUCUGGGAGCCUGGUGGCUUGUUAUAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUAC AAGCAGCUGAACAGGGCUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACAACCCGUGUAUCAG CUGAGCAAGUGGAAGGCGAACAGCAGCUGAUCAGGG CAGACCUGUGUCCAGCAGCUUCGACCUUAUCAAAGUCC UCAGGAUCAGUUCAGGUGGCCUGGACCAAGGUGUUCGA GAACAUCGAGAAUUCAGGCUUCUGGUGGACAGUCCAA CAGAAUCCUGUCUAGCGCCGAGAAGGGAACAACCGGCU CAUCAUCGUGAUCAUCCUGAUCGCGUGCUGGGCAGCUC CAUGAUCCUGGUGUCAUCUUAUCAUUAUCAAGAAGAC CAAGAAGCCACCGGCGUCUCCAGAACUGAGCGGAGU GACCAACAUGGCUUCAUCCUCACAAAC	146
HMPV_SUabilizeAlphaF196W	AUGAGCUGGAAGGUGGUCAUCAUCUUCAGCCUGCUGAU CACACCUCAGCACGGCCUGAAAGAGAGCUACCUGGAAGA GUCCUGCAGCACCAUCACAGAGGGCUACUGUCUGUGCU GAGAACC GGUGUACCAACGUGUUCACACUGGAAGU GGGCGACGUCGAGAAUCUGACAUGCUCUGAUGGCCUAG CCUGAUCAAGACCGAGCUGGAUCUGACCAAGAGCGCCU GAGAGAACUCAAGACCGUGUCUGCGAUCAGCUGGCCAG AGAGGAACAGAUCAAGAAUCCUGGACGCGGACGCUUUG UGCUGGGAGCCAUUGCUCUUGGAGUGGCGUCGUCUGCA GCUGUACAGCAGGCGUGGCCAUUCGUAAGACCAUCAGA CUGGAAGCGAAGUGACCGCCAUCAACAACGCCCUAGAAG AAGACAAACGAGGCCGUCAGCACACUCGGCAAUGGCGUU AGAGUGCUGGCCACAGCCGUGCGGAGCUGAAGGACUUC GUGUCCAAGAACCUGACACGGGCCAUUAAACAAGACAAG UGCGACAUCGACGACUGAAGAUGGCCGUGUCUUUAGC CAGUGGAACCGGCGUUUCUGAACGUCGUGCGGAGUU UAGCGACAACGCCGGAUACACACGACCAUCAGCCUGGA CCUGAUGACAGAUUGCUGAGCUGGCUAGAGCCGUGCCUAA CAUGCCUAUCAUCGCGGCCAGAUCAAGCUGAUGCUCGA GAAUAGAGCCAUUGGUCCGACGGAAGGCUUCGGCAUUC UGAUUGGCGUGUACGGCAGCAGCUGAUCUAUUGGUG CAGCUGCCUAUCUUCGGCGUGAUCGACACACCCUGCUG AUUGUGAAGGCCGUCUCCUAGCUGUAGCGAGAAGAAGG CAAUUAACGCCUGCCUGCUGAGAGAGGACCAAGGCUUGUA UUUGCAGAACCGGCGAGCACCGUGAUCUACCUAACGA GAAGGACUGCGAGACAAGAGGCGACCAAGUUCUGUG	147

TABLE 19-continued

Strain	Nucleic Acid Sequence	SEQ ID NO:
	AUACCGCCGCGUGGAAUCAUUGGGCCGAGCAGAGCAAAG AGUGCAACAUCAACAGCACCAACUAUCCUGCA AGGUGUCCACCGCAGGCACCCUAUUUCUAUGGUGGCUC UGUCUCUCUGGGAGCCUGGUGGCUUGUUAUAGGGC GUGUCCUGUAGCAUCGGCAGCAACAGAGUGGGCAUCAUC AAGCAGCUGAACAGGGCUGCAGCUACAUCACCAACCAG GACGCCGAUACCGUGACCAUCGACAACCCGUGUAUCAG CUGAGCAAGGUGGAAGGCGAACGACGUGAUCAGGG CAGACCUUGUCCAGCAGCUUCGACCCUAUCAAGUUC UGAGGAUCAGUUCAGGUGGCCUGGACAGGUGUUCG AGAACAUCGAGAAUUCAGGCUCUGGUGGACAGUCCA ACAGAAUCCUGUCUAGCGCCGAGAAGGGAACACCGGCU UCAUCAUCGUGAUCUCCUGAUCGCCGUGCUGGGCAGCU CCAUGAUCUGGUGUCCAUUCUACAUAUUAUCAAGAAGA CCAAGAAGCCACCGGCGCUCUCCAGAACUGAGCGGAG UGACCAACAAGGCUUCAUCCUCACAAAC	

Equivalents

[0931] Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the disclosure

described herein. Such equivalents are intended to be encompassed by the following claims.

[0932] All references, including patent documents, disclosed herein are incorporated by reference in their entirety.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 147

<210> SEQ ID NO 1

<211> LENGTH: 1620

<212> TYPE: DNA

<213> ORGANISM: Human metapneumovirus

<400> SEQUENCE: 1

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ctgaagaccg tgtccgccga ccagctggcc agagaggaac agatcgagaa ccctcggcag      300
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cccaacgaga aggactgcga gaccagaggc gaccacgtgt tctgcgacac cgctgccgga      1020
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<212> TYPE: DNA

<213> ORGANISM: Human metapneumovirus

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actgatggac ctgacttaac caaacagaa cttgatctaa caaaaagtc ttaaggga	240
ctcaaacag tctctgtga tcagttggcg agagaggagc aaattgaaaa tcccagacaa	300
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gatcaagtct tcgaaagcat tgagaacagt caggcactag tggaccagtc aaacaaaatt	1440
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<210> SEQ ID NO 3

<211> LENGTH: 1620

<212> TYPE: DNA

<213> ORGANISM: Human metapneumovirus

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<210> SEQ ID NO 4

<211> LENGTH: 1725

<212> TYPE: DNA

<213> ORGANISM: Human respiratory syncytial virus

<400> SEQUENCE: 4

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<210> SEQ ID NO 5
<211> LENGTH: 539
<212> TYPE: PRT
<213> ORGANISM: Human metapneumovirus isolate

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<400> SEQUENCE: 5

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                20           25          30

Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
                35           40          45

Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
50           55          60

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Ala	Ala	Ala	Ala	Ala	Val	Thr	Ala	Gly	Val	Ala	Ile	Ala	Lys	Thr	Ile	115	120	125	
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Phe	Ser	Gln	Phe	Asn	Arg	Arg	Phe	Leu	Asn	Val	Val	Arg	Gln	Phe	Ser	195	200	205	
Asp	Asn	Ala	Gly	Ile	Thr	Pro	Ala	Ile	Ser	Leu	Asp	Leu	Met	Thr	Asp	210	215	220	
Ala	Glu	Leu	Ala	Arg	Ala	Val	Pro	Asn	Met	Pro	Thr	Ser	Ala	Gly	Gln	225	230	235	240
Ile	Lys	Leu	Met	Leu	Glu	Asn	Arg	Ala	Met	Val	Arg	Arg	Lys	Gly	Phe	245	250	255	
Gly	Ile	Leu	Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln	260	265	270	
Leu	Pro	Ile	Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Val	Lys	Ala	275	280	285	
Ala	Pro	Ser	Cys	Ser	Glu	Lys	Lys	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg	290	295	300	
Glu	Asp	Gln	Gly	Trp	Tyr	Cys	Gln	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr	305	310	315	320
Pro	Asn	Glu	Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp	325	330	335	
Thr	Ala	Ala	Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Lys	Glu	Cys	Asn	Ile	340	345	350	
Asn	Ile	Ser	Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His	355	360	365	
Pro	Ile	Ser	Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys	370	375	380	
Tyr	Lys	Gly	Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile	385	390	395	400
Lys	Gln	Leu	Asn	Lys	Gly	Cys	Ser	Tyr	Ile	Thr	Asn	Gln	Asp	Ala	Asp	405	410	415	
Thr	Val	Thr	Ile	Asp	Asn	Thr	Val	Tyr	Gln	Leu	Ser	Lys	Val	Glu	Gly	420	425	430	
Glu	Gln	His	Val	Ile	Lys	Gly	Arg	Pro	Val	Ser	Ser	Ser	Phe	Asp	Pro	435	440	445	
Ile	Lys	Phe	Pro	Glu	Asp	Gln	Phe	Asn	Val	Ala	Leu	Asp	Gln	Val	Phe	450	455	460	

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Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
 465 470 475 480
 Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
 485 490 495
 Leu Ile Ala Val Leu Gly Ser Ser Met Ile Leu Val Ser Ile Phe Ile
 500 505 510
 Ile Ile Lys Lys Thr Lys Lys Pro Thr Gly Ala Pro Pro Glu Leu Ser
 515 520 525
 Gly Val Thr Asn Asn Gly Phe Ile Pro His Asn
 530 535

<210> SEQ ID NO 6
 <211> LENGTH: 539
 <212> TYPE: PRT
 <213> ORGANISM: Human metapneumovirus

<400> SEQUENCE: 6

Met Ser Trp Lys Val Met Ile Ile Ile Ser Leu Leu Ile Thr Pro Gln
 1 5 10 15
 His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
 20 25 30
 Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
 35 40 45
 Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Thr Asp Gly Pro
 50 55 60
 Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
 65 70 75 80
 Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
 85 90 95
 Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
 100 105 110
 Ala Thr Ala Ala Ala Val Thr Ala Gly Ile Ala Ile Ala Lys Thr Ile
 115 120 125
 Arg Leu Glu Ser Glu Val Asn Ala Ile Lys Gly Ala Leu Lys Gln Thr
 130 135 140
 Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
 145 150 155 160
 Ala Val Arg Glu Leu Lys Glu Phe Val Ser Lys Asn Leu Thr Ser Ala
 165 170 175
 Ile Asn Arg Asn Lys Cys Asp Ile Ala Asp Leu Lys Met Ala Val Ser
 180 185 190
 Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
 195 200 205
 Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
 210 215 220
 Ala Glu Leu Ala Arg Ala Val Ser Tyr Met Pro Thr Ser Ala Gly Gln
 225 230 235 240
 Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
 245 250 255
 Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
 260 265 270
 Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala
 275 280 285

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Ala	Pro	Ser	Cys	Ser	Glu	Lys	Asn	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg
290						295					300				
Glu	Asp	Gln	Gly	Trp	Tyr	Cys	Lys	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr
305					310					315					320
Pro	Asn	Glu	Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp
			325						330					335	
Thr	Ala	Ala	Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Arg	Glu	Cys	Asn	Ile
			340					345					350		
Asn	Ile	Ser	Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His
	355					360						365			
Pro	Ile	Ser	Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys
370						375				380					
Tyr	Lys	Gly	Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Trp	Val	Gly	Ile	Ile
385					390					395					400
Lys	Gln	Leu	Pro	Lys	Gly	Cys	Ser	Tyr	Ile	Thr	Asn	Gln	Asp	Ala	Asp
				405					410					415	
Thr	Val	Thr	Ile	Asp	Asn	Thr	Val	Tyr	Gln	Leu	Ser	Lys	Val	Glu	Gly
			420					425					430		
Glu	Gln	His	Val	Ile	Lys	Gly	Arg	Pro	Val	Ser	Ser	Ser	Phe	Asp	Pro
			435				440						445		
Ile	Lys	Phe	Pro	Glu	Asp	Gln	Phe	Asn	Val	Ala	Leu	Asp	Gln	Val	Phe
450					455					460					
Glu	Ser	Ile	Glu	Asn	Ser	Gln	Ala	Leu	Val	Asp	Gln	Ser	Asn	Lys	Ile
465					470					475					480
Leu	Asn	Ser	Ala	Glu	Lys	Gly	Asn	Thr	Gly	Phe	Ile	Ile	Val	Val	Ile
				485					490					495	
Leu	Val	Ala	Val	Leu	Gly	Leu	Thr	Met	Ile	Ser	Val	Ser	Ile	Ile	Ile
			500					505					510		
Ile	Ile	Lys	Lys	Thr	Arg	Lys	Pro	Thr	Gly	Ala	Pro	Pro	Glu	Leu	Asn
		515				520						525			
Gly	Val	Thr	Asn	Gly	Gly	Phe	Ile	Pro	His	Ser					
530					535										

<210> SEQ ID NO 7

<211> LENGTH: 539

<212> TYPE: PRT

<213> ORGANISM: Human metapneumovirus

<400> SEQUENCE: 7

Met	Ser	Trp	Lys	Val	Met	Ile	Ile	Ile	Ser	Leu	Leu	Ile	Thr	Pro	Gln
1			5						10				15		
His	Gly	Leu	Lys	Glu	Ser	Tyr	Leu	Glu	Glu	Ser	Cys	Ser	Thr	Ile	Thr
		20					25					30			
Glu	Gly	Tyr	Leu	Ser	Val	Leu	Arg	Thr	Gly	Trp	Tyr	Thr	Asn	Val	Phe
		35					40					45			
Thr	Leu	Glu	Val	Gly	Asp	Val	Glu	Asn	Leu	Thr	Cys	Thr	Asp	Gly	Pro
	50				55						60				
Ser	Leu	Ile	Lys	Thr	Glu	Leu	Asp	Leu	Thr	Lys	Ser	Ala	Leu	Arg	Glu
65				70					75				80		
Leu	Lys	Thr	Val	Ser	Ala	Asp	Gln	Leu	Ala	Arg	Glu	Glu	Gln	Ile	Glu
			85					90					95		
Asn	Pro	Arg	Gln	Ser	Arg	Phe	Val	Leu	Gly	Ala	Ile	Ala	Leu	Gly	Val

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100							105					110				
Ala	Thr	Ala	Ala	Ala	Val	Thr	Ala	Gly	Ile	Ala	Ile	Ala	Lys	Thr	Ile	
		115					120					125				
Arg	Leu	Glu	Ser	Glu	Val	Asn	Ala	Ile	Lys	Gly	Ala	Leu	Lys	Thr	Thr	
	130					135					140					
Asn	Glu	Ala	Val	Ser	Thr	Leu	Gly	Asn	Gly	Val	Arg	Val	Leu	Ala	Thr	
145					150					155					160	
Ala	Val	Arg	Glu	Leu	Lys	Glu	Phe	Val	Ser	Lys	Asn	Leu	Thr	Ser	Ala	
				165						170					175	
Ile	Asn	Lys	Asn	Lys	Cys	Asp	Ile	Ala	Asp	Leu	Lys	Met	Ala	Val	Ser	
			180					185					190			
Phe	Ser	Gln	Phe	Asn	Arg	Arg	Phe	Leu	Asn	Val	Val	Arg	Gln	Phe	Ser	
		195					200					205				
Asp	Asn	Ala	Gly	Ile	Thr	Pro	Ala	Ile	Ser	Leu	Asp	Leu	Met	Asn	Asp	
	210					215					220					
Ala	Glu	Leu	Ala	Arg	Ala	Val	Ser	Tyr	Met	Pro	Thr	Ser	Ala	Gly	Gln	
225					230					235					240	
Ile	Lys	Leu	Met	Leu	Glu	Asn	Arg	Ala	Met	Val	Arg	Arg	Lys	Gly	Phe	
				245					250					255		
Gly	Ile	Leu	Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln	
		260						265					270			
Leu	Pro	Ile	Phe	Gly	Val	Ile	Asn	Thr	Pro	Cys	Trp	Ile	Ile	Lys	Ala	
		275						280					285			
Ala	Pro	Ser	Cys	Ser	Glu	Lys	Asp	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg	
	290					295					300					
Glu	Asp	Gln	Gly	Trp	Tyr	Cys	Lys	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr	
305					310					315					320	
Pro	Asn	Glu	Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp	
			325						330					335		
Thr	Ala	Ala	Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Arg	Glu	Cys	Asn	Ile	
			340						345				350			
Asn	Ile	Ser	Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His	
		355					360					365				
Pro	Ile	Ser	Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys	
	370					375					380					
Tyr	Lys	Gly	Val	Ser	Cys	Ser	Thr	Gly	Ser	Asn	Gln	Val	Gly	Ile	Ile	
385					390					395					400	
Lys	Gln	Leu	Pro	Lys	Gly	Cys	Ser	Tyr	Ile	Thr	Asn	Gln	Asp	Ala	Asp	
			405						410					415		
Thr	Val	Thr	Ile	Asp	Asn	Thr	Val	Tyr	Gln	Leu	Ser	Lys	Val	Glu	Gly	
			420					425					430			
Glu	Gln	His	Val	Ile	Lys	Gly	Arg	Pro	Val	Ser	Ser	Ser	Phe	Asp	Pro	
			435				440					445				
Ile	Arg	Phe	Pro	Glu	Asp	Gln	Phe	Asn	Val	Ala	Leu	Asp	Gln	Val	Phe	
	450					455					460					
Glu	Ser	Ile	Glu	Asn	Ser	Gln	Ala	Leu	Val	Asp	Gln	Ser	Asn	Lys	Ile	
465					470					475					480	
Leu	Asn	Ser	Ala	Glu	Lys	Gly	Asn	Thr	Gly	Phe	Ile	Ile	Val	Ile	Ile	
				485					490					495		
Leu	Ile	Ala	Val	Leu	Gly	Leu	Thr	Met	Ile	Ser	Val	Ser	Ile	Ile	Ile	
			500					505					510			

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Ile Ile Lys Lys Thr Arg Lys Pro Thr Gly Ala Pro Pro Glu Leu Asn
 515 520 525

Gly Val Thr Asn Gly Gly Phe Ile Pro His Ser
 530 535

<210> SEQ ID NO 8

<211> LENGTH: 574

<212> TYPE: PRT

<213> ORGANISM: Human respiratory syncytial virus

<400> SEQUENCE: 8

Met Glu Leu Pro Ile Leu Lys Thr Asn Ala Ile Thr Thr Ile Leu Ala
 1 5 10 15

Ala Val Thr Leu Cys Phe Ala Ser Ser Gln Asn Ile Thr Glu Glu Phe
 20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
 35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
 50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
 65 70 75 80

Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
 85 90 95

Met Gln Ser Thr Pro Ala Ala Asn Asn Arg Ala Arg Arg Glu Leu Pro
 100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Thr Lys Asn Thr Asn Val Thr
 115 120 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
 130 135 140

Gly Ser Ala Ile Ala Ser Gly Ile Ala Val Ser Lys Val Leu His Leu
 145 150 155 160

Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys
 165 170 175

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val
 180 185 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Val Asn
 195 200 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
 210 215 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
 225 230 235 240

Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu
 245 250 255

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
 260 265 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
 275 280 285

Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
 290 295 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
 305 310 315 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg

[illegible]

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<210> SEQ ID NO 9
<211> LENGTH: 1617
<212> TYPE: DNA
<213> ORGANISM: Human parainfluenza virus 3
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<400> SEQUENCE: 9

atgccaat	tt caatactgtt	aattattaca	accatgatca	tggcatcaca	ctgccaaata	60
gacatcaca	aactacagca	tgtagggtga	ttggtcaaca	gtcccaaagg	gatgaagata	120
tcacaaaact	tcgaaacaag	atatctaata	ctgagttctca	tacaaaaaat	agaagattct	180
aactcttg	gtgaccaaca	gatcaagcaa	tacaagagg	tattggatag	actgatcatt	240
cctttatat	gtgactaag	attacagaag	gatgtgatag	tgactaatca	agaatccaat	300
gaaaaactg	atcccagaac	agaacgattc	tttggagggg	taattggaac	tattgtctca	360
ggagtagcaa	cctcagcaca	aattacagca	gcagttgctc	tggttgaagc	caagcaggca	420
agatcagaca	ttgaaaaact	caaggaagca	atcagggaca	caaataaagc	agtgcagtca	480
gttcagagct	ctgtaggaaa	tttgatagta	gcaattaaat	cagtcaggga	ttagtgcaac	540
aaagaaatcg	tgccatcgat	tgcgagacta	ggttgtgaag	cagcaggact	tcagttagg	600
attgcattaa	cacagcatta	ctcagaatta	acaaatatat	ttggtgataa	cataggatcg	660

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ttacaagaaa aaggaataaa attacaaggt atagcatcat tataccgtac aaatatcaca	720
gaaatattca caacatcaac agttgacaaa tatgatattt atgatctatt atttacagaa	780
tcaataaagg tgagagttaa agatgttgat ttgaatgatt actcaataac cctccaagtc	840
agactccctt tattgaccag actgctgaac actcaaatct acaaagtaga ttccatatca	900
tacaatatcc aaaatagaga atggtatatc cctcttccca gccatatcat gacgaaaggg	960
gcatttctag gtggagcaga tgcaaaagaa tgcatagaag cattcagcag ttatatatgc	1020
ccttctgata caggatttgt actaaacat gaaatggaga gctgtctatc aggaaacata	1080
tcccaatgtc caagaaccac agtcacatca gacatagttc ctaggtatgc atttgtcaat	1140
ggaggagtgg ttgcgaattg tataacaact acatgtacat gcaatgggat cggtaataga	1200
atcaaccaac cacctgatca aggagtcaaa attataacac ataaagaatg taatacaata	1260
ggatatcaac gaatgctatt caacacaaac aaagaaggaa ctcttgcatc ctacacacca	1320
gacgcataaa cattaaacaa ttctgttgca cttgatccga ttgacatata aatcgagctc	1380
aacaaggcca aatcagatct tgaggaaatca aaagaatgga taagaaggtc aaatcaaaag	1440
ctagattcta ttggaagtgg gcatcaatct agcactacaa tcatagttat ttgataatg	1500
atgattatat tgtttataat taatataaca ataattacaa ttgcaattaa gtattacaga	1560
attcaaaaga gaaatcgagt ggatcaaaat gataagccgt atgtattaac aaacaag	1617

<210> SEQ ID NO 10

<211> LENGTH: 1716

<212> TYPE: DNA

<213> ORGANISM: Human parainfluenza virus 3

<400> SEQUENCE: 10

atggaatact ggaagcacac caaccacgga aaggatgctg gtaatgagct ggagacatcc	60
acagccactc atggcaacaa gctcaccaac aagataacat atatattgtg gacgataacc	120
ctggtgttat tatcaatagt cttcatcata gtgctaacta attccatcaa aagtgaagag	180
gccccgaat cattgctaca agacataaat aatgagttaa tggaagtac agaaaagatc	240
caagtggcat cggataatac taatgatcta atacagtcag gagtgaatac aaggcttctt	300
acaattcaga gtcatgtcca gaattatata ccaatatcat tgacacaaca aatatcggat	360
cttaggaaat tcattagtga aattacaatt agaaatgata atcaagaagt gccaccacaa	420
agaataacac atgatgtggg tataaaacct ttaaatccag atgatttctg gagatgcacg	480
tctggtcttc catctttgat gaaaactcca aaaataagat taatgccggg accaggatta	540
ttagctatgc caacgactgt tgatggctgt gtcagaaccc cgtccttagt gataaatgat	600
ctgatttatg cttacacctc aaatctaatt actcgagggt gccaggatat agggaaatca	660
tatcaagtat tacagatagg gataataact gtaaactcag acttggtacc tgacttaaat	720
cctaggatct ctcatacctt caacataaat gacaatagaa agtcatgttc tctagcactc	780
ctaaatacag atgtatatca actgtgttca accccaaaag ttgatgaaag atcagattat	840
gcatcatcag gcatagaaga tattgtactt gatattgtca attatgatgg ctcaatctcg	900
acaacaagat ttaagaataa taatataagt ttgatcaac catatgcggc attataccca	960
tctgttgga cagggatata ctacaaaggc aaaataatat ttctcgggta tggaggtctt	1020
gaacatccaa taaatgagaa tgcaatctgc aacacaactg ggtgtcctgg gaaaacacag	1080

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agagactgta atcaagcatc tcatagtcca tggttttcag atagaaggat ggtcaactct 1140
ataattgttg ttgacaaggg cttgaactca gttccaaaat tgaaggatg gacgatatct 1200
atgagacaaa attactgggg gtcagaagga agattacttc tactaggtaa caagatctac 1260
atatacacia gatctacaag ttggcacagc aagttacaat taggaataat tgacattact 1320
gactacagtg atataaggat aaaatggaca tggcataatg tgctatcaag accaggaaac 1380
aatgaatgtc catggggaca ttcattgtcc gatggatgta taacgggagt atataccgat 1440
gcatatccac tcaatccac aggaagcatt gtatcatctg tcatattgga ctacacaaaa 1500
tcgagagtca acccagtcac aacttactca acagcaaccg aaagggtaaa cgagctggct 1560
atccgaaaca aaacactctc agctgggtac acaacaacaa gctgcattac aactataac 1620
aaagggtatt gttttcatat agtagaata aatcataaaa gcttaaacac atttcaacc 1680
atgttgttca aaacagagat tccaaaaagc tgcagt 1716

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<210> SEQ ID NO 11

<211> LENGTH: 1716

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 11

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atggaatact ggaagcacac caaccacggc aaggacgccc gcaacgagct ggaaaccagc 60
acagccacac acggaacaaa gctgaccaac aagatcacct acatcctgtg gaccatcacc 120
ctggtgctgc tgagcatcgt gttcatcacc gtgctgacca atagcatcaa gagcgagaag 180
gccagagaga gcctgctgca ggacatcaac aacgagttca tgggaagtgc cgagaagatc 240
caggtggcca gcgacaacac caacgacctg atccagagcg gcgtgaacac ccggtgctg 300
accatccaga gccacgtgca gaactacac cccatcagcc tgaccacgca gatcagcgac 360
ctgcggaagt tcatcagcga gatcaccac cggaacgaca accaggaagt gccccccag 420
agaatcacc acgacgtggg catcaagccc ctgaacccc acgatttctg gcggtgtaca 480
agcggcctgc ccagcctgat gaagaccccc aagatccggc tgatgcctgg ccctggactg 540
ctggccatgc ctaccacagt ggatggctgt gtgcggaccc ccagcctcgt gatcaacgat 600
ctgatctacg cctacaccag caacctgac acccggggct gccaggatat cggcaagagc 660
taccaggtgc tgcagatcgg catcaccac gtgaactccg acctggtgcc cgacctgaac 720
cctcggatca gccacacctt caacatcaac gacaacagaa agagctgcag cctggctctg 780
ctgaacaccg acgtgtacca gctgtgcagc acccccaagg tggacgagag aagcgactac 840
gccagcagcg gcatcgagga tatcgtgctg gacatcgtga actacgacgg cagcatcagc 900
accacccggt tcaagaacaa caacatcagc ttcgaccagc cctacgccgc cctgtaccct 960
tctgtgggcc ctggcatcta ctacaaggc aagatcatct tccctgggcta cgggcgctg 1020
gaacacccca tcaacgagaa cgccatctgc aacaccaccg gctgccctgg caagaccag 1080
agagactgca atcaggccag ccacagcccc tggttcagcg accgcagaat ggtcaactct 1140
atcatcgtgg tggacaaggg cctgaacagc gtgcccaagc tgaaagtgtg gacaatcagc 1200
atgcgccaga actactgggg cagcgagggc agacttctgc tgctgggaaa caagatctac 1260
atctacaccc ggtccaccag ctggcacagc aaactgcagc tgggaatcat cgacatcacc 1320

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gactacagcg acatccggat caagtggacc tggcacaacg tgctgagcag acccggaac	1380
aatgagtgcc cttggggcca cagctgcccc gatggatgta tcaccggcgt gtacaccgac	1440
gctaccccc tgaatcctac cggtccatc gtgtccagcg tgatcctgga cagccagaaa	1500
agcagagtga acccctgat cacatacagc accgccaccg agagagtga cgaactggcc	1560
atcagaaaca agaccctgag cgccggctac accaccacaa gctgcatac aactacaaac	1620
aagggtact gctcccatc cgtggaatc aaccacaagt ccctgaacac cttccagccc	1680
atgctgttca agaccgagat cccaagagc tgctcc	1716

<210> SEQ ID NO 12

<211> LENGTH: 1617

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 12

atgcccatca gcatactgct gatcatcacc acaatgatca tggccagcca ctgccagatc	60
gacatcacca agctgcagca cgtgggcgtg ctctgaaca gcccgaagg catgaagatc	120
agccagaact tcgagacacg ctacctgac ctgagcctga tcccgaagat cgaggacagc	180
aacagctgcg gcgaccagca gatcaagcag tacaagcgcc tgctggacag actgatcacc	240
cccctgtacg acggcctgcg gctgcagaaa gacgtgatcg tgaccaacca ggaaagcaac	300
gagaacacgg acccccgac cgagagattc ttcggcggcg tgatcgccac aatcgccctg	360
ggagtggcca caagcgcca gattacagcc gctgtggccc tgggtggaag caagcaggcc	420
agaagcgaca tcgagaagct gaaagaggcc atccgggaca ccaacaaggc cgtgcagagc	480
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attgccctga cacagcacta cagcgagctg accaacatct tcggcgacaa catcggcagc	660
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<210> SEQ ID NO 13

<211> LENGTH: 539

<212> TYPE: PRT

<213> ORGANISM: Human parainfluenza virus 3

<400> SEQUENCE: 13

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Met Pro Ile Ser Ile Leu Leu Ile Ile Thr Thr Met Ile Met Ala Ser
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His Cys Gln Ile Asp Ile Thr Lys Leu Gln His Val Gly Val Leu Val
20           25           30

Asn Ser Pro Lys Gly Met Lys Ile Ser Gln Asn Phe Glu Thr Arg Tyr
35           40           45

Leu Ile Leu Ser Leu Ile Pro Lys Ile Glu Asp Ser Asn Ser Cys Gly
50           55           60

Asp Gln Gln Ile Lys Gln Tyr Lys Arg Leu Leu Asp Arg Leu Ile Ile
65           70           75           80

Pro Leu Tyr Asp Gly Leu Arg Leu Gln Lys Asp Val Ile Val Thr Asn
85           90           95

Gln Glu Ser Asn Glu Asn Thr Asp Pro Arg Thr Glu Arg Phe Phe Gly
100          105          110

Gly Val Ile Gly Thr Ile Ala Leu Gly Val Ala Thr Ser Ala Gln Ile
115          120          125

Thr Ala Ala Val Ala Leu Val Glu Ala Lys Gln Ala Arg Ser Asp Ile
130          135          140

Glu Lys Leu Lys Glu Ala Ile Arg Asp Thr Asn Lys Ala Val Gln Ser
145          150          155          160

Val Gln Ser Ser Val Gly Asn Leu Ile Val Ala Ile Lys Ser Val Gln
165          170          175

Asp Tyr Val Asn Lys Glu Ile Val Pro Ser Ile Ala Arg Leu Gly Cys
180          185          190

Glu Ala Ala Gly Leu Gln Leu Gly Ile Ala Leu Thr Gln His Tyr Ser
195          200          205

Glu Leu Thr Asn Ile Phe Gly Asp Asn Ile Gly Ser Leu Gln Glu Lys
210          215          220

Gly Ile Lys Leu Gln Gly Ile Ala Ser Leu Tyr Arg Thr Asn Ile Thr
225          230          235          240

Glu Ile Phe Thr Thr Ser Thr Val Asp Lys Tyr Asp Ile Tyr Asp Leu
245          250          255

Leu Phe Thr Glu Ser Ile Lys Val Arg Val Ile Asp Val Asp Leu Asn
260          265          270

Asp Tyr Ser Ile Thr Leu Gln Val Arg Leu Pro Leu Leu Thr Arg Leu
275          280          285

Leu Asn Thr Gln Ile Tyr Lys Val Asp Ser Ile Ser Tyr Asn Ile Gln
290          295          300

Asn Arg Glu Trp Tyr Ile Pro Leu Pro Ser His Ile Met Thr Lys Gly
305          310          315          320

Ala Phe Leu Gly Gly Ala Asp Val Lys Glu Cys Ile Glu Ala Phe Ser
325          330          335

Ser Tyr Ile Cys Pro Ser Asp Pro Gly Phe Val Leu Asn His Glu Met
340          345          350

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Glu Ser Cys Leu Ser Gly Asn Ile Ser Gln Cys Pro Arg Thr Thr Val
 355 360 365
 Thr Ser Asp Ile Val Pro Arg Tyr Ala Phe Val Asn Gly Gly Val Val
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 Ala Asn Cys Ile Thr Thr Thr Cys Thr Cys Asn Gly Ile Gly Asn Arg
 385 390 395 400
 Ile Asn Gln Pro Pro Asp Gln Gly Val Lys Ile Ile Thr His Lys Glu
 405 410 415
 Cys Asn Thr Ile Gly Ile Asn Gly Met Leu Phe Asn Thr Asn Lys Glu
 420 425 430
 Gly Thr Leu Ala Phe Tyr Thr Pro Asp Asp Ile Thr Leu Asn Asn Ser
 435 440 445
 Val Ala Leu Asp Pro Ile Asp Ile Ser Ile Glu Leu Asn Lys Ala Lys
 450 455 460
 Ser Asp Leu Glu Glu Ser Lys Glu Trp Ile Arg Arg Ser Asn Gln Lys
 465 470 475 480
 Leu Asp Ser Ile Gly Ser Trp His Gln Ser Ser Thr Thr Ile Ile Val
 485 490 495
 Ile Leu Ile Met Met Ile Ile Leu Phe Ile Ile Asn Ile Thr Ile Ile
 500 505 510
 Thr Ile Ala Ile Lys Tyr Tyr Arg Ile Gln Lys Arg Asn Arg Val Asp
 515 520 525
 Gln Asn Asp Lys Pro Tyr Val Leu Thr Asn Lys
 530 535

<210> SEQ ID NO 14

<211> LENGTH: 572

<212> TYPE: PRT

<213> ORGANISM: Human parainfluenza virus 3

<400> SEQUENCE: 14

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 Leu Glu Thr Ser Thr Ala Thr His Gly Asn Lys Leu Thr Asn Lys Ile
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 Thr Tyr Ile Leu Trp Thr Ile Thr Leu Val Leu Leu Ser Ile Val Phe
 35 40 45
 Ile Ile Val Leu Thr Asn Ser Ile Lys Ser Glu Lys Ala Arg Glu Ser
 50 55 60
 Leu Leu Gln Asp Ile Asn Asn Glu Phe Met Glu Val Thr Glu Lys Ile
 65 70 75 80
 Gln Val Ala Ser Asp Asn Thr Asn Asp Leu Ile Gln Ser Gly Val Asn
 85 90 95
 Thr Arg Leu Leu Thr Ile Gln Ser His Val Gln Asn Tyr Ile Pro Ile
 100 105 110
 Ser Leu Thr Gln Gln Ile Ser Asp Leu Arg Lys Phe Ile Ser Glu Ile
 115 120 125
 Thr Ile Arg Asn Asp Asn Gln Glu Val Pro Pro Gln Arg Ile Thr His
 130 135 140
 Asp Val Gly Ile Lys Pro Leu Asn Pro Asp Asp Phe Trp Arg Cys Thr
 145 150 155 160
 Ser Gly Leu Pro Ser Leu Met Lys Thr Pro Lys Ile Arg Leu Met Pro

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165								170				175			
Gly	Pro	Gly	Leu	Leu	Ala	Met	Pro	Thr	Thr	Val	Asp	Gly	Cys	Val	Arg
			180					185					190		
Thr	Pro	Ser	Leu	Val	Ile	Asn	Asp	Leu	Ile	Tyr	Ala	Tyr	Thr	Ser	Asn
		195					200					205			
Leu	Ile	Thr	Arg	Gly	Cys	Gln	Asp	Ile	Gly	Lys	Ser	Tyr	Gln	Val	Leu
	210					215					220				
Gln	Ile	Gly	Ile	Ile	Thr	Val	Asn	Ser	Asp	Leu	Val	Pro	Asp	Leu	Asn
225					230					235					240
Pro	Arg	Ile	Ser	His	Thr	Phe	Asn	Ile	Asn	Asp	Asn	Arg	Lys	Ser	Cys
			245						250					255	
Ser	Leu	Ala	Leu	Leu	Asn	Thr	Asp	Val	Tyr	Gln	Leu	Cys	Ser	Thr	Pro
		260						265					270		
Lys	Val	Asp	Glu	Arg	Ser	Asp	Tyr	Ala	Ser	Ser	Gly	Ile	Glu	Asp	Ile
		275					280					285			
Val	Leu	Asp	Ile	Val	Asn	Tyr	Asp	Gly	Ser	Ile	Ser	Thr	Thr	Arg	Phe
	290					295					300				
Lys	Asn	Asn	Asn	Ile	Ser	Phe	Asp	Gln	Pro	Tyr	Ala	Ala	Leu	Tyr	Pro
305					310					315					320
Ser	Val	Gly	Pro	Gly	Ile	Tyr	Tyr	Lys	Gly	Lys	Ile	Ile	Phe	Leu	Gly
			325						330					335	
Tyr	Gly	Gly	Leu	Glu	His	Pro	Ile	Asn	Glu	Asn	Ala	Ile	Cys	Asn	Thr
		340						345					350		
Thr	Gly	Cys	Pro	Gly	Lys	Thr	Gln	Arg	Asp	Cys	Asn	Gln	Ala	Ser	His
		355					360					365			
Ser	Pro	Trp	Phe	Ser	Asp	Arg	Arg	Met	Val	Asn	Ser	Ile	Ile	Val	Val
	370					375					380				
Asp	Lys	Gly	Leu	Asn	Ser	Val	Pro	Lys	Leu	Lys	Val	Trp	Thr	Ile	Ser
385				390						395					400
Met	Arg	Gln	Asn	Tyr	Trp	Gly	Ser	Glu	Gly	Arg	Leu	Leu	Leu	Leu	Gly
			405					410						415	
Asn	Lys	Ile	Tyr	Ile	Tyr	Thr	Arg	Ser	Thr	Ser	Trp	His	Ser	Lys	Leu
		420						425					430		
Gln	Leu	Gly	Ile	Ile	Asp	Ile	Thr	Asp	Tyr	Ser	Asp	Ile	Arg	Ile	Lys
		435				440						445			
Trp	Thr	Trp	His	Asn	Val	Leu	Ser	Arg	Pro	Gly	Asn	Asn	Glu	Cys	Pro
	450				455						460				
Trp	Gly	His	Ser	Cys	Pro	Asp	Gly	Cys	Ile	Thr	Gly	Val	Tyr	Thr	Asp
465				470						475					480
Ala	Tyr	Pro	Leu	Asn	Pro	Thr	Gly	Ser	Ile	Val	Ser	Ser	Val	Ile	Leu
			485					490						495	
Asp	Ser	Gln	Lys	Ser	Arg	Val	Asn	Pro	Val	Ile	Thr	Tyr	Ser	Thr	Ala
		500						505					510		
Thr	Glu	Arg	Val	Asn	Glu	Leu	Ala	Ile	Arg	Asn	Lys	Thr	Leu	Ser	Ala
		515					520					525			
Gly	Tyr	Thr	Thr	Thr	Ser	Cys	Ile	Thr	His	Tyr	Asn	Lys	Gly	Tyr	Cys
	530					535					540				
Phe	His	Ile	Val	Glu	Ile	Asn	His	Lys	Ser	Leu	Asn	Thr	Phe	Gln	Pro
545					550					555					560
Met	Leu	Phe	Lys	Thr	Glu	Ile	Pro	Lys	Ser	Cys	Ser				
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<210> SEQ ID NO 15
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 15

Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro
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Asp Thr Thr Gly
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<210> SEQ ID NO 16
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 16

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser

<210> SEQ ID NO 17
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 17

Met Leu Gly Ser Asn Ser Gly Gln Arg Val Val Phe Thr Ile Leu Leu
1 5 10 15

Leu Leu Val Ala Pro Ala Tyr Ser
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<210> SEQ ID NO 18
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 18

Met Lys Cys Leu Leu Tyr Leu Ala Phe Leu Phe Ile Gly Val Asn Cys
1 5 10 15

Ala

<210> SEQ ID NO 19
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 19

Met Trp Leu Val Ser Leu Ala Ile Val Thr Ala Cys Ala Gly Ala
1 5 10 15

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<210> SEQ ID NO 20
<211> LENGTH: 4062
<212> TYPE: DNA
<213> ORGANISM: Middle East respiratory syndrome coronavirus

<400> SEQUENCE: 20
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gataaaactt ggccctaggcc aattgatgtt tctaaggctg acggtattat ataccctcaa      180
ggccgtacat attctaacat aactatcact tatcaaggtc tttttcccta tcagggagac      240
catggtgata tgtatgttta ctctgcagga catgctacag gcacaaactcc aaaaagtgtg      300
ttttagtagta actattctca ggacgtcaaa cagtttgcta atgggtttgt cgtccgtata      360
ggagcagctg ccaattccac tggcactgtt attattagcc catctaccag cgctactata      420
cgaaaaattt acctgctttt tatgctgggt tcttcagttg gtaatttctc agatggtaaa      480
atgggccgct tcttcaatca tactctagtt cttttgcccg atggatgtgg cactttactt      540
agagcttttt attgtattct agagcctcgc tctggaaatc attgtcctgc tggcaattcc      600
tatactttct ttgccactta tcacactcct gcaacagatt gttctgatgg caattacaat      660
cgtaatgcca gtctgaactc ttttaaggag tattttaatt tacgtaactg cactttatg      720
tacacttata acattaccga agatgagatt ttagagtggg ttggcattac aaaaactgct      780
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ctgatttttg attatttttc ataccactt agtatgaaat ccgatctcag tgttagttct      1380
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actggttggt gcacaaaactg tatgggaaaa cttaagtgt atcgttgttg tgatagatac	4020
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<210> SEQ ID NO 21

<211> LENGTH: 4062

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 21

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gataaaactt ggccctagggc aattgatgtt tctaaggctg acggtattat ataccctcaa	180
ggccgtacat attctaacat aactatcact tatcaaggtc tttttcccta tcagggagac	240
catggtgata tgtatgttta ctctgcagga catgctacag gcacaactcc aaaaagtgtg	300
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aacaagtgtc ctgctcttct ttctgatgat cgtactgaag tacctcagtt agtgaacgct	1560
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cacatttctt ctaccatgtc tcaatactcc cgttctacgc gatcaatgct taaacggcga	2100
gattctacat atggccccc ctacagacct gttggttgtg tcctaggact tgttaattcc	2160
tctttgttcg tagaggactg caagttgcct cttggtcaat ctctctgtgc tcttcctgac	2220

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acacctagta ctctcacacc tcgcagtgtg cgctctgttc caggtgaaat gcgcttggca	2280
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agtataccca ctaatttttc ctttggtgtg actcaggagt acattcagac aaccattcag	2400
aaagttactg ttgattgtaa acagtaactt tgcaatggtt tccagaagtg tgagcaatta	2460
ctgcgcgagt atggccaggt ttgttccaaa ataaaccagg ctctccatgg tgccaattta	2520
cgccaggatg attctgtacg taatttgttt gcgagcgtga aaagctctca atcatctcct	2580
atcataccag gttttggagg tgactttaat ttgacacttc tggaacctgt ttctatatct	2640
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gctgatccgt gttatatgca aggttacgat gattgcctgc agcaaggccc agcatcagct	2760
cgtgatctta tttgtgtcga atatgtggct ggttaccagg tattacctcc tcttatggat	2820
gttaatatgg aagccgcgta tacttcatct ttgcttggca gcatagcagg tgttggtcgg	2880
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actggttgtg gcacaaaactg tatgggaaaa cttaagtgtg atcgttgttg tgatagatac	4020
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<210> SEQ ID NO 22

<211> LENGTH: 1845

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 22

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tccgtgcggt	cgggtgcctgg	cgaaatgcgg	ctggcctcca	tcgccttcaa	tcaccaatc	180
caagtggatc	agctgaatag	ctcgtatttc	aagctgtcca	ccccacgaa	cttctcgttc	240
ggggtcaccc	aggagtacat	ccagaccaca	attcagaagg	tcaccgtcga	ttgcaagcaa	300
tacgtgtgca	acggcttcca	gaagtgcgag	cagctgctga	gagaatacgg	gcagttttgc	360
agcaagatca	accaggcgct	gcatggagct	aacttgccgc	aggacgactc	cgtgcgcaac	420
ctctttgcct	ctgtgaagtc	atcccagtc	tccccaatca	tcccggtgatt	cggaggggac	480
ttcaacctga	ccctcctgga	gcccggtgctg	atcagcaccg	gtageagatc	ggcgcgctca	540
gccattgaag	atcttctgtt	cgacaaggtc	accatcgccg	atccgggcta	catgcaggga	600
tacgacgact	gtatgcagca	gggaccagcc	tccgcgaggg	acctcatctg	cgcgcaatac	660
gtggccgggt	acaaagtgt	gcctcctctg	atggatgtga	acatggaggc	cgcttatact	720
tcgtccctgc	tcggtcttat	cgccggcgctg	gggtggaccg	cggcctgtc	ctccttcgcc	780
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aacgcccagg	cgtctctaaa	gctggcctcc	gaactcagca	acaccttcgg	agccatcagc	1020
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cttcaacaag	tggtaaggc	cctgaacgag	agctacatcg	acctgaagga	gctgggcaac	1740
tatacctact	acaacaagt	gccggacaag	attgaggaga	ttctgtcgaa	aatctaccac	1800
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<210> SEQ ID NO 23

<211> LENGTH: 4071

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 23

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agctatgtgg	acgtgggccc	cgatagcgtg	aagtcgcct	gtatcgaagt	ggacatccag	120
cagacctttt	tcgacaagac	ctggcccaga	cccatcgacg	tgtccaaggc	cgacggcatc	180
atctatccac	aaggccggac	ctacagcaac	atcaccatta	cctaccaggg	cctgttccca	240

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tatcaaggcg	accacggcga	tatgtacgtg	tactctgccg	gccacgccac	cggcaccaca	300
ccccagaaac	tggtcgtggc	caactacagc	caggacgtga	agcagttcgc	caacggcttc	360
gtcgtgcgga	ttggcgccgc	tgccaatagc	accggcacag	tgatcatcag	ccccagcacc	420
agcgccacca	tccggaagat	ctaccccgcc	ttcatgctgg	gcagctccgt	gggcaatttc	480
agcgacggca	agatgggcgc	gttcttcaac	cacacccctg	tgctgctgcc	cgatggctgt	540
ggcacactgc	tgagagcctt	ctactgcctc	ctggaaccca	gaagcggcaa	ccactgccct	600
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ccccacagca	tccgggtccat	ccagagcgac	agaaaagcct	gggcccgcct	ctacgtgtac	960
aagctgcagc	ccctgacctt	cctgctggac	ttcagcgtgg	acggtacatc	cagacggggc	1020
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caggctgagg	gcgtggaatg	cgacttcagc	cctctgctga	gcggcaccac	tcccaggtg	1200
tacaacttca	agcggctggg	gttcaccaac	tgcaattaca	acctgaccaa	gctgctgagc	1260
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accacaatcc	agaaagtgc	cgtggactgc	aagcagtacg	tgtgcaacgg	ctttcagaag	2460
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ggcgccaacc tgagacagga tgacagcgtg cggaacctgt tcgccagcgt gaaaagcagc 2580
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gtgtccatca gcaccggctc cagaagcgcc agatccgcca tcgaggacct gctgttcgac 2700
aaagtgacca ttgccgaccc cggtacatg cagggtacg acgattgcat gcagcagggc 2760
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<210> SEQ ID NO 24

<211> LENGTH: 1353

<212> TYPE: PRT

<213> ORGANISM: Middle East respiratory syndrome coronavirus

<400> SEQUENCE: 24

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Met Ile His Ser Val Phe Leu Leu Met Phe Leu Leu Thr Pro Thr Glu
1             5             10             15

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Ser Tyr Val Asp Val Gly Pro Asp Ser Val Lys Ser Ala Cys Ile Glu
20             25             30

```

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Val Asp Ile Gln Gln Thr Phe Phe Asp Lys Thr Trp Pro Arg Pro Ile
35             40             45

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Asp Val Ser Lys Ala Asp Gly Ile Ile Tyr Pro Gln Gly Arg Thr Tyr
50             55             60

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Ser Asn Ile Thr Ile Thr Tyr Gln Gly Leu Phe Pro Tyr Gln Gly Asp
65             70             75             80

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His Gly Asp Met Tyr Val Tyr Ser Ala Gly His Ala Thr Gly Thr Thr

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85								90					95				
Pro	Gln	Lys	Leu	Phe	Val	Ala	Asn	Tyr	Ser	Gln	Asp	Val	Lys	Gln	Phe		
			100					105					110				
Ala	Asn	Gly	Phe	Val	Val	Arg	Ile	Gly	Ala	Ala	Ala	Asn	Ser	Thr	Gly		
		115					120					125					
Thr	Val	Ile	Ile	Ser	Pro	Ser	Thr	Ser	Ala	Thr	Ile	Arg	Lys	Ile	Tyr		
		130					135					140					
Pro	Ala	Phe	Met	Leu	Gly	Ser	Ser	Val	Gly	Asn	Phe	Ser	Asp	Gly	Lys		
145					150					155					160		
Met	Gly	Arg	Phe	Phe	Asn	His	Thr	Leu	Val	Leu	Leu	Pro	Asp	Gly	Cys		
			165					170					175				
Gly	Thr	Leu	Leu	Arg	Ala	Phe	Tyr	Cys	Ile	Leu	Glu	Pro	Arg	Ser	Gly		
			180					185					190				
Asn	His	Cys	Pro	Ala	Gly	Asn	Ser	Tyr	Thr	Ser	Phe	Ala	Thr	Tyr	His		
		195					200					205					
Thr	Pro	Ala	Thr	Asp	Cys	Ser	Asp	Gly	Asn	Tyr	Asn	Arg	Asn	Ala	Ser		
		210					215					220					
Leu	Asn	Ser	Phe	Lys	Glu	Tyr	Phe	Asn	Leu	Arg	Asn	Cys	Thr	Phe	Met		
225					230					235					240		
Tyr	Thr	Tyr	Asn	Ile	Thr	Glu	Asp	Glu	Ile	Leu	Glu	Trp	Phe	Gly	Ile		
			245					250					255				
Thr	Gln	Thr	Ala	Gln	Gly	Val	His	Leu	Phe	Ser	Ser	Arg	Tyr	Val	Asp		
			260					265					270				
Leu	Tyr	Gly	Gly	Asn	Met	Phe	Gln	Phe	Ala	Thr	Leu	Pro	Val	Tyr	Asp		
		275					280					285					
Thr	Ile	Lys	Tyr	Tyr	Ser	Ile	Ile	Pro	His	Ser	Ile	Arg	Ser	Ile	Gln		
		290					295					300					
Ser	Asp	Arg	Lys	Ala	Trp	Ala	Ala	Phe	Tyr	Val	Tyr	Lys	Leu	Gln	Pro		
305					310					315					320		
Leu	Thr	Phe	Leu	Leu	Asp	Phe	Ser	Val	Asp	Gly	Tyr	Ile	Arg	Arg	Ala		
			325					330					335				
Ile	Asp	Cys	Gly	Phe	Asn	Asp	Leu	Ser	Gln	Leu	His	Cys	Ser	Tyr	Glu		
			340					345					350				
Ser	Phe	Asp	Val	Glu	Ser	Gly	Val	Tyr	Ser	Val	Ser	Ser	Phe	Glu	Ala		
		355					360					365					
Lys	Pro	Ser	Gly	Ser	Val	Val	Glu	Gln	Ala	Glu	Gly	Val	Glu	Cys	Asp		
		370					375					380					
Phe	Ser	Pro	Leu	Leu	Ser	Gly	Thr	Pro	Pro	Gln	Val	Tyr	Asn	Phe	Lys		
385					390					395					400		
Arg	Leu	Val	Phe	Thr	Asn	Cys	Asn	Tyr	Asn	Leu	Thr	Lys	Leu	Leu	Ser		
			405					410					415				
Leu	Phe	Ser	Val	Asn	Asp	Phe	Thr	Cys	Ser	Gln	Ile	Ser	Pro	Ala	Ala		
			420					425					430				
Ile	Ala	Ser	Asn	Cys	Tyr	Ser	Ser	Leu	Ile	Leu	Asp	Tyr	Phe	Ser	Tyr		
		435					440					445					
Pro	Leu	Ser	Met	Lys	Ser	Asp	Leu	Ser	Val	Ser	Ser	Ala	Gly	Pro	Ile		
		450					455					460					
Ser	Gln	Phe	Asn	Tyr	Lys	Gln	Ser	Phe	Ser	Asn	Pro	Thr	Cys	Leu	Ile		
465					470					475					480		
Leu	Ala	Thr	Val	Pro	His	Asn	Leu	Thr	Thr	Ile	Thr	Lys	Pro	Leu	Lys		
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Tyr	Ser	Tyr	Ile	Asn	Lys	Cys	Ser	Arg	Leu	Leu	Ser	Asp	Asp	Arg	Thr
			500					505					510		
Glu	Val	Pro	Gln	Leu	Val	Asn	Ala	Asn	Gln	Tyr	Ser	Pro	Cys	Val	Ser
		515					520					525			
Ile	Val	Pro	Ser	Thr	Val	Trp	Glu	Asp	Gly	Asp	Tyr	Tyr	Arg	Lys	Gln
	530					535					540				
Leu	Ser	Pro	Leu	Glu	Gly	Gly	Gly	Trp	Leu	Val	Ala	Ser	Gly	Ser	Thr
545				550					555						560
Val	Ala	Met	Thr	Glu	Gln	Leu	Gln	Met	Gly	Phe	Gly	Ile	Thr	Val	Gln
			565						570					575	
Tyr	Gly	Thr	Asp	Thr	Asn	Ser	Val	Cys	Pro	Lys	Leu	Glu	Phe	Ala	Asn
			580					585					590		
Asp	Thr	Lys	Ile	Ala	Ser	Gln	Leu	Gly	Asn	Cys	Val	Glu	Tyr	Ser	Leu
		595					600					605			
Tyr	Gly	Val	Ser	Gly	Arg	Gly	Val	Phe	Gln	Asn	Cys	Thr	Ala	Val	Gly
	610					615					620				
Val	Arg	Gln	Gln	Arg	Phe	Val	Tyr	Asp	Ala	Tyr	Gln	Asn	Leu	Val	Gly
625					630					635					640
Tyr	Tyr	Ser	Asp	Asp	Gly	Asn	Tyr	Tyr	Cys	Leu	Arg	Ala	Cys	Val	Ser
			645						650					655	
Val	Pro	Val	Ser	Val	Ile	Tyr	Asp	Lys	Glu	Thr	Lys	Thr	His	Ala	Thr
			660					665					670		
Leu	Phe	Gly	Ser	Val	Ala	Cys	Glu	His	Ile	Ser	Ser	Thr	Met	Ser	Gln
	675						680					685			
Tyr	Ser	Arg	Ser	Thr	Arg	Ser	Met	Leu	Lys	Arg	Arg	Asp	Ser	Thr	Tyr
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Gly	Pro	Leu	Gln	Thr	Pro	Val	Gly	Cys	Val	Leu	Gly	Leu	Val	Asn	Ser
705					710					715					720
Ser	Leu	Phe	Val	Glu	Asp	Cys	Lys	Leu	Pro	Leu	Gly	Gln	Ser	Leu	Cys
			725						730					735	
Ala	Leu	Pro	Asp	Thr	Pro	Ser	Thr	Leu	Thr	Pro	Arg	Ser	Val	Arg	Ser
			740					745					750		
Val	Pro	Gly	Glu	Met	Arg	Leu	Ala	Ser	Ile	Ala	Phe	Asn	His	Pro	Ile
		755					760					765			
Gln	Val	Asp	Gln	Leu	Asn	Ser	Ser	Tyr	Phe	Lys	Leu	Ser	Ile	Pro	Thr
	770				775						780				
Asn	Phe	Ser	Phe	Gly	Val	Thr	Gln	Glu	Tyr	Ile	Gln	Thr	Thr	Ile	Gln
785					790					795					800
Lys	Val	Thr	Val	Asp	Cys	Lys	Gln	Tyr	Val	Cys	Asn	Gly	Phe	Gln	Lys
			805						810					815	
Cys	Glu	Gln	Leu	Leu	Arg	Glu	Tyr	Gly	Gln	Phe	Cys	Ser	Lys	Ile	Asn
		820						825					830		
Gln	Ala	Leu	His	Gly	Ala	Asn	Leu	Arg	Gln	Asp	Asp	Ser	Val	Arg	Asn
		835					840					845			
Leu	Phe	Ala	Ser	Val	Lys	Ser	Ser	Gln	Ser	Ser	Pro	Ile	Ile	Pro	Gly
	850					855					860				
Phe	Gly	Gly	Asp	Phe	Asn	Leu	Thr	Leu	Leu	Glu	Pro	Val	Ser	Ile	Ser
865					870					875					880
Thr	Gly	Ser	Arg	Ser	Ala	Arg	Ser	Ala	Ile	Glu	Asp	Leu	Leu	Phe	Asp
					885				890						895

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Lys	Val	Thr	Ile	Ala	Asp	Pro	Gly	Tyr	Met	Gln	Gly	Tyr	Asp	Asp	Cys
			900					905					910		
Met	Gln	Gln	Gly	Pro	Ala	Ser	Ala	Arg	Asp	Leu	Ile	Cys	Ala	Gln	Tyr
		915					920					925			
Val	Ala	Gly	Tyr	Lys	Val	Leu	Pro	Pro	Leu	Met	Asp	Val	Asn	Met	Glu
	930					935					940				
Ala	Ala	Tyr	Thr	Ser	Ser	Leu	Leu	Gly	Ser	Ile	Ala	Gly	Val	Gly	Trp
945					950					955					960
Thr	Ala	Gly	Leu	Ser	Ser	Phe	Ala	Ala	Ile	Pro	Phe	Ala	Gln	Ser	Ile
				965					970					975	
Phe	Tyr	Arg	Leu	Asn	Gly	Val	Gly	Ile	Thr	Gln	Gln	Val	Leu	Ser	Glu
			980					985					990		
Asn	Gln	Lys	Leu	Ile	Ala	Asn	Lys	Phe	Asn	Gln	Ala	Leu	Gly	Ala	Met
		995					1000					1005			
Gln	Thr	Gly	Phe	Thr	Thr	Thr	Asn	Glu	Ala	Phe	Arg	Lys	Val	Gln	
	1010					1015					1020				
Asp	Ala	Val	Asn	Asn	Asn	Ala	Gln	Ala	Leu	Ser	Lys	Leu	Ala	Ser	
	1025					1030					1035				
Glu	Leu	Ser	Asn	Thr	Phe	Gly	Ala	Ile	Ser	Ala	Ser	Ile	Gly	Asp	
	1040					1045					1050				
Ile	Ile	Gln	Arg	Leu	Asp	Val	Leu	Glu	Gln	Asp	Ala	Gln	Ile	Asp	
	1055					1060					1065				
Arg	Leu	Ile	Asn	Gly	Arg	Leu	Thr	Thr	Leu	Asn	Ala	Phe	Val	Ala	
	1070					1075					1080				
Gln	Gln	Leu	Val	Arg	Ser	Glu	Ser	Ala	Ala	Leu	Ser	Ala	Gln	Leu	
	1085					1090					1095				
Ala	Lys	Asp	Lys	Val	Asn	Glu	Cys	Val	Lys	Ala	Gln	Ser	Lys	Arg	
	1100					1105					1110				
Ser	Gly	Phe	Cys	Gly	Gln	Gly	Thr	His	Ile	Val	Ser	Phe	Val	Val	
	1115					1120					1125				
Asn	Ala	Pro	Asn	Gly	Leu	Tyr	Phe	Met	His	Val	Gly	Tyr	Tyr	Pro	
	1130					1135					1140				
Ser	Asn	His	Ile	Glu	Val	Val	Ser	Ala	Tyr	Gly	Leu	Cys	Asp	Ala	
	1145					1150					1155				
Ala	Asn	Pro	Thr	Asn	Cys	Ile	Ala	Pro	Val	Asn	Gly	Tyr	Phe	Ile	
	1160					1165					1170				
Lys	Thr	Asn	Asn	Thr	Arg	Ile	Val	Asp	Glu	Trp	Ser	Tyr	Thr	Gly	
	1175					1180					1185				
Ser	Ser	Phe	Tyr	Ala	Pro	Glu	Pro	Ile	Thr	Ser	Leu	Asn	Thr	Lys	
	1190					1195					1200				
Tyr	Val	Ala	Pro	Gln	Val	Thr	Tyr	Gln	Asn	Ile	Ser	Thr	Asn	Leu	
	1205					1210					1215				
Pro	Pro	Pro	Leu	Leu	Gly	Asn	Ser	Thr	Gly	Ile	Asp	Phe	Gln	Asp	
	1220					1225					1230				
Glu															

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1280	1285	1290
Lys Trp Pro Trp Tyr Ile Trp Leu Gly Phe Ile Ala Gly Leu Val		
1295	1300	1305
Ala Leu Ala Leu Cys Val Phe Phe Ile Leu Cys Cys Thr Gly Cys		
1310	1315	1320
Gly Thr Asn Cys Met Gly Lys Leu Lys Cys Asn Arg Cys Cys Asp		
1325	1330	1335
Arg Tyr Glu Glu Tyr Asp Leu Glu Pro His Lys Val His Val His		
1340	1345	1350
<210> SEQ ID NO 25		
<211> LENGTH: 1353		
<212> TYPE: PRT		
<213> ORGANISM: Artificial Sequence		
<220> FEATURE:		
<223> OTHER INFORMATION: Synthetic Polypeptide		
<400> SEQUENCE: 25		
Met Ile His Ser Val Phe Leu Leu Met Phe Leu Leu Thr Pro Thr Glu		
1	5	10
Ser Tyr Val Asp Val Gly Pro Asp Ser Val Lys Ser Ala Cys Ile Glu		
20	25	30
Val Asp Ile Gln Gln Thr Phe Phe Asp Lys Thr Trp Pro Arg Pro Ile		
35	40	45
Asp Val Ser Lys Ala Asp Gly Ile Ile Tyr Pro Gln Gly Arg Thr Tyr		
50	55	60
Ser Asn Ile Thr Ile Thr Tyr Gln Gly Leu Phe Pro Tyr Gln Gly Asp		
65	70	75
His Gly Asp Met Tyr Val Tyr Ser Ala Gly His Ala Thr Gly Thr Thr		
85	90	95
Pro Gln Lys Leu Phe Val Ala Asn Tyr Ser Gln Asp Val Lys Gln Phe		
100	105	110
Ala Asn Gly Phe Val Val Arg Ile Gly Ala Ala Ala Asn Ser Thr Gly		
115	120	125
Thr Val Ile Ile Ser Pro Ser Thr Ser Ala Thr Ile Arg Lys Ile Tyr		
130	135	140
Pro Ala Phe Met Leu Gly Ser Ser Val Gly Asn Phe Ser Asp Gly Lys		
145	150	155
Met Gly Arg Phe Phe Asn His Thr Leu Val Leu Leu Pro Asp Gly Cys		
165	170	175
Gly Thr Leu Leu Arg Ala Phe Tyr Cys Ile Leu Glu Pro Arg Ser Gly		
180	185	190
Asn His Cys Pro Ala Gly Asn Ser Tyr Thr Ser Phe Ala Thr Tyr His		
195	200	205
Thr Pro Ala Thr Asp Cys Ser Asp Gly Asn Tyr Asn Arg Asn Ala Ser		
210	215	220
Leu Asn Ser Phe Lys Glu Tyr Phe Asn Leu Arg Asn Cys Thr Phe Met		
225	230	235
Tyr Thr Tyr Asn Ile Thr Glu Asp Glu Ile Leu Glu Trp Phe Gly Ile		
245	250	255
Thr Gln Thr Ala Gln Gly Val His Leu Phe Ser Ser Arg Tyr Val Asp		
260	265	270
Leu Tyr Gly Gly Asn Met Phe Gln Phe Ala Thr Leu Pro Val Tyr Asp		

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275						280						285					
Thr	Ile	Lys	Tyr	Tyr	Ser	Ile	Ile	Pro	His	Ser	Ile	Arg	Ser	Ile	Gln		
290						295					300						
Ser	Asp	Arg	Lys	Ala	Trp	Ala	Ala	Phe	Tyr	Val	Tyr	Lys	Leu	Gln	Pro		
305					310					315				320			
Leu	Thr	Phe	Leu	Leu	Asp	Phe	Ser	Val	Asp	Gly	Tyr	Ile	Arg	Arg	Ala		
			325						330					335			
Ile	Asp	Cys	Gly	Phe	Asn	Asp	Leu	Ser	Gln	Leu	His	Cys	Ser	Tyr	Glu		
			340					345					350				
Ser	Phe	Asp	Val	Glu	Ser	Gly	Val	Tyr	Ser	Val	Ser	Ser	Phe	Glu	Ala		
		355					360					365					
Lys	Pro	Ser	Gly	Ser	Val	Val	Glu	Gln	Ala	Glu	Gly	Val	Glu	Cys	Asp		
370						375					380						
Phe	Ser	Pro	Leu	Leu	Ser	Gly	Thr	Pro	Pro	Gln	Val	Tyr	Asn	Phe	Lys		
385					390					395					400		
Arg	Leu	Val	Phe	Thr	Asn	Cys	Asn	Tyr	Asn	Leu	Thr	Lys	Leu	Leu	Ser		
			405						410					415			
Leu	Phe	Ser	Val	Asn	Asp	Phe	Thr	Cys	Ser	Gln	Ile	Ser	Pro	Ala	Ala		
			420					425					430				
Ile	Ala	Ser	Asn	Cys	Tyr	Ser	Ser	Leu	Ile	Leu	Asp	Tyr	Phe	Ser	Tyr		
		435				440					445						
Pro	Leu	Ser	Met	Lys	Ser	Asp	Leu	Ser	Val	Ser	Ser	Ala	Gly	Pro	Ile		
450					455						460						
Ser	Gln	Phe	Asn	Tyr	Lys	Gln	Ser	Phe	Ser	Asn	Pro	Thr	Cys	Leu	Ile		
465					470					475				480			
Leu	Ala	Thr	Val	Pro	His	Asn	Leu	Thr	Thr	Ile	Thr	Lys	Pro	Leu	Lys		
			485						490					495			
Tyr	Ser	Tyr	Ile	Asn	Lys	Cys	Ser	Arg	Leu	Leu	Ser	Asp	Asp	Arg	Thr		
			500					505					510				
Glu	Val	Pro	Gln	Leu	Val	Asn	Ala	Asn	Gln	Tyr	Ser	Pro	Cys	Val	Ser		
		515				520						525					
Ile	Val	Pro	Ser	Thr	Val	Trp	Glu	Asp	Gly	Asp	Tyr	Tyr	Arg	Lys	Gln		
530					535						540						
Leu	Ser	Pro	Leu	Glu	Gly	Gly	Gly	Trp	Leu	Val	Ala	Ser	Gly	Ser	Thr		
545				550					555					560			
Val	Ala	Met	Thr	Glu	Gln	Leu	Gln	Met	Gly	Phe	Gly	Ile	Thr	Val	Gln		
			565						570					575			
Tyr	Gly	Thr	Asp	Thr	Asn	Ser	Val	Cys	Pro	Lys	Leu	Glu	Phe	Ala	Asn		
			580					585					590				
Asp	Thr	Lys	Ile	Ala	Ser	Gln	Leu	Gly	Asn	Cys	Val	Glu	Tyr	Ser	Leu		
595						600						605					
Tyr	Gly	Val	Ser	Gly	Arg	Gly	Val	Phe	Gln	Asn	Cys	Thr	Ala	Val	Gly		
610					615						620						
Val	Arg	Gln	Gln	Arg	Phe	Val	Tyr	Asp	Ala	Tyr	Gln	Asn	Leu	Val	Gly		
625					630					635				640			
Tyr	Tyr	Ser	Asp	Asp	Gly	Asn	Tyr	Tyr	Cys	Leu	Arg	Ala	Cys	Val	Ser		
			645					650					655				
Val	Pro	Val	Ser	Val	Ile	Tyr	Asp	Lys	Glu	Thr	Lys	Thr	His	Ala	Thr		
			660					665					670				
Leu	Phe	Gly	Ser	Val	Ala	Cys	Glu	His	Ile	Ser	Ser	Thr	Met	Ser	Gln		
675							680					685					

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Tyr	Ser	Arg	Ser	Thr	Arg	Ser	Met	Leu	Lys	Arg	Arg	Asp	Ser	Thr	Tyr
690						695					700				
Gly	Pro	Leu	Gln	Thr	Pro	Val	Gly	Cys	Val	Leu	Gly	Leu	Val	Asn	Ser
705					710					715				720	
Ser	Leu	Phe	Val	Glu	Asp	Cys	Lys	Leu	Pro	Leu	Gly	Gln	Ser	Leu	Cys
			725						730					735	
Ala	Leu	Pro	Asp	Thr	Pro	Ser	Thr	Leu	Thr	Pro	Arg	Ser	Val	Arg	Ser
			740					745					750		
Val	Pro	Gly	Glu	Met	Arg	Leu	Ala	Ser	Ile	Ala	Phe	Asn	His	Pro	Ile
		755					760					765			
Gln	Val	Asp	Gln	Leu	Asn	Ser	Ser	Tyr	Phe	Lys	Leu	Ser	Ile	Pro	Thr
	770				775						780				
Asn	Phe	Ser	Phe	Gly	Val	Thr	Gln	Glu	Tyr	Ile	Gln	Thr	Thr	Ile	Gln
785					790					795					800
Lys	Val	Thr	Val	Asp	Cys	Lys	Gln	Tyr	Val	Cys	Asn	Gly	Phe	Gln	Lys
			805						810					815	
Cys	Glu	Gln	Leu	Leu	Arg	Glu	Tyr	Gly	Gln	Phe	Cys	Ser	Lys	Ile	Asn
			820					825					830		
Gln	Ala	Leu	His	Gly	Ala	Asn	Leu	Arg	Gln	Asp	Asp	Ser	Val	Arg	Asn
			835				840					845			
Leu	Phe	Ala	Ser	Val	Lys	Ser	Ser	Gln	Ser	Ser	Pro	Ile	Ile	Pro	Gly
			850			855					860				
Phe	Gly	Gly	Asp	Phe	Asn	Leu	Thr	Leu	Leu	Glu	Pro	Val	Ser	Ile	Ser
865					870					875					880
Thr	Gly	Ser	Arg	Ser	Ala	Arg	Ser	Ala	Ile	Glu	Asp	Leu	Leu	Phe	Asp
			885						890					895	
Lys	Val	Thr	Ile	Ala	Asp	Pro	Gly	Tyr	Met	Gln	Gly	Tyr	Asp	Asp	Cys
			900					905					910		
Met	Gln	Gln	Gly	Pro	Ala	Ser	Ala	Arg	Asp	Leu	Ile	Cys	Ala	Gln	Tyr
			915				920					925			
Val	Ala	Gly	Tyr	Lys	Val	Leu	Pro	Pro	Leu	Met	Asp	Val	Asn	Met	Glu
	930					935					940				
Ala	Ala	Tyr	Thr	Ser	Ser	Leu	Leu	Gly	Ser	Ile	Ala	Gly	Val	Gly	Trp
945					950					955					960
Thr	Ala	Gly	Leu	Ser	Ser	Phe	Ala	Ala	Ile	Pro	Phe	Ala	Gln	Ser	Ile
			965						970					975	
Phe	Tyr	Arg	Leu	Asn	Gly	Val	Gly	Ile	Thr	Gln	Gln	Val	Leu	Ser	Glu
			980					985					990		
Asn	Gln	Lys	Leu	Ile	Ala	Asn	Lys	Phe	Asn	Gln	Ala	Leu	Gly	Ala	Met
		995					1000						1005		
Gln	Thr	Gly	Phe	Thr	Thr	Thr	Asn	Glu	Ala	Phe	Gln	Lys	Val	Gln	
	1010						1015					1020			
Asp	Ala	Val	Asn	Asn	Asn	Ala	Gln	Ala	Leu	Ser	Lys	Leu	Ala	Ser	
	1025						1030					1035			
Glu	Leu	Ser	Asn	Thr	Phe	Gly	Ala	Ile	Ser	Ala	Ser	Ile	Gly	Asp	
	1040					1045						1050			
Ile	Ile	Gln	Arg	Leu	Asp	Val	Leu	Glu	Gln	Asp	Ala	Gln	Ile	Asp	
	1055					1060						1065			
Arg	Leu	Ile	Asn	Gly	Arg	Leu	Thr	Thr	Leu	Asn	Ala	Phe	Val	Ala	
	1070					1075						1080			

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Gln	Gln	Leu	Val	Arg	Ser	Glu	Ser	Ala	Ala	Leu	Ser	Ala	Gln	Leu
1085						1090					1095			
Ala	Lys	Asp	Lys	Val	Asn	Glu	Cys	Val	Lys	Ala	Gln	Ser	Lys	Arg
1100						1105					1110			
Ser	Gly	Phe	Cys	Gly	Gln	Gly	Thr	His	Ile	Val	Ser	Phe	Val	Val
1115						1120					1125			
Asn	Ala	Pro	Asn	Gly	Leu	Tyr	Phe	Met	His	Val	Gly	Tyr	Tyr	Pro
1130						1135					1140			
Ser	Asn	His	Ile	Glu	Val	Val	Ser	Ala	Tyr	Gly	Leu	Cys	Asp	Ala
1145						1150					1155			
Ala	Asn	Pro	Thr	Asn	Cys	Ile	Ala	Pro	Val	Asn	Gly	Tyr	Phe	Ile
1160						1165					1170			
Lys	Thr	Asn	Asn	Thr	Arg	Ile	Val	Asp	Glu	Trp	Ser	Tyr	Thr	Gly
1175						1180					1185			
Ser	Ser	Phe	Tyr	Ala	Pro	Glu	Pro	Ile	Thr	Ser	Leu	Asn	Thr	Lys
1190						1195					1200			
Tyr	Val	Ala	Pro	Gln	Val	Thr	Tyr	Gln	Asn	Ile	Ser	Thr	Asn	Leu
1205						1210					1215			
Pro	Pro	Pro	Leu	Leu	Gly	Asn	Ser	Thr	Gly	Ile	Asp	Phe	Gln	Asp
1220						1225					1230			
Glu	Leu	Asp	Glu	Phe	Phe	Lys	Asn	Val	Ser	Thr	Ser	Ile	Pro	Asn
1235						1240					1245			
Phe	Gly	Ser	Leu	Thr	Gln	Ile	Asn	Thr	Thr	Leu	Leu	Asp	Leu	Thr
1250						1255					1260			
Tyr	Glu	Met	Leu	Ser	Leu	Gln	Gln	Val	Val	Lys	Ala	Leu	Asn	Glu
1265						1270					1275			
Ser	Tyr	Ile	Asp	Leu	Lys	Glu	Leu	Gly	Asn	Tyr	Thr	Tyr	Tyr	Asn
1280						1285					1290			
Lys	Trp	Pro	Trp	Tyr	Ile	Trp	Leu	Gly	Phe	Ile	Ala	Gly	Leu	Val
1295						1300					1305			
Ala	Leu	Ala	Leu	Cys	Val	Phe	Phe	Ile	Leu	Cys	Cys	Thr	Gly	Cys
1310						1315					1320			
Gly	Thr	Asn	Cys	Met	Gly	Lys	Leu	Lys	Cys	Asn	Arg	Cys	Cys	Asp
1325						1330					1335			
Arg	Tyr	Glu	Glu	Tyr	Asp	Leu	Glu	Pro	His	Lys	Val	His	Val	His
1340						1345					1350			

<210> SEQ ID NO 26

<211> LENGTH: 615

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 26

Met	Ile	His	Ser	Val	Phe	Leu	Leu	Met	Phe	Leu	Leu	Thr	Pro	Thr	Glu
1				5						10				15	

Ser	Asp	Cys	Lys	Leu	Pro	Leu	Gly	Gln	Ser	Leu	Cys	Ala	Leu	Pro	Asp
			20					25					30		

Thr	Pro	Ser	Thr	Leu	Thr	Pro	Arg	Ser	Val	Arg	Ser	Val	Pro	Gly	Glu
			35				40					45			

Met	Arg	Leu	Ala	Ser	Ile	Ala	Phe	Asn	His	Pro	Ile	Gln	Val	Asp	Gln
		50				55					60				

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Leu	Asn	Ser	Ser	Tyr	Phe	Lys	Leu	Ser	Ile	Pro	Thr	Asn	Phe	Ser	Phe
65					70					75					80
Gly	Val	Thr	Gln	Glu	Tyr	Ile	Gln	Thr	Thr	Ile	Gln	Lys	Val	Thr	Val
			85						90					95	
Asp	Cys	Lys	Gln	Tyr	Val	Cys	Asn	Gly	Phe	Gln	Lys	Cys	Glu	Gln	Leu
		100						105					110		
Leu	Arg	Glu	Tyr	Gly	Gln	Phe	Cys	Ser	Lys	Ile	Asn	Gln	Ala	Leu	His
		115					120					125			
Gly	Ala	Asn	Leu	Arg	Gln	Asp	Asp	Ser	Val	Arg	Asn	Leu	Phe	Ala	Ser
	130					135					140				
Val	Lys	Ser	Ser	Gln	Ser	Ser	Pro	Ile	Ile	Pro	Gly	Phe	Gly	Gly	Asp
145				150						155					160
Phe	Asn	Leu	Thr	Leu	Leu	Glu	Pro	Val	Ser	Ile	Ser	Thr	Gly	Ser	Arg
			165						170					175	
Ser	Ala	Arg	Ser	Ala	Ile	Glu	Asp	Leu	Leu	Phe	Asp	Lys	Val	Thr	Ile
		180						185					190		
Ala	Asp	Pro	Gly	Tyr	Met	Gln	Gly	Tyr	Asp	Asp	Cys	Met	Gln	Gln	Gly
		195					200					205			
Pro	Ala	Ser	Ala	Arg	Asp	Leu	Ile	Cys	Ala	Gln	Tyr	Val	Ala	Gly	Tyr
	210					215					220				
Lys	Val	Leu	Pro	Pro	Leu	Met	Asp	Val	Asn	Met	Glu	Ala	Ala	Tyr	Thr
225					230					235					240
Ser	Ser	Leu	Leu	Gly	Ser	Ile	Ala	Gly	Val	Gly	Trp	Thr	Ala	Gly	Leu
			245						250					255	
Ser	Ser	Phe	Ala	Ala	Ile	Pro	Phe	Ala	Gln	Ser	Ile	Phe	Tyr	Arg	Leu
		260						265					270		
Asn	Gly	Val	Gly	Ile	Thr	Gln	Gln	Val	Leu	Ser	Glu	Asn	Gln	Lys	Leu
		275					280						285		
Ile	Ala	Asn	Lys	Phe	Asn	Gln	Ala	Leu	Gly	Ala	Met	Gln	Thr	Gly	Phe
	290					295					300				
Thr	Thr	Thr	Asn	Glu	Ala	Phe	Gln	Lys	Val	Gln	Asp	Ala	Val	Asn	Asn
305				310						315					320
Asn	Ala	Gln	Ala	Leu	Ser	Lys	Leu	Ala	Ser	Glu	Leu	Ser	Asn	Thr	Phe
			325						330					335	
Gly	Ala	Ile	Ser	Ala	Ser	Ile	Gly	Asp	Ile	Ile	Gln	Arg	Leu	Asp	Val
		340						345					350		
Leu	Glu	Gln	Asp	Ala	Gln	Ile	Asp	Arg	Leu	Ile	Asn	Gly	Arg	Leu	Thr
		355					360					365			
Thr	Leu	Asn	Ala	Phe	Val	Ala	Gln	Gln	Leu	Val	Arg	Ser	Glu	Ser	Ala
	370					375					380				
Ala	Leu	Ser	Ala	Gln	Leu	Ala	Lys	Asp	Lys	Val	Asn	Glu	Cys	Val	Lys
385				390						395					400
Ala	Gln	Ser	Lys	Arg	Ser	Gly	Phe	Cys	Gly	Gln	Gly	Thr	His	Ile	Val
			405					410						415	
Ser	Phe	Val	Val	Asn	Ala	Pro	Asn	Gly	Leu	Tyr	Phe	Met	His	Val	Gly
		420						425					430		
Tyr	Tyr	Pro	Ser	Asn	His	Ile	Glu	Val	Val	Ser	Ala	Tyr	Gly	Leu	Cys
		435				440						445			
Asp	Ala	Ala	Asn	Pro	Thr	Asn	Cys	Ile	Ala	Pro	Val	Asn	Gly	Tyr	Phe
	450					455					460				
Ile	Lys	Thr	Asn	Asn	Thr	Arg	Ile	Val	Asp	Glu	Trp	Ser	Tyr	Thr	Gly

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465	470	475	480
Ser Ser Phe Tyr Ala Pro Glu Pro Ile Thr Ser Leu Asn Thr Lys Tyr	485	490	495
Val Ala Pro Gln Val Thr Tyr Gln Asn Ile Ser Thr Asn Leu Pro Pro	500	505	510
Pro Leu Leu Gly Asn Ser Thr Gly Ile Asp Phe Gln Asp Glu Leu Asp	515	520	525
Glu Phe Phe Lys Asn Val Ser Thr Ser Ile Pro Asn Phe Gly Ser Leu	530	535	540
Thr Gln Ile Asn Thr Thr Leu Leu Asp Leu Thr Tyr Glu Met Leu Ser	545	550	555
Leu Gln Gln Val Val Lys Ala Leu Asn Glu Ser Tyr Ile Asp Leu Lys	565	570	575
Glu Leu Gly Asn Tyr Thr Tyr Tyr Asn Lys Trp Pro Asp Lys Ile Glu	580	585	590
Glu Ile Leu Ser Lys Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile	595	600	605
Lys Lys Leu Ile Gly Glu Ala	610	615	

<210> SEQ ID NO 27

<211> LENGTH: 1353

<212> TYPE: PRT

<213> ORGANISM: Middle East respiratory syndrome coronavirus

<400> SEQUENCE: 27

Met Ile His Ser Val Phe Leu Leu Met Phe Leu Leu Thr Pro Thr Glu	1	5	10	15
Ser Tyr Val Asp Val Gly Pro Asp Ser Val Lys Ser Ala Cys Ile Glu	20	25	30	
Val Asp Ile Gln Gln Thr Phe Phe Asp Lys Thr Trp Pro Arg Pro Ile	35	40	45	
Asp Val Ser Lys Ala Asp Gly Ile Ile Tyr Pro Gln Gly Arg Thr Tyr	50	55	60	
Ser Asn Ile Thr Ile Thr Tyr Gln Gly Leu Phe Pro Tyr Gln Gly Asp	65	70	75	80
His Gly Asp Met Tyr Val Tyr Ser Ala Gly His Ala Thr Gly Thr Thr	85	90	95	
Pro Gln Lys Leu Phe Val Ala Asn Tyr Ser Gln Asp Val Lys Gln Phe	100	105	110	
Ala Asn Gly Phe Val Val Arg Ile Gly Ala Ala Ala Asn Ser Thr Gly	115	120	125	
Thr Val Ile Ile Ser Pro Ser Thr Ser Ala Thr Ile Arg Lys Ile Tyr	130	135	140	
Pro Ala Phe Met Leu Gly Ser Ser Val Gly Asn Phe Ser Asp Gly Lys	145	150	155	160
Met Gly Arg Phe Phe Asn His Thr Leu Val Leu Leu Pro Asp Gly Cys	165	170	175	
Gly Thr Leu Leu Arg Ala Phe Tyr Cys Ile Leu Glu Pro Arg Ser Gly	180	185	190	
Asn His Cys Pro Ala Gly Asn Ser Tyr Thr Ser Phe Ala Thr Tyr His	195	200	205	

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Thr	Pro	Ala	Thr	Asp	Cys	Ser	Asp	Gly	Asn	Tyr	Asn	Arg	Asn	Ala	Ser
210						215					220				
Leu	Asn	Ser	Phe	Lys	Glu	Tyr	Phe	Asn	Leu	Arg	Asn	Cys	Thr	Phe	Met
225				230						235					240
Tyr	Thr	Tyr	Asn	Ile	Thr	Glu	Asp	Glu	Ile	Leu	Glu	Trp	Phe	Gly	Ile
			245						250					255	
Thr	Gln	Thr	Ala	Gln	Gly	Val	His	Leu	Phe	Ser	Ser	Arg	Tyr	Val	Asp
			260					265					270		
Leu	Tyr	Gly	Gly	Asn	Met	Phe	Gln	Phe	Ala	Thr	Leu	Pro	Val	Tyr	Asp
		275					280					285			
Thr	Ile	Lys	Tyr	Tyr	Ser	Ile	Ile	Pro	His	Ser	Ile	Arg	Ser	Ile	Gln
290					295						300				
Ser	Asp	Arg	Lys	Ala	Trp	Ala	Ala	Phe	Tyr	Val	Tyr	Lys	Leu	Gln	Pro
305				310						315					320
Leu	Thr	Phe	Leu	Leu	Asp	Phe	Ser	Val	Asp	Gly	Tyr	Ile	Arg	Arg	Ala
			325						330					335	
Ile	Asp	Cys	Gly	Phe	Asn	Asp	Leu	Ser	Gln	Leu	His	Cys	Ser	Tyr	Glu
		340					345					350			
Ser	Phe	Asp	Val	Glu	Ser	Gly	Val	Tyr	Ser	Val	Ser	Ser	Phe	Glu	Ala
		355					360					365			
Lys	Pro	Ser	Gly	Ser	Val	Val	Glu	Gln	Ala	Glu	Gly	Val	Glu	Cys	Asp
370					375						380				
Phe	Ser	Pro	Leu	Leu	Ser	Gly	Thr	Pro	Pro	Gln	Val	Tyr	Asn	Phe	Lys
385				390						395					400
Arg	Leu	Val	Phe	Thr	Asn	Cys	Asn	Tyr	Asn	Leu	Thr	Lys	Leu	Leu	Ser
			405						410					415	
Leu	Phe	Ser	Val	Asn	Asp	Phe	Thr	Cys	Ser	Gln	Ile	Ser	Pro	Ala	Ala
			420					425					430		
Ile	Ala	Ser	Asn	Cys	Tyr	Ser	Ser	Leu	Ile	Leu	Asp	Tyr	Phe	Ser	Tyr
		435					440					445			
Pro	Leu	Ser	Met	Lys	Ser	Asp	Leu	Ser	Val	Ser	Ser	Ala	Gly	Pro	Ile
450					455						460				
Ser	Gln	Phe	Asn	Tyr	Lys	Gln	Ser	Phe	Ser	Asn	Pro	Thr	Cys	Leu	Ile
465				470						475					480
Leu	Ala	Thr	Val	Pro	His	Asn	Leu	Thr	Thr	Ile	Thr	Lys	Pro	Leu	Lys
			485					490						495	
Tyr	Ser	Tyr	Ile	Asn	Lys	Cys	Ser	Arg	Leu	Leu	Ser	Asp	Asp	Arg	Thr
			500					505					510		
Glu	Val	Pro	Gln	Leu	Val	Asn	Ala	Asn	Gln	Tyr	Ser	Pro	Cys	Val	Ser
		515					520					525			
Ile	Val	Pro	Ser	Thr	Val	Trp	Glu	Asp	Gly	Asp	Tyr	Tyr	Arg	Lys	Gln
530					535						540				
Leu	Ser	Pro	Leu	Glu	Gly	Gly	Gly	Trp	Leu	Val	Ala	Ser	Gly	Ser	Thr
545				550					555						560
Val	Ala	Met	Thr	Glu	Gln	Leu	Gln	Met	Gly	Phe	Gly	Ile	Thr	Val	Gln
			565					570						575	
Tyr	Gly	Thr	Asp	Thr	Asn	Ser	Val	Cys	Pro	Lys	Leu	Glu	Phe	Ala	Asn
			580				585						590		
Asp	Thr	Lys	Ile	Ala	Ser	Gln	Leu	Gly	Asn	Cys	Val	Glu	Tyr	Ser	Leu
		595				600						605			
Tyr	Gly	Val	Ser	Gly	Arg	Gly	Val	Phe	Gln	Asn	Cys	Thr	Ala	Val	Gly

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610	615	620
Val Arg Gln Gln Arg Phe	Val Tyr Asp Ala Tyr	Gln Asn Leu Val Gly
625	630	635 640
Tyr Tyr Ser Asp Asp Gly	Asn Tyr Tyr Cys Leu Arg Ala Cys	Val Ser
	645	650 655
Val Pro Val Ser Val Ile Tyr	Asp Lys Glu Thr Lys Thr His Ala Thr	
	660	665 670
Leu Phe Gly Ser Val Ala Cys	Glu His Ile Ser Ser Thr Met Ser Gln	
	675	680 685
Tyr Ser Arg Ser Thr Arg Ser	Met Leu Lys Arg Arg Asp Ser Thr Tyr	
	690	695 700
Gly Pro Leu Gln Thr Pro Val	Gly Cys Val Leu Gly Leu Val Asn Ser	
	705	710 715 720
Ser Leu Phe Val Glu Asp Cys	Lys Leu Pro Leu Gly Gln Ser Leu Cys	
	725	730 735
Ala Leu Pro Asp Thr Pro Ser	Thr Leu Thr Pro Arg Ser Val Arg Ser	
	740	745 750
Val Pro Gly Glu Met Arg Leu	Ala Ser Ile Ala Phe Asn His Pro Ile	
	755	760 765
Gln Val Asp Gln Leu Asn Ser	Ser Tyr Phe Lys Leu Ser Ile Pro Thr	
	770	775 780
Asn Phe Ser Phe Gly Val Thr	Gln Glu Tyr Ile Gln Thr Thr Ile Gln	
	785	790 795 800
Lys Val Thr Val Asp Cys Lys	Gln Tyr Val Cys Asn Gly Phe Gln Lys	
	805	810 815
Cys Glu Gln Leu Leu Arg Glu	Tyr Gly Gln Phe Cys Ser Lys Ile Asn	
	820	825 830
Gln Ala Leu His Gly Ala Asn	Leu Arg Gln Asp Asp Ser Val Arg Asn	
	835	840 845
Leu Phe Ala Ser Val Lys Ser	Ser Gln Ser Ser Pro Ile Ile Pro Gly	
	850	855 860
Phe Gly Gly Asp Phe Asn Leu	Thr Leu Leu Glu Pro Val Ser Ile Ser	
	865	870 875 880
Thr Gly Ser Arg Ser Ala Arg	Ser Ala Ile Glu Asp Leu Leu Phe Asp	
	885	890 895
Lys Val Thr Ile Ala Asp Pro	Gly Tyr Met Gln Gly Tyr Asp Asp Cys	
	900	905 910
Met Gln Gln Gly Pro Ala Ser	Ala Arg Asp Leu Ile Cys Ala Gln Tyr	
	915	920 925
Val Ala Gly Tyr Lys Val Leu	Pro Pro Leu Met Asp Val Asn Met Glu	
	930	935 940
Ala Ala Tyr Thr Ser Ser Leu	Leu Gly Ser Ile Ala Gly Val Gly Trp	
	945	950 955 960
Thr Ala Gly Leu Ser Ser Phe	Ala Ala Ile Pro Phe Ala Gln Ser Ile	
	965	970 975
Phe Tyr Arg Leu Asn Gly Val	Gly Ile Thr Gln Gln Val Leu Ser Glu	
	980	985 990
Asn Gln Lys Leu Ile Ala Asn	Lys Phe Asn Gln Ala Leu Gly Ala Met	
	995	1000 1005
Gln Thr Gly Phe Thr Thr Thr	Asn Glu Ala Phe Arg Lys Val Gln	
	1010	1015 1020

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Asp	Ala	Val	Asn	Asn	Asn	Ala	Gln	Ala	Leu	Ser	Lys	Leu	Ala	Ser
1025						1030					1035			
Glu	Leu	Ser	Asn	Thr	Phe	Gly	Ala	Ile	Ser	Ala	Ser	Ile	Gly	Asp
1040						1045					1050			
Ile	Ile	Gln	Arg	Leu	Asp	Val	Leu	Glu	Gln	Asp	Ala	Gln	Ile	Asp
1055						1060					1065			
Arg	Leu	Ile	Asn	Gly	Arg	Leu	Thr	Thr	Leu	Asn	Ala	Phe	Val	Ala
1070						1075					1080			
Gln	Gln	Leu	Val	Arg	Ser	Glu	Ser	Ala	Ala	Leu	Ser	Ala	Gln	Leu
1085						1090					1095			
Ala	Lys	Asp	Lys	Val	Asn	Glu	Cys	Val	Lys	Ala	Gln	Ser	Lys	Arg
1100						1105					1110			
Ser	Gly	Phe	Cys	Gly	Gln	Gly	Thr	His	Ile	Val	Ser	Phe	Val	Val
1115						1120					1125			
Asn	Ala	Pro	Asn	Gly	Leu	Tyr	Phe	Met	His	Val	Gly	Tyr	Tyr	Pro
1130						1135					1140			
Ser	Asn	His	Ile	Glu	Val	Val	Ser	Ala	Tyr	Gly	Leu	Cys	Asp	Ala
1145						1150					1155			
Ala	Asn	Pro	Thr	Asn	Cys	Ile	Ala	Pro	Val	Asn	Gly	Tyr	Phe	Ile
1160						1165					1170			
Lys	Thr	Asn	Asn	Thr	Arg	Ile	Val	Asp	Glu	Trp	Ser	Tyr	Thr	Gly
1175						1180					1185			
Ser	Ser	Phe	Tyr	Ala	Pro	Glu	Pro	Ile	Thr	Ser	Leu	Asn	Thr	Lys
1190						1195					1200			
Tyr	Val	Ala	Pro	His	Val	Thr	Tyr	Gln	Asn	Ile	Ser	Thr	Asn	Leu
1205						1210					1215			
Pro	Pro	Pro	Leu	Leu	Gly	Asn	Ser	Thr	Gly	Ile	Asp	Phe	Gln	Asp
1220						1225					1230			
Glu	Leu	Asp	Glu	Phe	Phe	Lys	Asn	Val	Ser	Thr	Ser	Ile	Pro	Asn
1235						1240					1245			
Phe	Gly	Ser	Leu	Thr	Gln	Ile	Asn	Thr	Thr	Leu	Leu	Asp	Leu	Thr
1250						1255					1260			
Tyr	Glu	Met	Leu	Ser	Leu	Gln	Gln	Val	Val	Lys	Ala	Leu	Asn	Glu
1265						1270					1275			
Ser	Tyr	Ile	Asp	Leu	Lys	Glu	Leu	Gly	Asn	Tyr	Thr	Tyr	Tyr	Asn
1280						1285					1290			
Lys	Trp	Pro	Trp	Tyr	Ile	Trp	Leu	Gly	Phe	Ile	Ala	Gly	Leu	Val
1295						1300					1305			
Ala	Leu	Ala	Leu	Cys	Val	Phe	Phe	Ile	Leu	Cys	Cys	Thr	Gly	Cys
1310						1315					1320			
Gly	Thr	Asn	Cys	Met	Gly	Lys	Leu	Lys	Cys	Asn	Arg	Cys	Cys	Asp
1325						1330					1335			
Arg	Tyr	Glu	Glu	Tyr	Asp	Leu	Glu	Pro	His	Lys	Val	His	Val	His
1340						1345					1350			

<210> SEQ ID NO 28

<211> LENGTH: 1353

<212> TYPE: PRT

<213> ORGANISM: Middle East respiratory syndrome coronavirus

<400> SEQUENCE: 28

Met Ile His Ser Val Phe Leu Leu Met Phe Leu Leu Thr Pro Thr Glu

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1	5	10	15
Ser Tyr Val Asp Val Gly Pro Asp Ser Val Lys Ser Ala Cys Ile Glu	20	25	30
Val Asp Ile Gln Gln Thr Phe Phe Asp Lys Thr Trp Pro Arg Pro Ile	35	40	45
Asp Val Ser Lys Ala Asp Gly Ile Ile Tyr Pro Gln Gly Arg Thr Tyr	50	55	60
Ser Asn Ile Thr Ile Thr Tyr Gln Gly Leu Phe Pro Tyr Gln Gly Asp	65	70	75
His Gly Asp Met Tyr Val Tyr Ser Ala Gly His Ala Thr Gly Thr Thr	85	90	95
Pro Gln Lys Leu Phe Val Ala Asn Tyr Ser Gln Asp Val Lys Gln Phe	100	105	110
Ala Asn Gly Phe Val Val Arg Ile Gly Ala Ala Ala Asn Ser Thr Gly	115	120	125
Thr Val Ile Ile Ser Pro Ser Thr Ser Ala Thr Ile Arg Lys Ile Tyr	130	135	140
Pro Ala Phe Met Leu Gly Ser Ser Val Gly Asn Phe Ser Asp Gly Lys	145	150	155
Met Gly Arg Phe Phe Asn His Thr Leu Val Leu Leu Pro Asp Gly Cys	165	170	175
Gly Thr Leu Leu Arg Ala Phe Tyr Cys Ile Leu Glu Pro Arg Ser Gly	180	185	190
Asn His Cys Pro Ala Gly Asn Ser Tyr Thr Ser Phe Ala Thr Tyr His	195	200	205
Thr Pro Ala Thr Asp Cys Ser Asp Gly Asn Tyr Asn Arg Asn Ala Ser	210	215	220
Leu Asn Ser Phe Lys Glu Tyr Phe Asn Leu Arg Asn Cys Thr Phe Met	225	230	235
Tyr Thr Tyr Asn Ile Thr Glu Asp Glu Ile Leu Glu Trp Phe Gly Ile	245	250	255
Thr Gln Thr Ala Gln Gly Val His Leu Phe Ser Ser Arg Tyr Val Asp	260	265	270
Leu Tyr Gly Gly Asn Met Phe Gln Phe Ala Thr Leu Pro Val Tyr Asp	275	280	285
Thr Ile Lys Tyr Tyr Ser Ile Ile Pro His Ser Ile Arg Ser Ile Gln	290	295	300
Ser Asp Arg Lys Ala Trp Ala Ala Phe Tyr Val Tyr Lys Leu Gln Pro	305	310	315
Leu Thr Phe Leu Leu Asp Phe Ser Val Asp Gly Tyr Ile Arg Arg Ala	325	330	335
Ile Asp Cys Gly Phe Asn Asp Leu Ser Gln Leu His Cys Ser Tyr Glu	340	345	350
Ser Phe Asp Val Glu Ser Gly Val Tyr Ser Val Ser Ser Phe Glu Ala	355	360	365
Lys Pro Ser Gly Ser Val Val Glu Gln Ala Glu Gly Val Glu Cys Asp	370	375	380
Phe Ser Pro Leu Leu Ser Gly Thr Pro Pro Gln Val Tyr Asn Phe Lys	385	390	395
Arg Leu Val Phe Thr Asn Cys Asn Tyr Asn Leu Thr Lys Leu Leu Ser	405	410	415

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Leu	Phe	Ser	Val	Asn	Asp	Phe	Thr	Cys	Ser	Gln	Ile	Ser	Pro	Ala	Ala	
			420					425					430			
Ile	Ala	Ser	Asn	Cys	Tyr	Ser	Ser	Leu	Ile	Leu	Asp	Tyr	Phe	Ser	Tyr	
			435					440				445				
Pro	Leu	Ser	Met	Lys	Ser	Asp	Leu	Ser	Val	Ser	Ser	Ala	Gly	Pro	Ile	
			450					455				460				
Ser	Gln	Phe	Asn	Tyr	Lys	Gln	Ser	Phe	Ser	Asn	Pro	Thr	Cys	Leu	Ile	
465					470					475					480	
Leu	Ala	Thr	Val	Pro	His	Asn	Leu	Thr	Thr	Ile	Thr	Lys	Pro	Leu	Lys	
				485						490					495	
Tyr	Ser	Tyr	Ile	Asn	Lys	Cys	Ser	Arg	Leu	Leu	Ser	Asp	Asp	Arg	Thr	
			500					505					510			
Glu	Val	Pro	Gln	Leu	Val	Asn	Ala	Asn	Gln	Tyr	Ser	Pro	Cys	Val	Ser	
			515					520					525			
Ile	Val	Pro	Ser	Thr	Val	Trp	Glu	Asp	Gly	Asp	Tyr	Tyr	Arg	Lys	Gln	
			530					535				540				
Leu	Ser	Pro	Leu	Glu	Gly	Gly	Gly	Trp	Leu	Val	Ala	Ser	Gly	Ser	Thr	
545					550					555					560	
Val	Ala	Met	Thr	Glu	Gln	Leu	Gln	Met	Gly	Phe	Gly	Ile	Thr	Val	Gln	
				565						570					575	
Tyr	Gly	Thr	Asp	Thr	Asn	Ser	Val	Cys	Pro	Lys	Leu	Glu	Phe	Ala	Asn	
			580					585					590			
Asp	Thr	Lys	Ile	Ala	Ser	Gln	Leu	Gly	Asn	Cys	Val	Glu	Tyr	Ser	Leu	
			595					600					605			
Tyr	Gly	Val	Ser	Gly	Arg	Gly	Val	Phe	Gln	Asn	Cys	Thr	Ala	Val	Gly	
			610					615				620				
Val	Arg	Gln	Gln	Arg	Phe	Val	Tyr	Asp	Ala	Tyr	Gln	Asn	Leu	Val	Gly	
625					630					635					640	
Tyr	Tyr	Ser	Asp	Asp	Gly	Asn	Tyr	Tyr	Cys	Leu	Arg	Ala	Cys	Val	Ser	
				645						650					655	
Val	Pro	Val	Ser	Val	Ile	Tyr	Asp	Lys	Glu	Thr	Lys	Thr	His	Ala	Thr	
				660					665					670		
Leu	Phe	Gly	Ser	Val	Ala	Cys	Glu	His	Ile	Ser	Ser	Thr	Met	Ser	Gln	
				675					680					685		
Tyr	Ser	Arg	Ser	Thr	Arg	Ser	Met	Leu	Lys	Arg	Arg	Asp	Ser	Thr	Tyr	
						695					700					
Gly	Pro	Leu	Gln	Thr	Pro	Val	Gly	Cys	Val	Leu	Gly	Leu	Val	Asn	Ser	
705					710						715				720	
Ser	Leu	Phe	Val	Glu	Asp	Cys	Lys	Leu	Pro	Leu	Gly	Gln	Ser	Leu	Cys	
				725						730					735	
Ala	Leu	Pro	Asp	Thr	Pro	Ser	Thr	Leu	Thr	Pro	Arg	Ser	Val	Arg	Ser	
				740						745				750		
Val	Pro	Gly	Glu	Met	Arg	Leu	Ala	Ser	Ile	Ala	Phe	Asn	His	Pro	Ile	
				755									765			
Gln	Val	Asp	Gln	Leu	Asn	Ser	Ser	Tyr	Phe	Lys	Leu	Ser	Ile	Pro	Thr	
				770				775					780			
Asn	Phe	Ser	Phe	Gly	Val	Thr	Gln	Glu	Tyr	Ile	Gln	Thr	Thr	Ile	Gln	
785					790						795				800	
Lys	Val	Thr	Val	Asp	Cys	Lys	Gln	Tyr	Val	Cys	Asn	Gly	Phe	Gln	Lys	
				805						810					815	

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Cys	Glu	Gln	Leu	Leu	Arg	Glu	Tyr	Gly	Gln	Phe	Cys	Ser	Lys	Ile	Asn
			820			825						830			
Gln	Ala	Leu	His	Gly	Ala	Asn	Leu	Arg	Gln	Asp	Asp	Ser	Val	Arg	Asn
			835			840						845			
Leu	Phe	Ala	Ser	Val	Lys	Ser	Ser	Gln	Ser	Ser	Pro	Ile	Ile	Pro	Gly
			850			855						860			
Phe	Gly	Gly	Asp	Phe	Asn	Leu	Thr	Leu	Leu	Glu	Pro	Val	Ser	Ile	Ser
			865			870						875			
Thr	Gly	Ser	Arg	Ser	Ala	Arg	Ser	Ala	Ile	Glu	Asp	Leu	Leu	Phe	Asp
			885			890						895			
Lys	Val	Thr	Ile	Ala	Asp	Pro	Gly	Tyr	Met	Gln	Gly	Tyr	Asp	Asp	Cys
			900			905						910			
Met	Gln	Gln	Gly	Pro	Ala	Ser	Ala	Arg	Asp	Leu	Ile	Cys	Ala	Gln	Tyr
			915			920						925			
Val	Ala	Gly	Tyr	Lys	Val	Leu	Pro	Pro	Leu	Met	Asp	Val	Asn	Met	Glu
			930			935						940			
Ala	Ala	Tyr	Thr	Ser	Ser	Leu	Leu	Gly	Ser	Ile	Ala	Gly	Val	Gly	Trp
			945			950						955			
Thr	Ala	Gly	Leu	Ser	Ser	Phe	Ala	Ala	Ile	Pro	Phe	Ala	Gln	Ser	Ile
			965			970						975			
Phe	Tyr	Arg	Leu	Asn	Gly	Val	Gly	Ile	Thr	Gln	Gln	Val	Leu	Ser	Glu
			980			985						990			
Asn	Gln	Lys	Leu	Ile	Ala	Asn	Lys	Phe	Asn	Gln	Ala	Leu	Gly	Ala	Met
			995			1000						1005			
Gln	Thr	Gly	Phe	Thr	Thr	Thr	Asn	Glu	Ala	Phe	Arg	Lys	Val	Gln	
			1010			1015						1020			
Asp	Ala	Val	Asn	Asn	Asn	Ala	Gln	Ala	Leu	Ser	Lys	Leu	Ala	Ser	
			1025			1030						1035			
Glu	Leu	Ser	Asn	Thr	Phe	Gly	Ala	Ile	Ser	Ala	Ser	Ile	Gly	Asp	
			1040			1045						1050			
Ile	Ile	Gln	Arg	Leu	Asp	Val	Leu	Glu	Gln	Asp	Ala	Gln	Ile	Asp	
			1055			1060						1065			
Arg	Leu	Ile	Asn	Gly	Arg	Leu	Thr	Thr	Leu	Asn	Ala	Phe	Val	Ala	
			1070			1075						1080			
Gln	Gln	Leu	Val	Arg	Ser	Glu	Ser	Ala	Ala	Leu	Ser	Ala	Gln	Leu	
			1085			1090						1095			
Ala	Lys	Asp	Lys	Val	Asn	Glu	Cys	Val	Lys	Ala	Gln	Ser	Lys	Arg	
			1100			1105						1110			
Ser	Gly	Phe	Cys	Gly	Gln	Gly	Thr	His	Ile	Val	Ser	Phe	Val	Val	
			1115			1120						1125			
Asn	Ala	Pro	Asn	Gly	Leu	Tyr	Phe	Met	His	Val	Gly	Tyr	Tyr	Pro	
			1130			1135						1140			
Ser	Asn	His	Ile	Glu	Val	Val	Ser	Ala	Tyr	Gly	Leu	Cys	Asp	Ala	
			1145			1150						1155			
Ala	Asn	Pro	Thr	Asn	Cys	Ile	Ala	Pro	Val	Asn	Gly	Tyr	Phe	Ile	
			1160			1165						1170			
Lys	Thr	Asn	Asn	Thr	Arg	Ile	Val	Asp	Glu	Trp	Ser	Tyr	Thr	Gly	
			1175			1180						1185			
Ser	Ser	Phe	Tyr	Ala	Pro	Glu	Pro	Ile	Thr	Ser	Leu	Asn	Thr	Lys	
			1190			1195						1200			
Tyr	Val	Ala	Pro	His	Val	Thr	Tyr	Gln	Asn	Ile	Ser	Thr	Asn	Leu	

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1205	1210	1215
Pro Pro Pro Leu Leu Gly Asn Ser Thr Gly Ile Asp Phe Gln Asp		
1220	1225	1230
Glu Leu Asp Glu Phe Phe Lys Asn Val Ser Thr Ser Ile Pro Asn		
1235	1240	1245
Phe Gly Ser Leu Thr Gln Ile Asn Thr Thr Leu Leu Asp Leu Thr		
1250	1255	1260
Tyr Glu Met Leu Ser Leu Gln Gln Val Val Lys Ala Leu Asn Glu		
1265	1270	1275
Ser Tyr Ile Asp Leu Lys Glu Leu Gly Asn Tyr Thr Tyr Tyr Asn		
1280	1285	1290
Lys Trp Pro Trp Tyr Ile Trp Leu Gly Phe Ile Ala Gly Leu Val		
1295	1300	1305
Ala Leu Ala Leu Cys Val Phe Phe Ile Leu Cys Cys Thr Gly Cys		
1310	1315	1320
Gly Thr Asn Cys Met Gly Lys Leu Lys Cys Asn Arg Cys Cys Asp		
1325	1330	1335
Arg Tyr Glu Glu Tyr Asp Leu Glu Pro His Lys Val His Val His		
1340	1345	1350

<210> SEQ ID NO 29

<211> LENGTH: 1255

<212> TYPE: PRT

<213> ORGANISM: Human SARS coronavirus

<400> SEQUENCE: 29

Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu		
1	5	10
Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln		
20	25	30
His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg		
35	40	45
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser		
50	55	60
Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val		
65	70	75
Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn		
85	90	95
Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln		
100	105	110
Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys		
115	120	125
Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met		
130	135	140
Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr		
145	150	155
Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser		
165	170	175
Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly		
180	185	190
Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp		
195	200	205

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Leu	Pro	Ser	Gly	Phe	Asn	Thr	Leu	Lys	Pro	Ile	Phe	Lys	Leu	Pro	Leu
210						215					220				
Gly	Ile	Asn	Ile	Thr	Asn	Phe	Arg	Ala	Ile	Leu	Thr	Ala	Phe	Ser	Pro
225					230					235					240
Ala	Gln	Asp	Ile	Trp	Gly	Thr	Ser	Ala	Ala	Ala	Tyr	Phe	Val	Gly	Tyr
			245						250					255	
Leu	Lys	Pro	Thr	Thr	Phe	Met	Leu	Lys	Tyr	Asp	Glu	Asn	Gly	Thr	Ile
			260					265					270		
Thr	Asp	Ala	Val	Asp	Cys	Ser	Gln	Asn	Pro	Leu	Ala	Glu	Leu	Lys	Cys
		275					280					285			
Ser	Val	Lys	Ser	Phe	Glu	Ile	Asp	Lys	Gly	Ile	Tyr	Gln	Thr	Ser	Asn
290						295					300				
Phe	Arg	Val	Val	Pro	Ser	Gly	Asp	Val	Val	Arg	Phe	Pro	Asn	Ile	Thr
305					310					315					320
Asn	Leu	Cys	Pro	Phe	Gly	Glu	Val	Phe	Asn	Ala	Thr	Lys	Phe	Pro	Ser
				325					330					335	
Val	Tyr	Ala	Trp	Glu	Arg	Lys	Lys	Ile	Ser	Asn	Cys	Val	Ala	Asp	Tyr
			340					345					350		
Ser	Val	Leu	Tyr	Asn	Ser	Thr	Phe	Phe	Ser	Thr	Phe	Lys	Cys	Tyr	Gly
		355					360					365			
Val	Ser	Ala	Thr	Lys	Leu	Asn	Asp	Leu	Cys	Phe	Ser	Asn	Val	Tyr	Ala
		370				375					380				
Asp	Ser	Phe	Val	Val	Lys	Gly	Asp	Asp	Val	Arg	Gln	Ile	Ala	Pro	Gly
385					390					395					400
Gln	Thr	Gly	Val	Ile	Ala	Asp	Tyr	Asn	Tyr	Lys	Leu	Pro	Asp	Asp	Phe
			405						410					415	
Met	Gly	Cys	Val	Leu	Ala	Trp	Asn	Thr	Arg	Asn	Ile	Asp	Ala	Thr	Ser
			420					425					430		
Thr	Gly	Asn	Tyr	Asn	Tyr	Lys	Tyr	Arg	Tyr	Leu	Arg	His	Gly	Lys	Leu
		435					440					445			
Arg	Pro	Phe	Glu	Arg	Asp	Ile	Ser	Asn	Val	Pro	Phe	Ser	Pro	Asp	Gly
		450				455					460				
Lys	Pro	Cys	Thr	Pro	Pro	Ala	Leu	Asn	Cys	Tyr	Trp	Pro	Leu	Asn	Asp
465					470					475					480
Tyr	Gly	Phe	Tyr	Thr	Thr	Thr	Gly	Ile	Gly	Tyr	Gln	Pro	Tyr	Arg	Val
			485						490					495	
Val	Val	Leu	Ser	Phe	Glu	Leu	Leu	Asn	Ala	Pro	Ala	Thr	Val	Cys	Gly
			500					505					510		
Pro	Lys	Leu	Ser	Thr	Asp	Leu	Ile	Lys	Asn	Gln	Cys	Val	Asn	Phe	Asn
		515					520					525			
Phe	Asn	Gly	Leu	Thr	Gly	Thr	Gly	Val	Leu	Thr	Pro	Ser	Ser	Lys	Arg
	530					535					540				
Phe	Gln	Pro	Phe	Gln	Gln	Phe	Gly	Arg	Asp	Val	Ser	Asp	Phe	Thr	Asp
545					550					555					560
Ser	Val	Arg	Asp	Pro	Lys	Thr	Ser	Glu	Ile	Leu	Asp	Ile	Ser	Pro	Cys
			565						570					575	
Ser	Phe	Gly	Gly	Val	Ser	Val	Ile	Thr	Pro	Gly	Thr	Asn	Ala	Ser	Ser
			580					585					590		
Glu	Val	Ala	Val	Leu	Tyr	Gln	Asp	Val	Asn	Cys	Thr	Asp	Val	Ser	Thr
		595					600					605			
Ala	Ile	His	Ala	Asp	Gln	Leu	Thr	Pro	Ala	Trp	Arg	Ile	Tyr	Ser	Thr

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610	615	620
Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu		
625	630	635 640
His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile		
	645	650 655
Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys		
	660	665 670
Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala		
	675	680 685
Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile		
	690	695 700
Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys		
	705	710 715 720
Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu		
	725	730 735
Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile		
	740	745 750
Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys		
	755	760 765
Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe		
	770	775 780
Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile		
	785	790 795 800
Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met		
	805	810 815
Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile		
	820	825 830
Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr		
	835	840 845
Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala		
	850	855 860
Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe		
	865	870 875 880
Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn		
	885	890 895
Val Leu Tyr Glu Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala		
	900	905 910
Ile Ser Gln Ile Gln Glu Ser Leu Thr Thr Thr Ser Thr Ala Leu Gly		
	915	920 925
Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu		
	930	935 940
Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn		
	945	950 955 960
Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp		
	965	970 975
Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln		
	980	985 990
Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu Ala Ala		
	995	1000 1005
Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg Val Asp		
	1010	1015 1020

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Phe	Cys	Gly	Lys	Gly	Tyr	His	Leu	Met	Ser	Phe	Pro	Gln	Ala	Ala
1025						1030					1035			
Pro	His	Gly	Val	Val	Phe	Leu	His	Val	Thr	Tyr	Val	Pro	Ser	Gln
1040						1045					1050			
Glu	Arg	Asn	Phe	Thr	Thr	Ala	Pro	Ala	Ile	Cys	His	Glu	Gly	Lys
1055						1060					1065			
Ala	Tyr	Phe	Pro	Arg	Glu	Gly	Val	Phe	Val	Phe	Asn	Gly	Thr	Ser
1070						1075					1080			
Trp	Phe	Ile	Thr	Gln	Arg	Asn	Phe	Phe	Ser	Pro	Gln	Ile	Ile	Thr
1085						1090					1095			
Thr	Asp	Asn	Thr	Phe	Val	Ser	Gly	Asn	Cys	Asp	Val	Val	Ile	Gly
1100						1105					1110			
Ile	Ile	Asn	Asn	Thr	Val	Tyr	Asp	Pro	Leu	Gln	Pro	Glu	Leu	Asp
1115						1120					1125			
Ser	Phe	Lys	Glu	Glu	Leu	Asp	Lys	Tyr	Phe	Lys	Asn	His	Thr	Ser
1130						1135					1140			
Pro	Asp	Val	Asp	Leu	Gly	Asp	Ile	Ser	Gly	Ile	Asn	Ala	Ser	Val
1145						1150					1155			
Val	Asn	Ile	Gln	Lys	Glu	Ile	Asp	Arg	Leu	Asn	Glu	Val	Ala	Lys
1160						1165					1170			
Asn	Leu	Asn	Glu	Ser	Leu	Ile	Asp	Leu	Gln	Glu	Leu	Gly	Lys	Tyr
1175						1180					1185			
Glu	Gln	Tyr	Ile	Lys	Trp	Pro	Trp	Tyr	Val	Trp	Leu	Gly	Phe	Ile
1190						1195					1200			
Ala	Gly	Leu	Ile	Ala	Ile	Val	Met	Val	Thr	Ile	Leu	Leu	Cys	Cys
1205						1210					1215			
Met	Thr	Ser	Cys	Cys	Ser	Cys	Leu	Lys	Gly	Ala	Cys	Ser	Cys	Gly
1220						1225					1230			
Ser	Cys	Cys	Lys	Phe	Asp	Glu	Asp	Asp	Ser	Glu	Pro	Val	Leu	Lys
1235						1240					1245			
Gly	Val	Lys	Leu	His	Tyr	Thr								
1250						1255								

<210> SEQ ID NO 30

<211> LENGTH: 1353

<212> TYPE: PRT

<213> ORGANISM: Human coronavirus

<400> SEQUENCE: 30

Met	Phe	Leu	Ile	Leu	Leu	Ile	Ser	Leu	Pro	Thr	Ala	Phe	Ala	Val	Ile
1			5					10						15	
Gly	Asp	Leu	Lys	Cys	Thr	Ser	Asp	Asn	Ile	Asn	Asp	Lys	Asp	Thr	Gly
		20						25				30			
Pro	Pro	Pro	Ile	Ser	Thr	Asp	Thr	Val	Asp	Val	Thr	Asn	Gly	Leu	Gly
		35					40					45			
Thr	Tyr	Tyr	Val	Leu	Asp	Arg	Val	Tyr	Leu	Asn	Thr	Thr	Leu	Phe	Leu
		50				55					60				
Asn	Gly	Tyr	Tyr	Pro	Thr	Ser	Gly	Ser	Thr	Tyr	Arg	Asn	Met	Ala	Leu
65				70					75					80	
Lys	Gly	Ser	Val	Leu	Leu	Ser	Arg	Leu	Trp	Phe	Lys	Pro	Pro	Phe	Leu
			85					90						95	
Ser	Asp	Phe	Ile	Asn	Gly	Ile	Phe	Ala	Lys	Val	Lys	Asn	Thr	Lys	Val

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100							105					110				
Ile	Lys	Asp	Arg	Val	Met	Tyr	Ser	Glu	Phe	Pro	Ala	Ile	Thr	Ile	Gly	
	115						120					125				
Ser	Thr	Phe	Val	Asn	Thr	Ser	Tyr	Ser	Val	Val	Val	Gln	Pro	Arg	Thr	
	130					135					140					
Ile	Asn	Ser	Thr	Gln	Asp	Gly	Asp	Asn	Lys	Leu	Gln	Gly	Leu	Leu	Glu	
145					150					155					160	
Val	Ser	Val	Cys	Gln	Tyr	Asn	Met	Cys	Glu	Tyr	Pro	Gln	Thr	Ile	Cys	
			165						170					175		
His	Pro	Asn	Leu	Gly	Asn	His	Arg	Lys	Glu	Leu	Trp	His	Leu	Asp	Thr	
		180						185					190			
Gly	Val	Val	Ser	Cys	Leu	Tyr	Lys	Arg	Asn	Phe	Thr	Tyr	Asp	Val	Asn	
	195						200					205				
Ala	Asp	Tyr	Leu	Tyr	Phe	His	Phe	Tyr	Gln	Glu	Gly	Gly	Thr	Phe	Tyr	
	210					215					220					
Ala	Tyr	Phe	Thr	Asp	Thr	Gly	Val	Val	Thr	Lys	Phe	Leu	Phe	Asn	Val	
225				230						235					240	
Tyr	Leu	Gly	Met	Ala	Leu	Ser	His	Tyr	Tyr	Val	Met	Pro	Leu	Thr	Cys	
			245						250					255		
Asn	Ser	Lys	Leu	Thr	Leu	Glu	Tyr	Trp	Val	Thr	Pro	Leu	Thr	Ser	Arg	
		260						265					270			
Gln	Tyr	Leu	Leu	Ala	Phe	Asn	Gln	Asp	Gly	Ile	Ile	Phe	Asn	Ala	Glu	
	275					280						285				
Asp	Cys	Met	Ser	Asp	Phe	Met	Ser	Glu	Ile	Lys	Cys	Lys	Thr	Gln	Ser	
	290				295						300					
Ile	Ala	Pro	Pro	Thr	Gly	Val	Tyr	Glu	Leu	Asn	Gly	Tyr	Thr	Val	Gln	
305				310						315					320	
Pro	Ile	Ala	Asp	Val	Tyr	Arg	Arg	Lys	Pro	Asn	Leu	Pro	Asn	Cys	Asn	
		325						330						335		
Ile	Glu	Ala	Trp	Leu	Asn	Asp	Lys	Ser	Val	Pro	Ser	Pro	Leu	Asn	Trp	
	340						345						350			
Glu	Arg	Lys	Thr	Phe	Ser	Asn	Cys	Asn	Phe	Asn	Met	Ser	Ser	Leu	Met	
	355					360						365				
Ser	Phe	Ile	Gln	Ala	Asp	Ser	Phe	Thr	Cys	Asn	Asn	Ile	Asp	Ala	Ala	
	370				375						380					
Lys	Ile	Tyr	Gly	Met	Cys	Phe	Ser	Ser	Ile	Thr	Ile	Asp	Lys	Phe	Ala	
385				390						395					400	
Ile	Pro	Asn	Gly	Arg	Lys	Val	Asp	Leu	Gln	Leu	Gly	Asn	Leu	Gly	Tyr	
		405						410						415		
Leu	Gln	Ser	Phe	Asn	Tyr	Arg	Ile	Asp	Thr	Thr	Ala	Thr	Ser	Cys	Gln	
	420						425						430			
Leu	Tyr	Tyr	Asn	Leu	Pro	Ala	Ala	Asn	Val	Ser	Val	Ser	Arg	Phe	Asn	
	435					440						445				
Pro	Ser	Thr	Trp	Asn	Lys	Arg	Phe	Gly	Phe	Ile	Glu	Asp	Ser	Val	Phe	
	450					455					460					
Lys	Pro	Arg	Pro	Ala	Gly	Val	Leu	Thr	Asn	His	Asp	Val	Val	Tyr	Ala	
465				470						475					480	
Gln	His	Cys	Phe	Lys	Ala	Pro	Lys	Asn	Phe	Cys	Pro	Cys	Lys	Leu	Asn	
		485						490						495		
Gly	Ser	Cys	Val	Gly	Ser	Gly	Pro	Gly	Lys	Asn	Asn	Gly	Ile	Gly	Thr	
		500						505					510			

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Cys	Pro	Ala	Gly	Thr	Asn	Tyr	Leu	Thr	Cys	Asp	Asn	Leu	Cys	Thr	Pro
	515						520					525			
Asp	Pro	Ile	Thr	Phe	Thr	Gly	Thr	Tyr	Lys	Cys	Pro	Gln	Thr	Lys	Ser
	530					535					540				
Leu	Val	Gly	Ile	Gly	Glu	His	Cys	Ser	Gly	Leu	Ala	Val	Lys	Ser	Asp
545					550					555					560
Tyr	Cys	Gly	Gly	Asn	Ser	Cys	Thr	Cys	Arg	Pro	Gln	Ala	Phe	Leu	Gly
				565					570					575	
Trp	Ser	Ala	Asp	Ser	Cys	Leu	Gln	Gly	Asp	Lys	Cys	Asn	Ile	Phe	Ala
		580						585					590		
Asn	Phe	Ile	Leu	His	Asp	Val	Asn	Ser	Gly	Leu	Thr	Cys	Ser	Thr	Asp
	595						600					605			
Leu	Gln	Lys	Ala	Asn	Thr	Asp	Ile	Ile	Leu	Gly	Val	Cys	Val	Asn	Tyr
	610					615					620				
Asp	Leu	Tyr	Gly	Ile	Leu	Gly	Gln	Gly	Ile	Phe	Val	Glu	Val	Asn	Ala
625					630					635					640
Thr	Tyr	Tyr	Asn	Ser	Trp	Gln	Asn	Leu	Leu	Tyr	Asp	Ser	Asn	Gly	Asn
				645					650					655	
Leu	Tyr	Gly	Phe	Arg	Asp	Tyr	Ile	Ile	Asn	Arg	Thr	Phe	Met	Ile	Arg
			660					665					670		
Ser	Cys	Tyr	Ser	Gly	Arg	Val	Ser	Ala	Ala	Phe	His	Ala	Asn	Ser	Ser
		675					680					685			
Glu	Pro	Ala	Leu	Leu	Phe	Arg	Asn	Ile	Lys	Cys	Asn	Tyr	Val	Phe	Asn
	690					695					700				
Asn	Ser	Leu	Thr	Arg	Gln	Leu	Gln	Pro	Ile	Asn	Tyr	Phe	Asp	Ser	Tyr
705					710					715					720
Leu	Gly	Cys	Val	Val	Asn	Ala	Tyr	Asn	Ser	Thr	Ala	Ile	Ser	Val	Gln
				725					730					735	
Thr	Cys	Asp	Leu	Thr	Val	Gly	Ser	Gly	Tyr	Cys	Val	Asp	Tyr	Ser	Lys
			740					745					750		
Asn	Arg	Arg	Ser	Arg	Gly	Ala	Ile	Thr	Thr	Gly	Tyr	Arg	Phe	Thr	Asn
		755					760						765		
Phe	Glu	Pro	Phe	Thr	Val	Asn	Ser	Val	Asn	Asp	Ser	Leu	Glu	Pro	Val
	770					775					780				
Gly	Gly	Leu	Tyr	Glu	Ile	Gln	Ile	Pro	Ser	Glu	Phe	Thr	Ile	Gly	Asn
785					790					795					800
Met	Val	Glu	Phe	Ile	Gln	Thr	Ser	Ser	Pro	Lys	Val	Thr	Ile	Asp	Cys
				805					810					815	
Ala	Ala	Phe	Val	Cys	Gly	Asp	Tyr	Ala	Ala	Cys	Lys	Ser	Gln	Leu	Val
			820					825					830		
Glu	Tyr	Gly	Ser	Phe	Cys	Asp	Asn	Ile	Asn	Ala	Ile	Leu	Thr	Glu	Val
	835						840					845			
Asn	Glu	Leu	Leu	Asp	Thr	Thr	Gln	Leu	Gln	Val	Ala	Asn	Ser	Leu	Met
	850					855					860				
Asn	Gly	Val	Thr	Leu	Ser	Thr	Lys	Leu	Lys	Asp	Gly	Val	Asn	Phe	Asn
865					870					875					880
Val	Asp	Asp	Ile	Asn	Phe	Ser	Pro	Val	Leu	Gly	Cys	Leu	Gly	Ser	Glu
				885					890					895	
Cys	Ser	Lys	Ala	Ser	Ser	Arg	Ser	Ala	Ile	Glu	Asp	Leu	Leu	Phe	Asp
			900					905						910	

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Lys Val	Lys Leu Ser Asp Val	Gly Phe Val Glu Ala Tyr Asn Asn Cys
915	920	925
Thr Gly	Gly Ala Glu Ile Arg Asp Leu Ile Cys Val Gln Ser Tyr Lys	
930	935	940
Gly Ile	Lys Val Leu Pro Pro Leu Leu Ser Glu Asn Gln Ile Ser Gly	
945	950	955 960
Tyr Thr	Leu Ala Ala Thr Ser Ala Ser Leu Phe Pro Pro Trp Thr Ala	
	965	970 975
Ala Ala	Gly Val Pro Phe Tyr Leu Asn Val Gln Tyr Arg Ile Asn Gly	
	980	985 990
Leu Gly	Val Thr Met Asp Val Leu Ser Gln Asn Gln Lys Leu Ile Ala	
	995	1000 1005
Asn Ala	Phe Asn Asn Ala Leu Tyr Ala Ile Gln Glu Gly Phe Asp	
1010	1015	1020
Ala Thr	Asn Ser Ala Leu Val Lys Ile Gln Ala Val Val Asn Ala	
1025	1030	1035
Asn Ala	Glu Ala Leu Asn Asn Leu Leu Gln Gln Leu Ser Asn Arg	
1040	1045	1050
Phe Gly	Ala Ile Ser Ala Ser Leu Gln Glu Ile Leu Ser Arg Leu	
1055	1060	1065
Asp Ala	Leu Glu Ala Glu Ala Gln Ile Asp Arg Leu Ile Asn Gly	
1070	1075	1080
Arg Leu	Thr Ala Leu Asn Ala Tyr Val Ser Gln Gln Leu Ser Asp	
1085	1090	1095
Ser Thr	Leu Val Lys Phe Ser Ala Ala Gln Ala Met Glu Lys Val	
1100	1105	1110
Asn Glu	Cys Val Lys Ser Gln Ser Ser Arg Ile Asn Phe Cys Gly	
1115	1120	1125
Asn Gly	Asn His Ile Ile Ser Leu Val Gln Asn Ala Pro Tyr Gly	
1130	1135	1140
Leu Tyr	Phe Ile His Phe Ser Tyr Val Pro Thr Lys Tyr Val Thr	
1145	1150	1155
Ala Arg	Val Ser Pro Gly Leu Cys Ile Ala Gly Asp Arg Gly Ile	
1160	1165	1170
Ala Pro	Lys Ser Gly Tyr Phe Val Asn Val Asn Asn Thr Trp Met	
1175	1180	1185
Tyr Thr	Gly Ser Gly Tyr Tyr Tyr Pro Glu Pro Ile Thr Glu Asn	
1190	1195	1200
Asn Val	Val Val Met Ser Thr Cys Ala Val Asn Tyr Thr Lys Ala	
1205	1210	1215
Pro Tyr	Val Met Leu Asn Thr Ser Ile Pro Asn Leu Pro Asp Phe	
1220	1225	1230
Lys Glu	Glu Leu Asp Gln Trp Phe Lys Asn Gln Thr Ser Val Ala	
1235	1240	1245
Pro Asp	Leu Ser Leu Asp Tyr Ile Asn Val Thr Phe Leu Asp Leu	
1250	1255	1260
Gln Val	Glu Met Asn Arg Leu Gln Glu Ala Ile Lys Val Leu Asn	
1265	1270	1275
Gln Ser	Tyr Ile Asn Leu Lys Asp Ile Gly Thr Tyr Glu Tyr Tyr	
1280	1285	1290
Val Lys	Trp Pro Trp Tyr Val Trp Leu Leu Ile Cys Leu Ala Gly	

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1295	1300	1305
Val Ala Met Leu Val Leu Leu Phe Phe Ile Cys Cys Cys Thr Gly		
1310	1315	1320
Cys Gly Thr Ser Cys Phe Lys Lys Cys Gly Gly Cys Cys Asp Asp		
1325	1330	1335
Tyr Thr Gly Tyr Gln Glu Leu Val Ile Lys Thr Ser His Asp Asp		
1340	1345	1350

<210> SEQ ID NO 31
 <211> LENGTH: 1351
 <212> TYPE: PRT
 <213> ORGANISM: Human coronavirus

<400> SEQUENCE: 31

Met Phe Leu Ile Ile Phe Ile Leu Pro Thr Thr Leu Ala Val Ile Gly		
1	5	10 15
Asp Phe Asn Cys Thr Asn Ser Phe Ile Asn Asp Tyr Asn Lys Thr Ile		
	20	25 30
Pro Arg Ile Ser Glu Asp Val Val Asp Val Ser Leu Gly Leu Gly Thr		
	35	40 45
Tyr Tyr Val Leu Asn Arg Val Tyr Leu Asn Thr Thr Leu Leu Phe Thr		
	50	55 60
Gly Tyr Phe Pro Lys Ser Gly Ala Asn Phe Arg Asp Leu Ala Leu Lys		
65	70	75 80
Gly Ser Ile Tyr Leu Ser Thr Leu Trp Tyr Lys Pro Pro Phe Leu Ser		
	85	90 95
Asp Phe Asn Asn Gly Ile Phe Ser Lys Val Lys Asn Thr Lys Leu Tyr		
	100	105 110
Val Asn Asn Thr Leu Tyr Ser Glu Phe Ser Thr Ile Val Ile Gly Ser		
	115	120 125
Val Phe Val Asn Thr Ser Tyr Thr Ile Val Val Gln Pro His Asn Gly		
	130	135 140
Ile Leu Glu Ile Thr Ala Cys Gln Tyr Thr Met Cys Glu Tyr Pro His		
145	150	155 160
Thr Val Cys Lys Ser Lys Gly Ser Ile Arg Asn Glu Ser Trp His Ile		
	165	170 175
Asp Ser Ser Glu Pro Leu Cys Leu Phe Lys Lys Asn Phe Thr Tyr Asn		
	180	185 190
Val Ser Ala Asp Trp Leu Tyr Phe His Phe Tyr Gln Glu Arg Gly Val		
	195	200 205
Phe Tyr Ala Tyr Tyr Ala Asp Val Gly Met Pro Thr Thr Phe Leu Phe		
210	215	220
Ser Leu Tyr Leu Gly Thr Ile Leu Ser His Tyr Tyr Val Met Pro Leu		
225	230	235 240
Thr Cys Asn Ala Ile Ser Ser Asn Thr Asp Asn Glu Thr Leu Glu Tyr		
	245	250 255
Trp Val Thr Pro Leu Ser Arg Arg Gln Tyr Leu Leu Asn Phe Asp Glu		
	260	265 270
His Gly Val Ile Thr Asn Ala Val Asp Cys Ser Ser Ser Phe Leu Ser		
	275	280 285
Glu Ile Gln Cys Lys Thr Gln Ser Phe Ala Pro Asn Thr Gly Val Tyr		
290	295	300

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Asp	Leu	Ser	Gly	Phe	Thr	Val	Lys	Pro	Val	Ala	Thr	Val	Tyr	Arg	Arg		
305					310					315					320		
Ile	Pro	Asn	Leu	Pro	Asp	Cys	Asp	Ile	Asp	Asn	Trp	Leu	Asn	Asn	Val		
			325						330					335			
Ser	Val	Pro	Ser	Pro	Leu	Asn	Trp	Glu	Arg	Arg	Ile	Phe	Ser	Asn	Cys		
			340					345					350				
Asn	Phe	Asn	Leu	Ser	Thr	Leu	Leu	Arg	Leu	Val	His	Val	Asp	Ser	Phe		
		355					360					365					
Ser	Cys	Asn	Asn	Leu	Asp	Lys	Ser	Lys	Ile	Phe	Gly	Ser	Cys	Phe	Asn		
	370					375					380						
Ser	Ile	Thr	Val	Asp	Lys	Phe	Ala	Ile	Pro	Asn	Arg	Arg	Arg	Asp	Asp		
385					390					395					400		
Leu	Gln	Leu	Gly	Ser	Ser	Gly	Phe	Leu	Gln	Ser	Ser	Asn	Tyr	Lys	Ile		
			405						410					415			
Asp	Ile	Ser	Ser	Ser	Ser	Cys	Gln	Leu	Tyr	Tyr	Ser	Leu	Pro	Leu	Val		
			420					425					430				
Asn	Val	Thr	Ile	Asn	Asn	Phe	Asn	Pro	Ser	Ser	Trp	Asn	Arg	Arg	Tyr		
		435					440					445					
Gly	Phe	Gly	Ser	Phe	Asn	Leu	Ser	Ser	Tyr	Asp	Val	Val	Tyr	Ser	Asp		
	450					455					460						
His	Cys	Phe	Ser	Val	Asn	Ser	Asp	Phe	Cys	Pro	Cys	Ala	Asp	Pro	Ser		
465					470					475					480		
Val	Val	Asn	Ser	Cys	Ala	Lys	Ser	Lys	Pro	Pro	Ser	Ala	Ile	Cys	Pro		
			485						490					495			
Ala	Gly	Thr	Lys	Tyr	Arg	His	Cys	Asp	Leu	Asp	Thr	Thr	Leu	Tyr	Val		
			500					505					510				
Lys	Asn	Trp	Cys	Arg	Cys	Ser	Cys	Leu	Pro	Asp	Pro	Ile	Ser	Thr	Tyr		
		515					520					525					
Ser	Pro	Asn	Thr	Cys	Pro	Gln	Lys	Lys	Val	Val	Val	Gly	Ile	Gly	Glu		
	530					535						540					
His	Cys	Pro	Gly	Leu	Gly	Ile	Asn	Glu	Glu	Lys	Cys	Gly	Thr	Gln	Leu		
545					550					555					560		
Asn	His	Ser	Ser	Cys	Phe	Cys	Ser	Pro	Asp	Ala	Phe	Leu	Gly	Trp	Ser		
			565						570					575			
Phe	Asp	Ser	Cys	Ile	Ser	Asn	Asn	Arg	Cys	Asn	Ile	Phe	Ser	Asn	Phe		
			580					585					590				
Ile	Phe	Asn	Gly	Ile	Asn	Ser	Gly	Thr	Thr	Cys	Ser	Asn	Asp	Leu	Leu		
		595					600					605					
Tyr	Ser	Asn	Thr	Glu	Ile	Ser	Thr	Gly	Val	Cys	Val	Asn	Tyr	Asp	Leu		
	610					615						620					
Tyr	Gly	Ile	Thr	Gly	Gln	Gly	Ile	Phe	Lys	Glu	Val	Ser	Ala	Ala	Tyr		
625					630					635					640		
Tyr	Asn	Asn	Trp	Gln	Asn	Leu	Leu	Tyr	Asp	Ser	Asn	Gly	Asn	Ile	Ile		
			645						650					655			
Gly	Phe	Lys	Asp	Phe	Leu	Thr	Asn	Lys	Thr	Tyr	Thr	Ile	Leu	Pro	Cys		
			660					665					670				
Tyr	Ser	Gly	Arg	Val	Ser	Ala	Ala	Phe	Tyr	Gln	Asn	Ser	Ser	Ser	Pro		
		675					680					685					
Ala	Leu	Leu	Tyr	Arg	Asn	Leu	Lys	Cys	Ser	Tyr	Val	Leu	Asn	Asn	Ile		
	690					695					700						
Ser	Phe	Ile	Ser	Gln	Pro	Phe	Tyr	Phe	Asp	Ser	Tyr	Leu	Gly	Cys	Val		

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705	710	715	720
Leu Asn Ala Val Asn Leu Thr Ser Tyr Ser Val Ser Ser Cys Asp Leu	725	730	735
Arg Met Gly Ser Gly Phe Cys Ile Asp Tyr Ala Leu Pro Ser Ser Arg	740	745	750
Arg Lys Arg Arg Gly Ile Ser Ser Pro Tyr Arg Phe Val Thr Phe Glu	755	760	765
Pro Phe Asn Val Ser Phe Val Asn Asp Ser Val Glu Thr Val Gly Gly	770	775	780
Leu Phe Glu Ile Gln Ile Pro Thr Asn Phe Thr Ile Ala Gly His Glu	785	790	795
Glu Phe Ile Gln Thr Ser Ser Pro Lys Val Thr Ile Asp Cys Ser Ala	805	810	815
Phe Val Cys Ser Asn Tyr Ala Ala Cys His Asp Leu Leu Ser Glu Tyr	820	825	830
Gly Thr Phe Cys Asp Asn Ile Asn Ser Ile Leu Asn Glu Val Asn Asp	835	840	845
Leu Leu Asp Ile Thr Gln Leu Gln Val Ala Asn Ala Leu Met Gln Gly	850	855	860
Val Thr Leu Ser Ser Asn Leu Asn Thr Asn Leu His Ser Asp Val Asp	865	870	875
Asn Ile Asp Phe Lys Ser Leu Leu Gly Cys Leu Gly Ser Gln Cys Gly	885	890	895
Ser Ser Ser Arg Ser Leu Leu Glu Asp Leu Leu Phe Asn Lys Val Lys	900	905	910
Leu Ser Asp Val Gly Phe Val Glu Ala Tyr Asn Asn Cys Thr Gly Gly	915	920	925
Ser Glu Ile Arg Asp Leu Leu Cys Val Gln Ser Phe Asn Gly Ile Lys	930	935	940
Val Leu Pro Pro Ile Leu Ser Glu Thr Gln Ile Ser Gly Tyr Thr Thr	945	950	955
Ala Ala Thr Val Ala Ala Met Phe Pro Pro Trp Ser Ala Ala Ala Gly	965	970	975
Val Pro Phe Ser Leu Asn Val Gln Tyr Arg Ile Asn Gly Leu Gly Val	980	985	990
Thr Met Asp Val Leu Asn Lys Asn Gln Lys Leu Ile Ala Asn Ala Phe	995	1000	1005
Asn Lys Ala Leu Leu Ser Ile Gln Asn Gly Phe Thr Ala Thr Asn	1010	1015	1020
Ser Ala Leu Ala Lys Ile Gln Ser Val Val Asn Ala Asn Ala Gln	1025	1030	1035
Ala Leu Asn Ser Leu Leu Gln Gln Leu Phe Asn Lys Phe Gly Ala	1040	1045	1050
Ile Ser Ser Ser Leu Gln Glu Ile Leu Ser Arg Leu Asp Asn Leu	1055	1060	1065
Glu Ala Gln Val Gln Ile Asp Arg Leu Ile Asn Gly Arg Leu Thr	1070	1075	1080
Ala Leu Asn Ala Tyr Val Ser Gln Gln Leu Ser Asp Ile Thr Leu	1085	1090	1095
Ile Lys Ala Gly Ala Ser Arg Ala Ile Glu Lys Val Asn Glu Cys	1100	1105	1110

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Val	Lys	Ser	Gln	Ser	Pro	Arg	Ile	Asn	Phe	Cys	Gly	Asn	Gly	Asn
1115						1120					1125			
His	Ile	Leu	Ser	Leu	Val	Gln	Asn	Ala	Pro	Tyr	Gly	Leu	Leu	Phe
1130						1135					1140			
Ile	His	Phe	Ser	Tyr	Lys	Pro	Thr	Ser	Phe	Lys	Thr	Val	Leu	Val
1145						1150					1155			
Ser	Pro	Gly	Leu	Cys	Leu	Ser	Gly	Asp	Arg	Gly	Ile	Ala	Pro	Lys
1160						1165					1170			
Gln	Gly	Tyr	Phe	Ile	Lys	Gln	Asn	Asp	Ser	Trp	Met	Phe	Thr	Gly
1175						1180					1185			
Ser	Ser	Tyr	Tyr	Tyr	Pro	Glu	Pro	Ile	Ser	Asp	Lys	Asn	Val	Val
1190						1195					1200			
Phe	Met	Asn	Ser	Cys	Ser	Val	Asn	Phe	Thr	Lys	Ala	Pro	Phe	Ile
1205						1210					1215			
Tyr	Leu	Asn	Asn	Ser	Ile	Pro	Asn	Leu	Ser	Asp	Phe	Glu	Ala	Glu
1220						1225					1230			
Leu	Ser	Leu	Trp	Phe	Lys	Asn	His	Thr	Ser	Ile	Ala	Pro	Asn	Leu
1235						1240					1245			
Thr	Phe	Asn	Ser	His	Ile	Asn	Ala	Thr	Phe	Leu	Asp	Leu	Tyr	Tyr
1250						1255					1260			
Glu	Met	Asn	Val	Ile	Gln	Glu	Ser	Ile	Lys	Ser	Leu	Asn	Ser	Ser
1265						1270					1275			
Phe	Ile	Asn	Leu	Lys	Glu	Ile	Gly	Thr	Tyr	Glu	Met	Tyr	Val	Lys
1280						1285					1290			
Trp	Pro	Trp	Tyr	Ile	Trp	Leu	Leu	Ile	Val	Ile	Leu	Phe	Ile	Ile
1295						1300					1305			
Phe	Leu	Met	Ile	Leu	Phe	Phe	Ile	Cys	Cys	Cys	Thr	Gly	Cys	Gly
1310						1315					1320			
Ser	Ala	Cys	Phe	Ser	Lys	Cys	His	Asn	Cys	Cys	Asp	Glu	Tyr	Gly
1325						1330					1335			
Gly	His	Asn	Asp	Phe	Val	Ile	Lys	Ala	Ser	His	Asp	Asp		
1340						1345					1350			

<210> SEQ ID NO 32

<211> LENGTH: 526

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 32

Met	Phe	Ile	Phe	Leu	Phe	Leu	Thr	Leu	Thr	Ser	Gly	Ser	Asp	Leu
1				5				10				15		
Asp	Arg	Ala	Leu	Ser	Gly	Ile	Ala	Ala	Glu	Gln	Asp	Arg	Asn	Thr
			20					25				30		
Glu	Val	Phe	Ala	Gln	Val	Lys	Gln	Met	Tyr	Lys	Thr	Pro	Thr	Leu
		35				40					45			
Tyr	Phe	Gly	Gly	Phe	Asn	Phe	Ser	Gln	Ile	Leu	Pro	Asp	Pro	Leu
	50				55					60				
Pro	Thr	Lys	Arg	Ser	Phe	Ile	Glu	Asp	Leu	Leu	Phe	Asn	Lys	Val
65					70					75			80	
Leu	Ala	Asp	Ala	Gly	Phe	Met	Lys	Gln	Tyr	Gly	Glu	Cys	Leu	Gly
			85					90					95	

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Ile	Asn	Ala	Arg	Asp	Leu	Ile	Cys	Ala	Gln	Lys	Phe	Asn	Gly	Leu	Thr	100	105	110
Val	Leu	Pro	Pro	Leu	Leu	Thr	Asp	Asp	Met	Ile	Ala	Ala	Tyr	Thr	Ala	115	120	125
Ala	Leu	Val	Ser	Gly	Thr	Ala	Thr	Ala	Gly	Trp	Thr	Phe	Gly	Ala	Gly	130	135	140
Ala	Ala	Leu	Gln	Ile	Pro	Phe	Ala	Met	Gln	Met	Ala	Tyr	Arg	Phe	Asn	145	150	155
Gly	Ile	Gly	Val	Thr	Gln	Asn	Val	Leu	Tyr	Glu	Asn	Gln	Lys	Gln	Ile	165	170	175
Ala	Asn	Gln	Phe	Asn	Lys	Ala	Ile	Ser	Gln	Ile	Gln	Glu	Ser	Leu	Thr	180	185	190
Thr	Thr	Ser	Thr	Ala	Leu	Gly	Lys	Leu	Gln	Asp	Val	Val	Asn	Gln	Asn	195	200	205
Ala	Gln	Ala	Leu	Asn	Thr	Leu	Val	Lys	Gln	Leu	Ser	Ser	Asn	Phe	Gly	210	215	220
Ala	Ile	Ser	Ser	Val	Leu	Asn	Asp	Ile	Leu	Ser	Arg	Leu	Asp	Lys	Val	225	230	235
Glu	Ala	Glu	Val	Gln	Ile	Asp	Arg	Leu	Ile	Thr	Gly	Arg	Leu	Gln	Ser	245	250	255
Leu	Gln	Thr	Tyr	Val	Thr	Gln	Gln	Leu	Ile	Arg	Ala	Ala	Glu	Ile	Arg	260	265	270
Ala	Ser	Ala	Asn	Leu	Ala	Ala	Thr	Lys	Met	Ser	Glu	Cys	Val	Leu	Gly	275	280	285
Gln	Ser	Lys	Arg	Val	Asp	Phe	Cys	Gly	Lys	Gly	Tyr	His	Leu	Met	Ser	290	295	300
Phe	Pro	Gln	Ala	Ala	Pro	His	Gly	Val	Val	Phe	Leu	His	Val	Thr	Tyr	305	310	315
Val	Pro	Ser	Gln	Glu	Arg	Asn	Phe	Thr	Thr	Ala	Pro	Ala	Ile	Cys	His	325	330	335
Glu	Gly	Lys	Ala	Tyr	Phe	Pro	Arg	Glu	Gly	Val	Phe	Val	Phe	Asn	Gly	340	345	350
Thr	Ser	Trp	Phe	Ile	Thr	Gln	Arg	Asn	Phe	Phe	Ser	Pro	Gln	Ile	Ile	355	360	365
Thr	Thr	Asp	Asn	Thr	Phe	Val	Ser	Gly	Asn	Cys	Asp	Val	Val	Ile	Gly	370	375	380
Ile	Ile	Asn	Asn	Thr	Val	Tyr	Asp	Pro	Leu	Gln	Pro	Glu	Leu	Asp	Ser	385	390	395
Phe	Lys	Glu	Glu	Leu	Asp	Lys	Tyr	Phe	Lys	Asn	His	Thr	Ser	Pro	Asp	405	410	415
Val	Asp	Leu	Gly	Asp	Ile	Ser	Gly	Ile	Asn	Ala	Ser	Val	Val	Asn	Ile	420	425	430
Gln	Lys	Glu	Ile	Asp	Arg	Leu	Asn	Glu	Val	Ala	Lys	Asn	Leu	Asn	Glu	435	440	445
Ser	Leu	Ile	Asp	Leu	Gln	Glu	Leu	Gly	Lys	Tyr	Glu	Gln	Tyr	Ile	Lys	450	455	460
Trp	Pro	Trp	Tyr	Val	Trp	Leu	Gly	Phe	Ile	Ala	Gly	Leu	Ile	Ala	Ile	465	470	475
Val	Met	Val	Thr	Ile	Leu	Leu	Cys	Cys	Met	Thr	Ser	Cys	Cys	Ser	Cys	485	490	495

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Leu Lys Gly Ala Cys Ser Cys Gly Ser Cys Cys Lys Phe Asp Glu Asp
 500 505 510

Asp Ser Glu Pro Val Leu Lys Gly Val Lys Leu His Tyr Thr
 515 520 525

<210> SEQ ID NO 33
 <211> LENGTH: 588
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 33

Met Ile His Ser Val Phe Leu Leu Met Phe Leu Leu Thr Pro Thr Glu
 1 5 10 15

Ser Asp Cys Lys Leu Pro Leu Gly Gln Ser Leu Cys Ala Leu Pro Asp
 20 25 30

Thr Pro Ser Thr Leu Thr Pro Arg Ser Val Arg Ser Val Pro Gly Glu
 35 40 45

Met Arg Leu Ala Ser Ile Ala Phe Asn His Pro Ile Gln Val Asp Gln
 50 55 60

Leu Asn Ser Ser Tyr Phe Lys Leu Ser Ile Pro Thr Asn Phe Ser Phe
 65 70 75 80

Gly Val Thr Gln Glu Tyr Ile Gln Thr Thr Ile Gln Lys Val Thr Val
 85 90 95

Asp Cys Lys Gln Tyr Val Cys Asn Gly Phe Gln Lys Cys Glu Gln Leu
 100 105 110

Leu Arg Glu Tyr Gly Gln Phe Cys Ser Lys Ile Asn Gln Ala Leu His
 115 120 125

Gly Ala Asn Leu Arg Gln Asp Asp Ser Val Arg Asn Leu Phe Ala Ser
 130 135 140

Val Lys Ser Ser Gln Ser Ser Pro Ile Ile Pro Gly Phe Gly Gly Asp
 145 150 155 160

Phe Asn Leu Thr Leu Leu Glu Pro Val Ser Ile Ser Thr Gly Ser Arg
 165 170 175

Ser Ala Arg Ser Ala Ile Glu Asp Leu Leu Phe Asp Lys Val Thr Ile
 180 185 190

Ala Asp Pro Gly Tyr Met Gln Gly Tyr Asp Asp Cys Met Gln Gln Gly
 195 200 205

Pro Ala Ser Ala Arg Asp Leu Ile Cys Ala Gln Tyr Val Ala Gly Tyr
 210 215 220

Lys Val Leu Pro Pro Leu Met Asp Val Asn Met Glu Ala Ala Tyr Thr
 225 230 235 240

Ser Ser Leu Leu Gly Ser Ile Ala Gly Val Gly Trp Thr Ala Gly Leu
 245 250 255

Ser Ser Phe Ala Ala Ile Pro Phe Ala Gln Ser Ile Phe Tyr Arg Leu
 260 265 270

Asn Gly Val Gly Ile Thr Gln Gln Val Leu Ser Glu Asn Gln Lys Leu
 275 280 285

Ile Ala Asn Lys Phe Asn Gln Ala Leu Gly Ala Met Gln Thr Gly Phe
 290 295 300

Thr Thr Thr Asn Glu Ala Phe Gln Lys Val Gln Asp Ala Val Asn Asn
 305 310 315 320

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Asn	Ala	Gln	Ala	Leu	Ser	Lys	Leu	Ala	Ser	Glu	Leu	Ser	Asn	Thr	Phe
				325					330					335	
Gly	Ala	Ile	Ser	Ala	Ser	Ile	Gly	Asp	Ile	Ile	Gln	Arg	Leu	Asp	Val
			340					345					350		
Leu	Glu	Gln	Asp	Ala	Gln	Ile	Asp	Arg	Leu	Ile	Asn	Gly	Arg	Leu	Thr
		355					360					365			
Thr	Leu	Asn	Ala	Phe	Val	Ala	Gln	Gln	Leu	Val	Arg	Ser	Glu	Ser	Ala
	370					375					380				
Ala	Leu	Ser	Ala	Gln	Leu	Ala	Lys	Asp	Lys	Val	Asn	Glu	Cys	Val	Lys
	385				390					395					400
Ala	Gln	Ser	Lys	Arg	Ser	Gly	Phe	Cys	Gly	Gln	Gly	Thr	His	Ile	Val
			405						410					415	
Ser	Phe	Val	Val	Asn	Ala	Pro	Asn	Gly	Leu	Tyr	Phe	Met	His	Val	Gly
		420						425					430		
Tyr	Tyr	Pro	Ser	Asn	His	Ile	Glu	Val	Val	Ser	Ala	Tyr	Gly	Leu	Cys
		435					440					445			
Asp	Ala	Ala	Asn	Pro	Thr	Asn	Cys	Ile	Ala	Pro	Val	Asn	Gly	Tyr	Phe
	450					455					460				
Ile	Lys	Thr	Asn	Asn	Thr	Arg	Ile	Val	Asp	Glu	Trp	Ser	Tyr	Thr	Gly
	465				470					475					480
Ser	Ser	Phe	Tyr	Ala	Pro	Glu	Pro	Ile	Thr	Ser	Leu	Asn	Thr	Lys	Tyr
			485					490						495	
Val	Ala	Pro	Gln	Val	Thr	Tyr	Gln	Asn	Ile	Ser	Thr	Asn	Leu	Pro	Pro
			500					505					510		
Pro	Leu	Leu	Gly	Asn	Ser	Thr	Gly	Ile	Asp	Phe	Gln	Asp	Glu	Leu	Asp
		515					520					525			
Glu	Phe	Phe	Lys	Asn	Val	Ser	Thr	Ser	Ile	Pro	Asn	Phe	Gly	Ser	Leu
	530					535					540				
Thr	Gln	Ile	Asn	Thr	Thr	Leu	Leu	Asp	Leu	Thr	Tyr	Glu	Met	Leu	Ser
	545				550					555					560
Leu	Gln	Gln	Val	Val	Lys	Ala	Leu	Asn	Glu	Ser	Tyr	Ile	Asp	Leu	Lys
			565						570					575	
Glu	Leu	Gly	Asn	Tyr	Thr	Tyr	Tyr	Asn	Lys	Trp	Pro				
		580						585							

<210> SEQ ID NO 34

<211> LENGTH: 526

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 34

Met	Phe	Ile	Phe	Leu	Leu	Phe	Leu	Thr	Leu	Thr	Ser	Gly	Ser	Asp	Leu
1				5					10					15	
Asp	Arg	Ala	Leu	Ser	Gly	Ile	Ala	Ala	Glu	Gln	Asp	Arg	Asn	Thr	Arg
		20						25					30		
Glu	Val	Phe	Ala	Gln	Val	Lys	Gln	Met	Tyr	Lys	Thr	Pro	Thr	Leu	Lys
		35					40					45			
Tyr	Phe	Gly	Gly	Phe	Asn	Phe	Ser	Gln	Ile	Leu	Pro	Asp	Pro	Leu	Lys
	50				55						60				
Pro	Thr	Lys	Arg	Ser	Phe	Ile	Glu	Asp	Leu	Leu	Phe	Asn	Lys	Val	Thr
	65				70					75				80	

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Leu	Ala	Asp	Ala	Gly	Phe	Met	Lys	Gln	Tyr	Gly	Glu	Cys	Leu	Gly	Asp	85	90	95
Ile	Asn	Ala	Arg	Asp	Leu	Ile	Cys	Ala	Gln	Lys	Phe	Asn	Gly	Leu	Thr	100	105	110
Val	Leu	Pro	Pro	Leu	Leu	Thr	Asp	Asp	Met	Ile	Ala	Ala	Tyr	Thr	Ala	115	120	125
Ala	Leu	Val	Ser	Gly	Thr	Ala	Thr	Ala	Gly	Trp	Thr	Phe	Gly	Ala	Gly	130	135	140
Ala	Ala	Leu	Gln	Ile	Pro	Phe	Ala	Met	Gln	Met	Ala	Tyr	Arg	Phe	Asn	145	150	155
Gly	Ile	Gly	Val	Thr	Gln	Asn	Val	Leu	Tyr	Glu	Asn	Gln	Lys	Gln	Ile	165	170	175
Ala	Asn	Gln	Phe	Asn	Lys	Ala	Ile	Ser	Gln	Ile	Gln	Glu	Ser	Leu	Thr	180	185	190
Thr	Thr	Ser	Thr	Ala	Leu	Gly	Lys	Leu	Gln	Asp	Val	Val	Asn	Gln	Asn	195	200	205
Ala	Gln	Ala	Leu	Asn	Thr	Leu	Val	Lys	Gln	Leu	Ser	Ser	Asn	Phe	Gly	210	215	220
Ala	Ile	Ser	Ser	Val	Leu	Asn	Asp	Ile	Leu	Ser	Arg	Leu	Asp	Lys	Val	225	230	235
Glu	Ala	Glu	Val	Gln	Ile	Asp	Arg	Leu	Ile	Thr	Gly	Arg	Leu	Gln	Ser	245	250	255
Leu	Gln	Thr	Tyr	Val	Thr	Gln	Gln	Leu	Ile	Arg	Ala	Ala	Glu	Ile	Arg	260	265	270
Ala	Ser	Ala	Asn	Leu	Ala	Ala	Thr	Lys	Met	Ser	Glu	Cys	Val	Leu	Gly	275	280	285
Gln	Ser	Lys	Arg	Val	Asp	Phe	Cys	Gly	Lys	Gly	Tyr	His	Leu	Met	Ser	290	295	300
Phe	Pro	Gln	Ala	Ala	Pro	His	Gly	Val	Val	Phe	Leu	His	Val	Thr	Tyr	305	310	315
Val	Pro	Ser	Gln	Glu	Arg	Asn	Phe	Thr	Thr	Ala	Pro	Ala	Ile	Cys	His	325	330	335
Glu	Gly	Lys	Ala	Tyr	Phe	Pro	Arg	Glu	Gly	Val	Phe	Val	Phe	Asn	Gly	340	345	350
Thr	Ser	Trp	Phe	Ile	Thr	Gln	Arg	Asn	Phe	Phe	Ser	Pro	Gln	Ile	Ile	355	360	365
Thr	Thr	Asp	Asn	Thr	Phe	Val	Ser	Gly	Asn	Cys	Asp	Val	Val	Ile	Gly	370	375	380
Ile	Ile	Asn	Asn	Thr	Val	Tyr	Asp	Pro	Leu	Gln	Pro	Glu	Leu	Asp	Ser	385	390	395
Phe	Lys	Glu	Glu	Leu	Asp	Lys	Tyr	Phe	Lys	Asn	His	Thr	Ser	Pro	Asp	405	410	415
Val	Asp	Leu	Gly	Asp	Ile	Ser	Gly	Ile	Asn	Ala	Ser	Val	Val	Asn	Ile	420	425	430
Gln	Lys	Glu	Ile	Asp	Arg	Leu	Asn	Glu	Val	Ala	Lys	Asn	Leu	Asn	Glu	435	440	445
Ser	Leu	Ile	Asp	Leu	Gln	Glu	Leu	Gly	Lys	Tyr	Glu	Gln	Tyr	Ile	Lys	450	455	460
Trp	Pro	Trp	Tyr	Val	Trp	Leu	Gly	Phe	Ile	Ala	Gly	Leu	Ile	Ala	Ile	465	470	475
Val	Met	Val	Thr	Ile	Leu	Leu	Cys	Cys	Met	Thr	Ser	Cys	Cys	Ser	Cys	480		

-continued

485				490				495							
Leu	Lys	Gly	Ala	Cys	Ser	Cys	Gly	Ser	Cys	Cys	Lys	Phe	Asp	Glu	Asp
			500				505								510
Asp	Ser	Glu	Pro	Val	Leu	Lys	Gly	Val	Lys	Leu	His	Tyr	Thr		
			515				520								525

<210> SEQ ID NO 35
 <211> LENGTH: 1864
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 35

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tcaagctttt ggaccctcgt acagaagcta atacgactca ctataggga atagagaga      60
aaagaagagt aagaagaaat ataagagcca ccatgggtct caaggatgaac gtctctgccg    120
tattcatggc agtactgtta actctccaaa caccgcgcgg tcaaattcat tggggcaatc    180
tctctaagat aggggtagta ggaataggaa gtgcaagcta caaagttatg actcgttcca    240
gccatcaatc attagtcata aaattaatgc ccaatataac tctcctcaat aactgcacga    300
gggtagagat tgcagaatac aggagactac taagaacagt tttggaacca attagggatg    360
cacttaatgc aatgacccag aacataaggc cggttcagag cgtagcttca agtaggagac    420
acaagagatt tgcgggagta gtctctggcag gtgcggccct aggtgttgcc acagctgctc    480
agataacagc cggcattgca cttcacccgt ccatgctgaa ctctcaggcc atcgacaatc    540
tgagagcgag cctgaaaact actaatcagg caattgaggc aatcagacaa gcagggcagg    600
agatgatatt ggctgttcag ggtgtccaag actacatcaa taatgagctg ataccgtcta    660
tgaaccagct atcttgtgat ctaatcggtc agaagctcgg gctcaaattg cttagatact    720
atacagaaat cctgtcatta tttggcccca gcctacggga ccccatatct gcggagatat    780
ctatccaggc tttgagttat gcacttggag gagatatcaa taagggtgta gaaaagctcg    840
gatacagtgg aggcgattta ctaggcatct tagagagcag aggaataaag gctcggataa    900
ctcacgtcga cacagagtcc tacttcatag tcctcagtat agcctatccg acgctgtccg    960
agattaaggg ggtgatgtgc caccggctag aggggggtctc gtacaacata ggctctcaag   1020
agtgtgtatac cactgtgccc aagtatgttg caaccaaggc gtaccttata tcgaattttg   1080
atgagtcatac atgtactttc atgccagagg ggactgtgtg cagccaaaat gccttgtaac   1140
cgatgagtcc tctgctccaa gaatgcctcc gggggtccac caagtctgtg gctcgtacac   1200
tcgtatccgg gtcttttggg aaccggttca ttttatcaca agggaaccta atagccaatt   1260
gtgcatcaat tctttgtaag tgttacacaa caggtacgat tattaatcaa gaccctgaca   1320
agatcctaac atacattgct gccgatcgct gcccggtagt cgaggatgaac ggcgtgacca   1380
tccaagtcgg gagcaggagg tatccagacg ctgtgtactt gcacagaatt gacctcggtc   1440
ctcccatatc attggagagg ttggacgtag ggacaaatct ggggaatgca attgccaaat   1500
tggaggatgc caaggaattg ttggaatcat cggaccagat attgagaagt atgaaaggtt   1560
tatcgagcac tagcatagtc tacatcctga ttgcagtgtg tcttgagggg ttgataggga   1620
tccccacttt aatatgttgc tgcagggggc gttgtaacaa aaaggagaaa caagttggta   1680
tgtcaagacc aggcctaagc cctgacctta caggaacatc aaaatcctat gtaagatcgc   1740
  
```


-continued

tttgatgata ataggctgga gcctcgggtgg ccaagcttct tgcccccttg gcctccccc	1800
agccccctct ccccttcctg cacccggtacc cccgtggtct ttgaataaag tctgagtggg	1860
cggc	1864

<210> SEQ ID NO 36
 <211> LENGTH: 1653
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 36

atgggtctca aggtgaacgt ctctgccgta ttcattggcag tactgttaac tctccaaaca	60
cccgccggtc aaattcattg gggcaatctc tctaagatag gggtagtagg aataggaagt	120
gcaagctaca aagttatgac tcgttccagc catcaatcat tagtcataaa attaatgccc	180
aatataactc tctcaataa ctgcacgagg gtagagattg cagaatacag gagactacta	240
agaacagttt tggaaccaat tagggatgca cttaatgcaa tgaccagaa cataaggccg	300
gttcagagcg tagcttcaag taggagacac aagagatttg cgggagtagt cctggcagggt	360
gcgcccttag gtgttgccac agctgctcag ataacagccg gcattgcact tcaccgggcc	420
atgctgaact ctccagccat cgacaatctg agagcgagcc tggaaactac taatcaggca	480
attgaggcaa tcagacaagc agggcaggag atgatattgg ctgttcaggg tgtccaagac	540
tacatcaata atgagctgat accgtctatg aaccagctat cttgtgatct aatcggtcag	600
aagctcgggc tcaaattgct tagatactat acagaaatcc tgtcattatt tggccccagc	660
ctacgggacc ccatatctgc ggagatatct atccaggctt tgagtattgc acttgaggga	720
gatatcaata aggtgttaga aaagctcgga tacagtggag gcgatttact aggcattctta	780
gagagcagag gaataaaggc tcggataact cacgtcgaca cagagtccta ctccatagtc	840
ctcagtatag cctatccgac gctgtccgag attaaggggg tgattgtcca ccggctagag	900
gggggtctctg acaacatagg ctctcaagag tgggtatacca ctgtgcccga gtatgttgca	960
acccaagggt accttatctc gaattttgat gagtcacat gtactttcat gccagagggg	1020
actgtgtgca gccaaaatgc cttgtaccgg atgagtcctc tgctccaaga atgcctccgg	1080
gggtccacca agtcctgtgc tcgtacactc gtatccgggt cttttgggaa ccgggttcatt	1140
ttatcacaag ggaacctaat agccaattgt gcatcaattc tttgtaagtg ttacacaaca	1200
ggtagcatta ttaatcaaga ccttgacaag atcctaact acattgtctc cgatcgctgc	1260
ccggtagtcg aggtgaacgg cgtgaccatc caagtcggga gcaggaggta tccagacgct	1320
gtgtacttgc acagaattga cctcggtcct cccatatcat tggagagggt ggacgtaggg	1380
acaaatctgg ggaatgcaat tgccaaattg gaggatgcca aggaattgtt ggaatcatcg	1440
gaccagatat tgagaagtat gaaagggtta tcgagcacta gcatagtcta catcctgatt	1500
gcagtgtgtc ttggagggtt gatagggatc cccactttaa tatgttgctg cagggggcgt	1560
tgtaacaaaa agggagaaca agttggtatg tcaagaccag gcctaaagcc tgaccttaca	1620
ggaacatcaa aatcctatgt aagatcgctt tga	1653

<210> SEQ ID NO 37
 <211> LENGTH: 1925
 <212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 37

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gtgaacgtct ctgccgtatt catggcagta ctgttaactc tccaaacacc cgccgggtcaa      120
attcattggg gcaatctctc taagataggg gtagtaggaa taggaagtgc aagctacaaa      180
gttatgactc gttccagcca tcaatcatta gtcataaaat taatgcccaa tataactctc      240
ctcaataact gcacgagggg agagattgca gaatacagga gactactaag aacagttttg      300
gaaccaatta gggatgcact taatgcaatg acccagaaca taaggccggg tcagagcgta      360
gcttcaagta ggagacacaa gagatttgcg ggagtagtcc tggcaggtgc ggccctaggt      420
gttgccacag ctgctcagat aacagccggc attgcacttc accgggtccat gctgaactct      480
caggccatcg acaatctgag agcagcctg gaaactacta atcaggcaat tgaggcaatc      540
agacaagcag ggcaggagat gatattggct gttcagggtg tccaagacta catcaataat      600
gagctgatac cgtctatgaa ccagctatct tgtgatctaa tcggtcagaa gctcgggctc      660
aaattgctta gatactatac agaaatcctg tcattatttg gcccagcct acggggacccc      720
atatctgcgg agatatctat ccaggctttg agttatgcac ttggaggaga tatcaataag      780
gtgttagaaa agctcggata cagtggaggc gatttactag gcatcttaga gagcagagga      840
ataaaggctc ggataactca cgtcgacaca gagtcctact tcatagtcct cagtatagcc      900
tatccgacgc tgtccgagat taaggggggtg attgtccacc ggctagaggg ggtctcgtac      960
aacataggct ctcaagagtg gtataccact gtgcccaagt atgttgcaac ccaagggtag      1020
cttatctcga attttgatga gtcacatgtg actttcatgc cagaggggac tgtgtgcagc      1080
caaaatgcct tgtaccgat gagtcctctg ctccaagaat gcctccgggg gtccaccaag      1140
tcctgtgctc gtacactcgt atccgggtct tttgggaacc gggttcatttt atcacaaggg      1200
aacctaatag ccaattgtgc atcaattctt tgtaagtgtt acacaacagg tacgattatt      1260
aatcaagacc ctgacaagat cctaacatac attgctgccg atcgtgcccc ggtagtcgag      1320
gtgaacggcg tgaccatcca agtcgggagc aggaggtatc cagacgctgt gtacttgcac      1380
agaattgacc tcggtctctc catatcattg gagagggttg acgtagggac aaatctgggg      1440
aatgcaattg ccaaatgga ggatgccaag gaattgttg aatcatcgga ccagatattg      1500
agaagtatga aaggtttatc gagcactagc atagtctaca tcctgattgc agtgtgtctt      1560
ggagggttga tagggatccc cactttaata tgttgctgca gggggcggtg taacaaaaag      1620
ggagaacaag ttggtatgtc aagaccaggc ctaaagcctg accttacagg aacatcaaaa      1680
tcctatgtaa gatcgctttg atgataatag gctggagcct cggtggccaa gcttcttgcc      1740
ccttgggcct ccccccagcc cctctcccc ttcctgcacc cgtacccccg tggcttttga      1800
ataaagtctg agtggcgggc aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa      1860
aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa      1920
tctag                                             1925
```

<210> SEQ ID NO 38

<211> LENGTH: 1864

<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 38

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tcaagctttt ggaccctcgt acagaagcta atacgactca ctataggga ataagagaga      60
aaagaagagt aagaagaaat ataagagcca ccatgggtct caaggtgaac gtctctgtca      120
tattcatggc agtactgtta actcttcaaa caccaccgg tcaaatccat tggggcaatc      180
tctctaagat aggggtggta ggggtaggaa gtgcaagcta caaagttatg actcgttcca      240
gccatcaatc attagtcata aagttaatgc ccaatataac tctcctcaac aattgcacga      300
gggtagggat tgcagaatac aggagactac tgagaacagt tctggaacca attagagatg      360
cacttaatgc aatgaccagc aatataagac cggttcagag tgtagcttca agtaggagac      420
acaagagatt tgcgggagtt gtctcggcag gtgcggccct aggcgttgcc acagctgctc      480
aaataacagc cggtattgca cttcaccagt ccatgctgaa ctctcaagcc atcgacaatc      540
tgagagcgag cctagaaact actaatcagg caattgaggc aatcagacaa gcagggcagg      600
agatgatatt ggctgttcag ggtgtccaag actacatcaa taatgagctg ataccgtcta      660
tgaatcaact atcttgtgat ttaatcggcc agaagctagg gctcaaattg ctgagatact      720
atacagaaat cctgtcatta tttggcccca gcttacggga ccccatatct gcggagatat      780
ctatccaggc tttgagctat gcgcttgagg gagatatcaa taagggtgtg gaaaagctcg      840
gatacagtgg aggtgatcta ctgggcatct tagagagcag aggaataaag gcccgataa      900
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agattaaggg ggtgatgtgc caccggctag aggggggtctc gtacaacata ggctctcaag      1020
agtgtgtata cactgtgccc aagtatgttg caacccaagg gtaccttata tcgaattttg      1080
atgagtcata atgcactttc atgccagagg ggactgtgtg cagccagaat gccttgtaac      1140
cgatgagtcc tctgctccaa gaatgcctcc ggggggtccac taagtctgtg gctcgtacac      1200
tcgtatccgg gtctttcggg aaccggttca ttttatcaca ggggaaccta atagccaatt      1260
gtgcatcaat cctttgcaag tgttacacaa caggaacaat cattaatcaa gaccctgaca      1320
agatcctaac atacattgct gccgatcact gcccggtggt cgagggtgaat ggcgtgacca      1380
tccaagtcgg gagcaggagg tatccggacg ctgtgtactt gcacaggatt gacctcggtc      1440
ctcccatatc tttggagagg ttggacgtag ggacaaatct ggggaatgca attgctaagt      1500
tggaggatgc caaggaattg ttggagtcac cggaccagat attgaggagt atgaaagggt      1560
tatcgagcac tagtatagtt tacatcctga ttgcagtgtg tcttgaggga ttgataggga      1620
tccccgcttt aatatgttgc tgcagggggc gttgtaacaa gaaggagaa caagttggta      1680
tgtcaagacc aggccataag cctgatctta caggaacatc aaaatcctat gtaaggtcac      1740
tctgatgata ataggctgga gctcgggtgg ccaagcttct tgccccctgg gctccccccc      1800
agccccctct ccccttctct caccctgacc cccgtggtct ttgaataaag tctgagtggg      1860
cggc

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<210> SEQ ID NO 39

<211> LENGTH: 1653

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

-continued

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 39

```

atgggtctca aggtgaacgt ctctgtcata ttcattggcag tactgttaac ttttcaaaca    60
ccccccggtc aaatccattg gggcaatctc tctaagatag ggggtgtagg ggttaggaagt    120
gcaagctaca aagttatgac tcgttccagc catcaatcat tagtcataaa gttaattgccc    180
aatataactc tcctcaacaa ttgcacgagg gttaggattg cagaatacag gagactactg    240
agaacagttc tggaaccaat tagagatgca cttaatgcaa tgaccagaa tataagaccg    300
gttcagagtg tagcttcaag taggagacac aagagatttg cgggagttgt cctggcagggt    360
gcgggccctag gcgttgccac agctgctcaa ataacagccg gtattgcact tcaccagtcc    420
atgctgaact ctcaagccat cgacaatctg agagcgagcc tagaaactac taatcaggca    480
attgaggcaa tcagacaagc agggcaggag atgatattgg ctgttcaggg tgtccaagac    540
tacatcaata atgagctgat accgtctatg aatcaactat cttgtgattt aatcggccag    600
aagctagggc tcaaattgct cagatactat acagaaatcc tgtcattatt tggccccagc    660
ttacgggacc ccatatctgc ggagatatct atccaggctt tgagctatgc gcttgaggga    720
gatatcaata aggtgttgga aaagctcgga tacagtggag gtgatctact gggcatctta    780
gagagcagag gaataaaggc ccggataact cacgtcgaca cagagtccta cttcattgta    840
ctcagtatag cctatccgac gctatccgag attaaggggg tgattgtcca ccggctagag    900
ggggtctctg acaacatagg ctctcaagag tggatatacca ctgtgcccc gatatgttga    960
acccaagggt accttatctc gaattttgat gagtcatcat gcaactttcat gccagagggg    1020
actgtgtgca gccagaatgc cttgtaccgc atgagtcctc tgctccaaga atgcctccgg    1080
gggtccacta agtcctgtgc tcgtacactc gtatccgggt ctttcgggaa ccgggttcatt    1140
ttatcacagg ggaacctaat agccaattgt gcatcaatcc tttgcaagtg ttacacaaca    1200
ggaacaatca ttaatcaaga ccttgacaag atcctaacat acattgctgc cgatcactgc    1260
ccgggtggtc aggtgaatgg cgtgaccatc caagtcggga gcaggaggta tccggacgct    1320
gtgtacttgc acaggattga cctcggtcct cccatatctt tggagagggt ggaagtaggg    1380
acaaatctgg ggaatgcaat tgctaagttg gaggatgcca aggaattgtt ggagtcacgc    1440
gaccagatat tgaggagtat gaaaggttta tcgagcacta gtatagttta catcctgatt    1500
gcagtgtgtc ttggaggatt gatagggatc cccgctttaa tatgttctgc cagggggcgt    1560
tgtaacaaga agggagaaca agttggtatg tcaagaccag gcctaaagcc tgatcttaca    1620
ggaacatcaa aatcctatgt aaggtcactc tga                                1653

```

<210> SEQ ID NO 40

<211> LENGTH: 1925

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 40

```

ggggaaataa gagagaaaag aagagtaaga agaaatataa gagccaccat gggctctcaag    60
gtgaacgtct ctgtcatatt catggcagta ctgttaactc ttcaaaccac caccgggtcaa    120
atccattggg gcaatctctc taagataggg gtggtagggg taggaagtgc aagctacaaa    180

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-continued

gttatgactc gttccagcca tcaatcatta gtcataaagt taatgcccaa tataactctc	240
ctcaacaatt gcacgagggg agggattgca gaatacagga gactactgag aacagttctg	300
gaaccaatta gagatgcact taatgcaatg acccagaata taagaccggg tcagagtgtg	360
gcttcaagta ggagacacaa gagatttgcg ggagttgtcc tggcaggtgc ggccctaggc	420
gttgccacag ctgctcaaat aacagccggg attgcacttc accagtccat gctgaactct	480
caagccatcg acaatctgag agcgagccta gaaactacta atcaggcaat tgaggcaatc	540
agacaagcag ggcaggagat gatattggct gttcaggggtg tccaagacta catcaataat	600
gagctgtatc cgtctatgaa tcaactatct tgtgatttaa tcggccagaa gctagggctc	660
aaattgctca gatactatac agaaatcctg tcattatttg gcccagctt acgggacccc	720
atatctgcgg agatatctat ccaggctttg agctatgcgc ttggaggaga tatcaataag	780
gtgttgaaa agctcggata cagtggaggt gatctactgg gcatcttaga gagcagagga	840
ataaaggccc ggataactca cgtcgacaca gagtccactt tcattgtact cagtatagcc	900
tatccgacgc tatccgagat taaggggggtg attgtccacc ggctagaggg ggtctcgta	960
aacataggct ctcaagagtg gtataccact gtgcccaggt atgttgcaac ccaagggtag	1020
cttatctcga attttgatga gtcacatgc actttcatgc cagaggggac tgtgtgcagc	1080
cagaatgcct tgtaccgat gagtcctctg ctccaagaat gcctccgggg gtccactaag	1140
tcctgtgctc gtacactcgt atccgggtct ttcgggaacc gggtcatttt atcacagggg	1200
aacctaatag ccaattgtgc atcaatcctt tgcaagtgtt acacaacagg aacaatcatt	1260
aatcaagacc ctgacaagat cctaacatac attgctgccg atcactgccc ggtggctcag	1320
gtgaatggcg tgaccatcca agtcgggagc aggaggtatc cggacgctgt gtacttgca	1380
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aatgcaattg ctaagttgga ggatgccaa gaattgttgg agtcacgga ccagatattg	1500
aggagtatga aaggtttatc gagcactagt atagtttaca tcctgattgc agtgtgtctt	1560
ggaggattga tagggatccc cgtctttaata tgttgctgca gggggcggtg taacaagaag	1620
ggagaacaag ttggtatgtc aagaccaggc ctaaagcctg atcttacagg aacatcaaaa	1680
tcctatgtaa ggtcactctg atgataatag gctggagcct cggtgggcaa gcttcttgcc	1740
ccttggggct ccccccagcc cctcctcccc ttctgcacc cgtacccccg tggctcttga	1800
ataaagtctg agtggggcgc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1860
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1920
tctag	1925

<210> SEQ ID NO 41

<211> LENGTH: 2065

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 41

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aaagaagagt aagaagaat ataagagcca ccatgtcacc gcaacgagac cggataaatg	120
ccttctacaa agataaccct tatcccaagg gaagtaggat agttattaac agagaacatc	180

-continued

ttatgattga cagaccctat gttctgctgg ctgttctgtt cgtcatgttt ctgagcttga	240
tcggattgct ggcaattgca gccattagac ttcacgccc agccatctac accgcggaga	300
tccataaaag cctcagtagc aatctggatg tgactaactc catcgagcat caggcaagg	360
acgtgctgac accactcttt aaaatcatcg gggatgaagt gggcctgaga acacctcaga	420
gattcactga cctagtgaat ttcacgctcg acaagattaa attccttaat ccgcataggg	480
agtagcactt cagagatctc acttggtgca tcaacccgcc agagaggatc aaactagatt	540
atgatcaata ctgtgcagat gtggctgctg aagagctcat gaatgcattg gtgaactcaa	600
ctctactgga gaccagaaca accactcagt tctagctgt ctcaaaggga aactgctcag	660
ggcccactac aatcagaggt caattctcaa acatgctgct gtcttctgtg gacttgact	720
taggtcgagg ttacaatgtg tcactatag tcactatgac atcccaggga atgtatggg	780
gaacctacct agttgaaaag cctaactctga acagcaaagg gtcagagttg tcacaactga	840
gcctgtaccg agtgtttgaa gtggtgtgga tcagaaaccc ggggttgagg gctccggtgt	900
tccatagcag aaactatttt gagcaaccag tcagtaatgg tctcggcaac tgtatgggtg	960
ctttggggga gctcaaacct gcagcccttt gtcacgggga cgattctatc ataattccct	1020
atcagggatc agggaaaagg gtcagcttcc agctcgtcaa gctgggtgct tggaaatccc	1080
caaccgacat gcaatcctgg gtccccttat caacggatga tccagtggta gacagcttt	1140
acctctctac tcacagaggt gtcacgctg acaatcaagc aaaatgggct gtcccagaaa	1200
cacgaacaga tgacaagtgt cgaatggaga catgcttcca gcaggcgtgt aaaggtaaaa	1260
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gattcggggc attgatcaca cagggctcag ggatggacct atacaaatcc aactgcaaca	1440
atgtgtattg gctgactatt ccgccaatga gaaatctagc cttaggcgta atcaacacat	1500
tggagtggat accgagatc aagggttagc ccaacctctt cactgtccca attaaggga	1560
caggcgaaga ctgccatgcc ccaacatacc tacctgcgga ggtggacggt gatgtcaaac	1620
tcagttccaa cctggtgatt ctacctgggc aagatctcca atatgttttg gcaacctacg	1680
atactccag ggttgagcat gctgtggttt attacgttta cagcccaagc cgctcatttt	1740
cttactttta tccttttagg ttgcctataa aggggggtccc aatcgaacta caagtggaat	1800
gcttcacatg ggatcaaaaa ctctggtgcc gtcacttctg tgtgcttgcg gactcagaat	1860
ccggtggact tatcactcac tctgggatgg tgggcatggg agtcagctgc acagctaccc	1920
gggaagatgg aaccaatgc agataatgat aataggtg agcctcggtg gccaaagcttc	1980
ttgccccttg ggctccccc cagccctccc tccccttctt gcacccgtac ccccggtgct	2040
tttgaataaa gtctgagtg gcggc	2065

<210> SEQ ID NO 42

<211> LENGTH: 1854

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 42

atgtcaccgc aacgagaccg gataaatgcc ttctacaaag ataaccctta tcccaaggga	60
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agtaggatag ttattaacag agaacatctt atgattgaca gacctatgt tctgctggct	120
gttctgttcg tcatgtttct gagcttgatc ggattgctgg caattgcagg cattagactt	180
catcgggcag ccactctacac cgcggagatc cataaaagcc tcagtaccaa tctggatgtg	240
actaactcca tcgagcatca ggtcaaggac gtgctgacac cactctttaa aatcatcggg	300
gatgaagtgg gcctgagaac acctcagaga ttcactgacc tagtgaaatt catctcggac	360
aagattaaat tccttaatcc ggatagggag tacgacttca gagatctcac ttggtgcac	420
aaccgccag agaggatcaa actagattat gatcaatact gtgcagatgt ggctgctgaa	480
gagctcatga atgcattggg gaactcaact ctactggaga ccagaacaac cactcagttc	540
ctagctgtct caaagggaaa ctgctcaggc ccactacaa tcagaggta attctcaaac	600
atgtcgtgt ccttgttga cttgtactta ggtcgaggtt acaatgtgtc atctatagtc	660
actatgacat ccagggaat gtatggggga acctacctag ttgaaaagcc taatctgaac	720
agcaaagggt cagagtgttc acaactgagc atgtaccgag tgtttgaagt aggtgtgac	780
agaaaccgg gtttgggggc tccggtgttc catatgacaa actattttga gcaaccagtc	840
agtaatggtc tcggcaactg tatggtggct ttgggggagc tcaaactcgc agccctttgt	900
cacggggagc attctatcat aattccctat cagggatcag ggaaagggtg cagcttcag	960
ctcgtcaagc tgggtgtctg gaaatcccca accgacatgc aatcctgggt ccccttatca	1020
acggatgac cagtggtaga caggctttac ctctcatctc acagagggtg catcgtgac	1080
aatcaagcaa aatgggtgtt ccgcacaaca cgaacagatg acaagttgcg aatggagaca	1140
tgcttcacgc aggcgtgtaa aggtaaaatc caagcactct gcgagaatcc cgagtgggta	1200
ccattgaagg ataacaggat tccttcatac ggggtcctgt ctgttgatct gactctgacg	1260
gttgagctta aaatcaaaat tgcttcggga ttcggggccat tgatcacaca cggctcaggg	1320
atggacctat acaaatccaa ctgcaacaat gtgtattggc tgactattcc gccaatgaga	1380
aatctagcct taggcgtaat caacacattg gagtggatgc cgagattcaa ggtagtccc	1440
aacctcttca ctgtcccaat taagggaagc ggcgaagact gccatgcccc aacataccta	1500
cctgcggagg tggacggtga tgtcaaaact agttccaacc tggtagattct acctggtcaa	1560
gactctcaat atgttttggc aaacctacgat acctccaggg ttgagcatgc tgtggtttat	1620
tacgtttaca gcccagcgc ctcatcttct tacttttacc cttttagggt gcctataaag	1680
ggggtcccaa tcgaactaca agtggaatgc ttcacatggg atcaaaaact ctggtgccgt	1740
cacttctgtg tgcttgcgga ctcagaatcc ggtggactta tcaactcactc tgggaggtg	1800
ggcatgggag tcagctgcac agctaccggg gaagatggaa ccaatcgcag ataa	1854

<210> SEQ ID NO 43

<211> LENGTH: 2126

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 43

ggggaaataa gagagaaaag aagagtaaga agaaatataa gagccacat gtcaccgcaa	60
cgagaccgga taaatgcctt ctacaaagat aacccttacc ccaagggaag taggatagtt	120
attaacagag aacatcttat gattgacaga cccatgttgc tgctggctgt tctgttcgtc	180

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atgtttctga gcttgatcgg attgctggca attgcaggca ttagacttca tcgggcagcc	240
atctacaccg cggagatcca taaaagcctc agtaccaatc tggatgtgac taactccatc	300
gagcatcagg tcaaggacgt gctgacacca ctctttaaaa tcatcgggga tgaagtgggc	360
ctgagaacac ctcagagatt cactgaccta gtgaaattca tctcggacaa gattaaattc	420
cttaatccgg atagggagta cgacttcaga gatctcactt ggtgcatcaa cccgccagag	480
aggatcaaac tagattatga tcaatactgt gcagatgtgg ctgctgaaga gctcatgaat	540
gcattggtga actcaactct actggagacc agaacaacca ctcagttcct agctgtctca	600
aagggaaact gctcagggcc cactacaatc agaggtcaat tctcaaacat gtcgctgtcc	660
ttgttggaact tgtacttagg tcgaggttac aatgtgtcat ctatagtcaac tatgacatcc	720
cagggaaatgt atgggggaac ctacctagtt gaaaagccta atctgaacag caaagggta	780
gagttgtcac aactgagcat gtaccgagtg tttgaagtag gtgtgatcag aaacccgggt	840
ttgggggctc cggtgttcca tatgacaaac tattttgagc aaccagtcag taatggtctc	900
ggcaactgta tgggtggcttt gggggagctc aaactcgag ccctttgtca cggggacgat	960
tctatcataa ttccctatca gggatcaggg aaaggtgtca gcttcagct cgtcaagctg	1020
ggtgtctgga aatccccaac cgacatgcaa tcttgggtcc ccttatcaac ggatgatcca	1080
gtggtagaca ggctttacct ctcatctcac agaggtgtca tcgctgacaa tcaagcaaaa	1140
tgggtgtgctc cgacaacacg aacagatgac aagttgcgaa tggagacatg cttccagcag	1200
gcgtgtaaag gtaaaatcca agcactctgc gagaatcccg agtgggtacc attgaaggat	1260
aacaggattc cttcatacgg ggtcctgtct gttgatctga gtctgacggg tgagcttaaa	1320
atcaaaaattg cttcgggatt cggggcattg atcacacacg gctcagggat ggacctatac	1380
aaatccaact gcaacaatgt gtattggctg actattccgc caatgagaaa tctagcctta	1440
ggcgtaatca acacattgga gtggataccg agattcaagg ttagtcccaa cctcttccact	1500
gtcccaatta aggaagcagg cgaagactgc catgccccaa catacctacc tgcggagggtg	1560
gacggtgatg tcaaaactcag ttccaacctg gtgattctac ctggtcaaga tctccaatat	1620
gttttggaac cctacgatac ctccaggggt gagcatgctg tggtttatta cgtttacagc	1680
ccaagccgct cattttctta cttttatcct tttaggttgc ctataaaggg ggtcccaatc	1740
gaactacaag tggaatgctt cacatgggat caaaaactct ggtgccgtca cttctgtgtg	1800
cttgccgact cagaatccgg tggacttata actcactctg ggatgggtggg catgggagtc	1860
agctgcacag ctaccgagg agatggaacc aatcgagat aatgataata ggctggagcc	1920
tcggtggcca agcttcttgc cccttgggcc tccccccagc cctctctccc cttctgtcac	1980
ccgtaccccc gtggtctttg aataaagtct gagtgggcgg caaaaaaaaa aaaaaaaaaa	2040
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	2100
aaaaaaaaaa aaaaaaaaaa atctag	2126

<210> SEQ ID NO 44

<211> LENGTH: 2065

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 44

-continued

tcaagctttt	ggaccctcgt	acagaagcta	atagcactca	ctatagggaa	ataagagaga	60
aaagaagagt	aagaagaaat	ataagagcca	ccatgtcacc	acaacgagac	cggataaatg	120
ccttctacaa	agacaacccc	catcctaagg	gaagtaggat	agttattaac	agagaacatc	180
ttatgattga	tagaccttat	gttttgctgg	ctgttctatt	cgtcagtgtt	ctgagcttga	240
tcgggttgct	agccattgca	ggcattagac	ttcatcgggc	agccatctac	accgcagaga	300
tccataaaag	cctcagcacc	aatctggatg	taactaactc	aatcgagcat	cagggttaagg	360
acgtgctgac	accactcttc	aagatcatcg	gtgatgaagt	gggcttgagg	acacctcaga	420
gattcactga	cctagtgaag	ttcatctctg	acaagattaa	attccttaat	cgggacaggg	480
aatacgactt	cagagatctc	acttggtgta	tcaaccgcgc	agagagaatc	aaattggatt	540
atgatcaata	ctgtgcagat	gtggctgctg	aagaactcat	gaatgcattg	gtgaactcaa	600
ctctactgga	gaccagggca	accaatcagt	tcttagctgt	ctcaaaggga	aactgctcag	660
ggcccaactac	aatcagaggc	caattctcaa	acatgtcgct	gtccctgttg	gacttgtatt	720
taagtcgagg	ttacaatgtg	tcacttatag	tcactatgac	atcccaggga	atgtacgggg	780
gaacttacct	agtggaaaag	cctaactctga	gcagcaaagg	gtcagagtgt	tcacaactga	840
gcctgcaccg	agtgtttgaa	gtagggtgta	tcagaaatcc	gggtttgggg	gtcccggtat	900
tccatattgac	aaactatctt	gagcaaccag	tcagtaatga	tttcagcaac	tgcattggtg	960
ctttggggga	gctcaagttc	gcagccctct	gtcacaggga	agattctatc	acaattccct	1020
atcagggatc	agggaaaagg	gtcagcttcc	agcttggtcaa	gctaggtgtc	tggaaatccc	1080
caaccgacat	gcaatcctgg	gtccccctat	caacggatga	tccagtgata	gacaggcttt	1140
acctctcatc	tcacagaggc	gttatcgctg	acaatcaagc	aaaatgggct	gtcccagaaa	1200
cacggacaga	tgacaagttg	cgaatggaga	catgcttcca	gcaggcggtg	aagggtaaaa	1260
tccaagcact	ttgcgagaat	cccagtgga	caccattgaa	ggataacagg	attccttcat	1320
acggggctct	gtctgttgat	ctgagctctga	cagttgagct	taaaatcaaa	attgtttcag	1380
gattcggggc	attgatcaca	cacggttcag	ggatggacct	atacaaatcc	aaccacaaca	1440
atatgtattg	gctgactatc	ccgccaatga	agaacctggc	cttaggtgta	atcaacacat	1500
tggagtggat	accgagattc	aagggttagtc	ccaacctctt	cactgttcca	attaagggaag	1560
caggcgagga	ctgccatgcc	ccaacatacc	tacctgcgga	gggtggatgg	gatgtcaaac	1620
tcagttccaa	tctggtgatt	ctacctggtc	aagatctcca	atatgttctg	gcaacctacg	1680
atacttccag	agttgaacat	gctgtagttt	attacgttta	cagcccaagc	cgctcatttt	1740
cttactttta	tccttttagg	ttgctgtgaa	gggggggtccc	cattgaatta	caagtggaat	1800
gcttcacatg	ggacaaaaaa	ctctggtgcc	gtcacttctg	tgtgcttgcg	gactcagaat	1860
ctggtggaca	tatcactcac	tctgggatgg	tgggcatggg	agtcagctgc	acagccactc	1920
gggaagatgg	aaccagccgc	agatagtgat	aataggctgg	agcctcggtg	gccaagcttc	1980
ttgccccttg	ggcctccccc	cagccctccc	tccccttccc	gcacccgtac	ccccgtggtc	2040
tttgaataaa	gtctgagtgg	gcgggc				2065

<210> SEQ ID NO 45

<211> LENGTH: 1854

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

-continued

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 45

```

atgtcaccac aacgagaccg gataaatgcc ttctacaaag acaaccccca tectaaggga      60
agtaggatag ttattaacag agaacatctt atgattgata gaccttatgt ttgctggct      120
gttctattcg tcatgtttct gagcttgatc gggttgctag ccattgcagg cattagactt      180
catcgggcag ccattctacac cgcagagatc cataaaagcc tcagcaccaa tctggatgta      240
actaactcaa tcgagcatca ggtaaggac gtgctgacac cactcttcaa gatcatcggt      300
gatgaagtgg gcttgaggac acctcagaga ttactgacc tagtgaagtt catctctgac      360
aagattaaat tccttaatcc ggacaggga tacgacttca gagatctcac ttggtgtatc      420
aaccgcgcag agagaatcaa attggattat gatcaatact gtgcagatgt ggctgctgaa      480
gaactcatga atgcattggg gaactcaact ctactggaga ccagggaac caatcagttc      540
ctagctgtct caaagggaaa ctgctcaggg ccactacaa tcagaggcca attctcaaac      600
atgtcgcgtg ccctgttggg cttgtattta agtcgaggtt acaatgtgtc atctatagtc      660
actatgacat cccagggaat gtacggggga acttacctag tggaaaagcc taatctgagc      720
agcaaagggt cagagttgtc acaactgagc atgcaccgag tgtttgaagt aggtgttate      780
agaaatccgg gtttgggggc tccggtattc catatgacaa actatcttga gcaaccagtc      840
agtaatgatt tcagcaactg catggtggct ttgggggagc tcaagttcgc agccctctgt      900
cacagggaag attctatcac aattccctat cagggatcag ggaaagggtg cagcttcacg      960
cttgtcaagc taggtgtctg gaaatcccca accgacatgc aatcctgggt cccctatca     1020
acggatgac cagtgataga caggctttac ctctcatctc acagaggcgt tatcgctgac     1080
aatcaagcaa aatgggtgtg cccgacaaca cggacagatg acaagttgag aatggagaca     1140
tgcttccagc aggcgtgtaa gggtaaaatc caagcacttt gcgagaatcc cgagtggaca     1200
ccattgaagg ataacaggat tccttcatac ggggtcttgt ctgttgatct gagtctgaca     1260
gttgagctta aaatcaaaat tgtttcagga ttccgggcat tgatcacaca cggttcaggg     1320
atggacctat acaaatccaa ccacaacaat atgtattggc tgactatccc gccaatgaag     1380
aacctggcct taggtgtaat caacacattg gagtggatgc cgagattcaa ggtagtccc     1440
aacctcttca ctgttccaat taaggaagca ggcgaggact gccatgcccc aacataccta     1500
cctgcggagg tggatggtga tgcaaaactc agttccaatc tggtgattct acctggtcaa     1560
gatctccaat atgttctggc aacctacgat acttccagag ttgaacatgc ttagtattat     1620
tacgtttaca gccaagccg ctcatcttct tacttttata cttttagggt gcctgtaagg     1680
ggggtcccca ttgaattaca agtggaatgc ttcacatggg accaaaaact ctggtgccgt     1740
cacttctgtg tgcttgcgga ctcagaatct ggtggacata tcaactactc tgggatgggt     1800
ggcatgggag tcagctgcac agccactcgg gaagatggaa ccagccgcag atag         1854

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<210> SEQ ID NO 46

<211> LENGTH: 2126

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 46

-continued

ggggaataa gagagaaaag aagagtaaga agaaatataa gagccaccat gtcaccacaa	60
cgagaccgga taaatgcctt ctacaagac aacccccatc ctaagggaag taggatagtt	120
attaacagag aacatcttat gattgataga ccttatgttt tgetggctgt tctattcgtc	180
atgtttctga gcttgatcgg gttgctagcc attgcaggca ttagacttca tcgggcagcc	240
atctacacg cagagatcca taaaagcctc agcaccaatc tggatgtaac taactcaatc	300
gagcatcagg ttaaggacgt gctgacacca ctcttcaaga tcatcggtga tgaagtgggc	360
ttgaggacac ctgagagatt cactgaccta gtgaagtcca tctctgacaa gattaaattc	420
cttaatccgg acagggaata cgacttcaga gatctcactt ggtgtatcaa cccgccagag	480
agaatcaaat tggattatga tcaatactgt gcagatgtgg ctgctgaaga actcatgaat	540
gcattggtga actcaactct actggagacc agggcaacca atcagttcct agctgtctca	600
aagggaact gctcagggcc cactacaatc agaggccaat tctcaaacat gtcgctgtcc	660
ctgttggaact tgtatttaag tcgaggttac aatgtgtcat ctatagtcac tatgacatcc	720
cagggaatgt acgggggaac ttacctagtg gaaaagccta atctgagcag caaagggtca	780
gagttgtcac aactgagcat gcaccgagtg tttgaagtag gtgttatcag aaatccgggt	840
ttgggggctc cggtattcca tatgacaaac tatcttgagc aaccagtcag taatgatttc	900
agcaactgca tgggtggcttt gggggagctc aagttcgcag ccctctgtca cagggaagat	960
tctatcacia ttccctatca gggatcaggg aaaggtgtca gcttcagct tgtcaagcta	1020
ggtgtctgga aatccccaac cgacatgcaa tccctgggtcc ccctatcaac ggatgatcca	1080
gtgatagaca ggctttacct ctcatctcac agaggcggtta tcgctgacaa tcaagcaaaa	1140
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aacaggattc cttcatacgg ggtcttgtct gttgatctga gtctgacagt tgagcttaaa	1320
atcaaaattg tttcaggatt cggggcattg atcacacacg gttcagggat ggacctatac	1380
aaatccaacc acaacaatat gtattggctg actatccgcg caatgaagaa cctggcctta	1440
ggtgtaatca acacattgga gtggataccg agattcaagg ttagtcccaa cctcttact	1500
gttccaatta aggaagcagg cgaggactgc catgccccaa catacctacc tgcggagggtg	1560
gatggtgatg tcaaaactcag ttccaatctg gtgattctac ctggtcaaga tctccaatat	1620
gttctggcaa cctacgatac ttccagagtt gaacatgctg tagtttatta cgtttacagc	1680
ccaagccgct cattttctta cttttatcct tttaggttgc ctgtaagggg ggtccccatt	1740
gaattacaag tggaatgctt cacatgggac caaaaactct ggtgccgtca cttctgtgtg	1800
cttgccgact cagaatctgg tggacatatc actcactctg ggatgggtggg catgggagtc	1860
agctgcacag ccactcggga agatggaacc agccgcagat agtgataata ggctggagcc	1920
tcggtggcca agcttcttgc ccttggggcc tccccccagc ccctcctccc cttctgtcac	1980
ccgtaccccc gtggtctttg aataaagtct gagtgggcgg caaaaaaaaaa aaaaaaaaaa	2040
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	2100
aaaaaaaaaa aaaaaaaaaa atctag	2126

<210> SEQ ID NO 47

<211> LENGTH: 550

<212> TYPE: PRT

-continued

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 47

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Met Gly Leu Lys Val Asn Val Ser Ala Val Phe Met Ala Val Leu Leu
 1          5          10          15

Thr Leu Gln Thr Pro Ala Gly Gln Ile His Trp Gly Asn Leu Ser Lys
 20          25          30

Ile Gly Val Val Gly Ile Gly Ser Ala Ser Tyr Lys Val Met Thr Arg
 35          40          45

Ser Ser His Gln Ser Leu Val Ile Lys Leu Met Pro Asn Ile Thr Leu
 50          55          60

Leu Asn Asn Cys Thr Arg Val Glu Ile Ala Glu Tyr Arg Arg Leu Leu
 65          70          75          80

Arg Thr Val Leu Glu Pro Ile Arg Asp Ala Leu Asn Ala Met Thr Gln
 85          90          95

Asn Ile Arg Pro Val Gln Ser Val Ala Ser Ser Arg Arg His Lys Arg
100          105          110

Phe Ala Gly Val Val Leu Ala Gly Ala Ala Leu Gly Val Ala Thr Ala
115          120          125

Ala Gln Ile Thr Ala Gly Ile Ala Leu His Arg Ser Met Leu Asn Ser
130          135          140

Gln Ala Ile Asp Asn Leu Arg Ala Ser Leu Glu Thr Thr Asn Gln Ala
145          150          155          160

Ile Glu Ala Ile Arg Gln Ala Gly Gln Glu Met Ile Leu Ala Val Gln
165          170          175

Gly Val Gln Asp Tyr Ile Asn Asn Glu Leu Ile Pro Ser Met Asn Gln
180          185          190

Leu Ser Cys Asp Leu Ile Gly Gln Lys Leu Gly Leu Lys Leu Leu Arg
195          200          205

Tyr Tyr Thr Glu Ile Leu Ser Leu Phe Gly Pro Ser Leu Arg Asp Pro
210          215          220

Ile Ser Ala Glu Ile Ser Ile Gln Ala Leu Ser Tyr Ala Leu Gly Gly
225          230          235          240

Asp Ile Asn Lys Val Leu Glu Lys Leu Gly Tyr Ser Gly Gly Asp Leu
245          250          255

Leu Gly Ile Leu Glu Ser Arg Gly Ile Lys Ala Arg Ile Thr His Val
260          265          270

Asp Thr Glu Ser Tyr Phe Ile Val Leu Ser Ile Ala Tyr Pro Thr Leu
275          280          285

Ser Glu Ile Lys Gly Val Ile Val His Arg Leu Glu Gly Val Ser Tyr
290          295          300

Asn Ile Gly Ser Gln Glu Trp Tyr Thr Thr Val Pro Lys Tyr Val Ala
305          310          315          320

Thr Gln Gly Tyr Leu Ile Ser Asn Phe Asp Glu Ser Ser Cys Thr Phe
325          330          335

Met Pro Glu Gly Thr Val Cys Ser Gln Asn Ala Leu Tyr Pro Met Ser
340          345          350

Pro Leu Leu Gln Glu Cys Leu Arg Gly Ser Thr Lys Ser Cys Ala Arg
355          360          365

Thr Leu Val Ser Gly Ser Phe Gly Asn Arg Phe Ile Leu Ser Gln Gly

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370	375	380
Asn Leu Ile Ala Asn Cys Ala Ser Ile Leu Cys Lys Cys Tyr Thr Thr		
385	390	395 400
Gly Thr Ile Ile Asn Gln Asp Pro Asp Lys Ile Leu Thr Tyr Ile Ala		
	405	410 415
Ala Asp Arg Cys Pro Val Val Glu Val Asn Gly Val Thr Ile Gln Val		
	420	425 430
Gly Ser Arg Arg Tyr Pro Asp Ala Val Tyr Leu His Arg Ile Asp Leu		
	435	440 445
Gly Pro Pro Ile Ser Leu Glu Arg Leu Asp Val Gly Thr Asn Leu Gly		
	450	455 460
Asn Ala Ile Ala Lys Leu Glu Asp Ala Lys Glu Leu Leu Glu Ser Ser		
	465	470 475 480
Asp Gln Ile Leu Arg Ser Met Lys Gly Leu Ser Ser Thr Ser Ile Val		
	485	490 495
Tyr Ile Leu Ile Ala Val Cys Leu Gly Gly Leu Ile Gly Ile Pro Thr		
	500	505 510
Leu Ile Cys Cys Cys Arg Gly Arg Cys Asn Lys Lys Gly Glu Gln Val		
	515	520 525
Gly Met Ser Arg Pro Gly Leu Lys Pro Asp Leu Thr Gly Thr Ser Lys		
	530	535 540
Ser Tyr Val Arg Ser Leu		
545	550	

<210> SEQ ID NO 48

<211> LENGTH: 550

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 48

Met Gly Leu Lys Val Asn Val Ser Val Ile Phe Met Ala Val Leu Leu		
1	5	10 15
Thr Leu Gln Thr Pro Thr Gly Gln Ile His Trp Gly Asn Leu Ser Lys		
	20	25 30
Ile Gly Val Val Gly Val Gly Ser Ala Ser Tyr Lys Val Met Thr Arg		
	35	40 45
Ser Ser His Gln Ser Leu Val Ile Lys Leu Met Pro Asn Ile Thr Leu		
	50	55 60
Leu Asn Asn Cys Thr Arg Val Gly Ile Ala Glu Tyr Arg Arg Leu Leu		
	65	70 75 80
Arg Thr Val Leu Glu Pro Ile Arg Asp Ala Leu Asn Ala Met Thr Gln		
	85	90 95
Asn Ile Arg Pro Val Gln Ser Val Ala Ser Ser Arg Arg His Lys Arg		
	100	105 110
Phe Ala Gly Val Val Leu Ala Gly Ala Ala Leu Gly Val Ala Thr Ala		
	115	120 125
Ala Gln Ile Thr Ala Gly Ile Ala Leu His Gln Ser Met Leu Asn Ser		
	130	135 140
Gln Ala Ile Asp Asn Leu Arg Ala Ser Leu Glu Thr Thr Asn Gln Ala		
	145	150 155 160
Ile Glu Ala Ile Arg Gln Ala Gly Gln Glu Met Ile Leu Ala Val Gln		

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165								170					175				
Gly	Val	Gln	Asp	Tyr	Ile	Asn	Asn	Glu	Leu	Ile	Pro	Ser	Met	Asn	Gln		
			180				185						190				
Leu	Ser	Cys	Asp	Leu	Ile	Gly	Gln	Lys	Leu	Gly	Leu	Lys	Leu	Leu	Arg		
		195				200					205						
Tyr	Tyr	Thr	Glu	Ile	Leu	Ser	Leu	Phe	Gly	Pro	Ser	Leu	Arg	Asp	Pro		
		210				215					220						
Ile	Ser	Ala	Glu	Ile	Ser	Ile	Gln	Ala	Leu	Ser	Tyr	Ala	Leu	Gly	Gly		
		225				230					235		240				
Asp	Ile	Asn	Lys	Val	Leu	Glu	Lys	Leu	Gly	Tyr	Ser	Gly	Gly	Asp	Leu		
			245				250						255				
Leu	Gly	Ile	Leu	Glu	Ser	Arg	Gly	Ile	Lys	Ala	Arg	Ile	Thr	His	Val		
			260				265						270				
Asp	Thr	Glu	Ser	Tyr	Phe	Ile	Val	Leu	Ser	Ile	Ala	Tyr	Pro	Thr	Leu		
			275				280						285				
Ser	Glu	Ile	Lys	Gly	Val	Ile	Val	His	Arg	Leu	Glu	Gly	Val	Ser	Tyr		
		290				295					300						
Asn	Ile	Gly	Ser	Gln	Glu	Trp	Tyr	Thr	Thr	Val	Pro	Lys	Tyr	Val	Ala		
		305				310					315		320				
Thr	Gln	Gly	Tyr	Leu	Ile	Ser	Asn	Phe	Asp	Glu	Ser	Ser	Cys	Thr	Phe		
			325				330						335				
Met	Pro	Glu	Gly	Thr	Val	Cys	Ser	Gln	Asn	Ala	Leu	Tyr	Pro	Met	Ser		
			340				345						350				
Pro	Leu	Leu	Gln	Glu	Cys	Leu	Arg	Gly	Ser	Thr	Lys	Ser	Cys	Ala	Arg		
		355				360					365						
Thr	Leu	Val	Ser	Gly	Ser	Phe	Gly	Asn	Arg	Phe	Ile	Leu	Ser	Gln	Gly		
		370				375					380						
Asn	Leu	Ile	Ala	Asn	Cys	Ala	Ser	Ile	Leu	Cys	Lys	Cys	Tyr	Thr	Thr		
		385				390					395		400				
Gly	Thr	Ile	Ile	Asn	Gln	Asp	Pro	Asp	Lys	Ile	Leu	Thr	Tyr	Ile	Ala		
			405				410						415				
Ala	Asp	His	Cys	Pro	Val	Val	Glu	Val	Asn	Gly	Val	Thr	Ile	Gln	Val		
			420				425						430				
Gly	Ser	Arg	Arg	Tyr	Pro	Asp	Ala	Val	Tyr	Leu	His	Arg	Ile	Asp	Leu		
		435				440					445						
Gly	Pro	Pro	Ile	Ser	Leu	Glu	Arg	Leu	Asp	Val	Gly	Thr	Asn	Leu	Gly		
		450				455					460						
Asn	Ala	Ile	Ala	Lys	Leu	Glu	Asp	Ala	Lys	Glu	Leu	Leu	Glu	Ser	Ser		
		465				470					475		480				
Asp	Gln	Ile	Leu	Arg	Ser	Met	Lys	Gly	Leu	Ser	Ser	Thr	Ser	Ile	Val		
			485				490						495				
Tyr	Ile	Leu	Ile	Ala	Val	Cys	Leu	Gly	Gly	Leu	Ile	Gly	Ile	Pro	Ala		
			500				505						510				
Leu	Ile	Cys	Cys	Cys	Arg	Gly	Arg	Cys	Asn	Lys	Lys	Gly	Glu	Gln	Val		
		515				520					525						
Gly	Met	Ser	Arg	Pro	Gly	Leu	Lys	Pro	Asp	Leu	Thr	Gly	Thr	Ser	Lys		
		530				535					540						
Ser	Tyr	Val	Arg	Ser	Leu												
		545	550														

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<211> LENGTH: 617
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 49

Met Ser Pro Gln Arg Asp Arg Ile Asn Ala Phe Tyr Lys Asp Asn Pro
1      5      10      15

Tyr Pro Lys Gly Ser Arg Ile Val Ile Asn Arg Glu His Leu Met Ile
      20      25      30

Asp Arg Pro Tyr Val Leu Leu Ala Val Leu Phe Val Met Phe Leu Ser
      35      40      45

Leu Ile Gly Leu Leu Ala Ile Ala Gly Ile Arg Leu His Arg Ala Ala
50      55      60

Ile Tyr Thr Ala Glu Ile His Lys Ser Leu Ser Thr Asn Leu Asp Val
65      70      75      80

Thr Asn Ser Ile Glu His Gln Val Lys Asp Val Leu Thr Pro Leu Phe
      85      90      95

Lys Ile Ile Gly Asp Glu Val Gly Leu Arg Thr Pro Gln Arg Phe Thr
100     105     110

Asp Leu Val Lys Phe Ile Ser Asp Lys Ile Lys Phe Leu Asn Pro Asp
115     120     125

Arg Glu Tyr Asp Phe Arg Asp Leu Thr Trp Cys Ile Asn Pro Pro Glu
130     135     140

Arg Ile Lys Leu Asp Tyr Asp Gln Tyr Cys Ala Asp Val Ala Ala Glu
145     150     155     160

Glu Leu Met Asn Ala Leu Val Asn Ser Thr Leu Leu Glu Thr Arg Thr
165     170     175

Thr Thr Gln Phe Leu Ala Val Ser Lys Gly Asn Cys Ser Gly Pro Thr
180     185     190

Thr Ile Arg Gly Gln Phe Ser Asn Met Ser Leu Ser Leu Leu Asp Leu
195     200     205

Tyr Leu Gly Arg Gly Tyr Asn Val Ser Ser Ile Val Thr Met Thr Ser
210     215     220

Gln Gly Met Tyr Gly Gly Thr Tyr Leu Val Glu Lys Pro Asn Leu Asn
225     230     235     240

Ser Lys Gly Ser Glu Leu Ser Gln Leu Ser Met Tyr Arg Val Phe Glu
245     250     255

Val Gly Val Ile Arg Asn Pro Gly Leu Gly Ala Pro Val Phe His Met
260     265     270

Thr Asn Tyr Phe Glu Gln Pro Val Ser Asn Gly Leu Gly Asn Cys Met
275     280     285

Val Ala Leu Gly Glu Leu Lys Leu Ala Ala Leu Cys His Gly Asp Asp
290     295     300

Ser Ile Ile Ile Pro Tyr Gln Gly Ser Gly Lys Gly Val Ser Phe Gln
305     310     315     320

Leu Val Lys Leu Gly Val Trp Lys Ser Pro Thr Asp Met Gln Ser Trp
325     330     335

Val Pro Leu Ser Thr Asp Asp Pro Val Val Asp Arg Leu Tyr Leu Ser
340     345     350

Ser His Arg Gly Val Ile Ala Asp Asn Gln Ala Lys Trp Ala Val Pro
355     360     365

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Thr	Thr	Arg	Thr	Asp	Asp	Lys	Leu	Arg	Met	Glu	Thr	Cys	Phe	Gln	Gln
370						375					380				
Ala	Cys	Lys	Gly	Lys	Ile	Gln	Ala	Leu	Cys	Glu	Asn	Pro	Glu	Trp	Val
385					390					395					400
Pro	Leu	Lys	Asp	Asn	Arg	Ile	Pro	Ser	Tyr	Gly	Val	Leu	Ser	Val	Asp
				405					410					415	
Leu	Ser	Leu	Thr	Val	Glu	Leu	Lys	Ile	Lys	Ile	Ala	Ser	Gly	Phe	Gly
			420					425						430	
Pro	Leu	Ile	Thr	His	Gly	Ser	Gly	Met	Asp	Leu	Tyr	Lys	Ser	Asn	Cys
		435					440					445			
Asn	Asn	Val	Tyr	Trp	Leu	Thr	Ile	Pro	Pro	Met	Arg	Asn	Leu	Ala	Leu
	450					455					460				
Gly	Val	Ile	Asn	Thr	Leu	Glu	Trp	Ile	Pro	Arg	Phe	Lys	Val	Ser	Pro
465					470					475					480
Asn	Leu	Phe	Thr	Val	Pro	Ile	Lys	Glu	Ala	Gly	Glu	Asp	Cys	His	Ala
				485					490						495
Pro	Thr	Tyr	Leu	Pro	Ala	Glu	Val	Asp	Gly	Asp	Val	Lys	Leu	Ser	Ser
			500					505					510		
Asn	Leu	Val	Ile	Leu	Pro	Gly	Gln	Asp	Leu	Gln	Tyr	Val	Leu	Ala	Thr
		515					520					525			
Tyr	Asp	Thr	Ser	Arg	Val	Glu	His	Ala	Val	Val	Tyr	Tyr	Val	Tyr	Ser
	530					535					540				
Pro	Ser	Arg	Ser	Phe	Ser	Tyr	Phe	Tyr	Pro	Phe	Arg	Leu	Pro	Ile	Lys
545					550					555					560
Gly	Val	Pro	Ile	Glu	Leu	Gln	Val	Glu	Cys	Phe	Thr	Trp	Asp	Gln	Lys
				565					570					575	
Leu	Trp	Cys	Arg	His	Phe	Cys	Val	Leu	Ala	Asp	Ser	Glu	Ser	Gly	Gly
			580					585					590		
Leu	Ile	Thr	His	Ser	Gly	Met	Val	Gly	Met	Gly	Val	Ser	Cys	Thr	Ala
		595				600						605			
Thr	Arg	Glu	Asp	Gly	Thr	Asn	Arg	Arg							
	610					615									

<210> SEQ ID NO 50

<211> LENGTH: 617

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 50

Met	Ser	Pro	Gln	Arg	Asp	Arg	Ile	Asn	Ala	Phe	Tyr	Lys	Asp	Asn	Pro
1					5				10					15	
His	Pro	Lys	Gly	Ser	Arg	Ile	Val	Ile	Asn	Arg	Glu	His	Leu	Met	Ile
			20				25						30		
Asp	Arg	Pro	Tyr	Val	Leu	Leu	Ala	Val	Leu	Phe	Val	Met	Phe	Leu	Ser
		35					40					45			
Leu	Ile	Gly	Leu	Leu	Ala	Ile	Ala	Gly	Ile	Arg	Leu	His	Arg	Ala	Ala
	50					55					60				
Ile	Tyr	Thr	Ala	Glu	Ile	His	Lys	Ser	Leu	Ser	Thr	Asn	Leu	Asp	Val
65				70						75				80	
Thr	Asn	Ser	Ile	Glu	His	Gln	Val	Lys	Asp	Val	Leu	Thr	Pro	Leu	Phe
			85						90					95	

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Lys	Ile	Ile	Gly	Asp	Glu	Val	Gly	Leu	Arg	Thr	Pro	Gln	Arg	Phe	Thr	100	105	110
Asp	Leu	Val	Lys	Phe	Ile	Ser	Asp	Lys	Ile	Lys	Phe	Leu	Asn	Pro	Asp	115	120	125
Arg	Glu	Tyr	Asp	Phe	Arg	Asp	Leu	Thr	Trp	Cys	Ile	Asn	Pro	Pro	Glu	130	135	140
Arg	Ile	Lys	Leu	Asp	Tyr	Asp	Gln	Tyr	Cys	Ala	Asp	Val	Ala	Ala	Glu	145	150	155
Glu	Leu	Met	Asn	Ala	Leu	Val	Asn	Ser	Thr	Leu	Leu	Glu	Thr	Arg	Ala	165	170	175
Thr	Asn	Gln	Phe	Leu	Ala	Val	Ser	Lys	Gly	Asn	Cys	Ser	Gly	Pro	Thr	180	185	190
Thr	Ile	Arg	Gly	Gln	Phe	Ser	Asn	Met	Ser	Leu	Ser	Leu	Leu	Asp	Leu	195	200	205
Tyr	Leu	Ser	Arg	Gly	Tyr	Asn	Val	Ser	Ser	Ile	Val	Thr	Met	Thr	Ser	210	215	220
Gln	Gly	Met	Tyr	Gly	Gly	Thr	Tyr	Leu	Val	Glu	Lys	Pro	Asn	Leu	Ser	225	230	235
Ser	Lys	Gly	Ser	Glu	Leu	Ser	Gln	Leu	Ser	Met	His	Arg	Val	Phe	Glu	245	250	255
Val	Gly	Val	Ile	Arg	Asn	Pro	Gly	Leu	Gly	Ala	Pro	Val	Phe	His	Met	260	265	270
Thr	Asn	Tyr	Leu	Glu	Gln	Pro	Val	Ser	Asn	Asp	Phe	Ser	Asn	Cys	Met	275	280	285
Val	Ala	Leu	Gly	Glu	Leu	Lys	Phe	Ala	Ala	Leu	Cys	His	Arg	Glu	Asp	290	295	300
Ser	Ile	Thr	Ile	Pro	Tyr	Gln	Gly	Ser	Gly	Lys	Gly	Val	Ser	Phe	Gln	305	310	315
Leu	Val	Lys	Leu	Gly	Val	Trp	Lys	Ser	Pro	Thr	Asp	Met	Gln	Ser	Trp	325	330	335
Val	Pro	Leu	Ser	Thr	Asp	Asp	Pro	Val	Ile	Asp	Arg	Leu	Tyr	Leu	Ser	340	345	350
Ser	His	Arg	Gly	Val	Ile	Ala	Asp	Asn	Gln	Ala	Lys	Trp	Ala	Val	Pro	355	360	365
Thr	Thr	Arg	Thr	Asp	Asp	Lys	Leu	Arg	Met	Glu	Thr	Cys	Phe	Gln	Gln	370	375	380
Ala	Cys	Lys	Gly	Lys	Ile	Gln	Ala	Leu	Cys	Glu	Asn	Pro	Glu	Trp	Thr	385	390	395
Pro	Leu	Lys	Asp	Asn	Arg	Ile	Pro	Ser	Tyr	Gly	Val	Leu	Ser	Val	Asp	405	410	415
Leu	Ser	Leu	Thr	Val	Glu	Leu	Lys	Ile	Lys	Ile	Val	Ser	Gly	Phe	Gly	420	425	430
Pro	Leu	Ile	Thr	His	Gly	Ser	Gly	Met	Asp	Leu	Tyr	Lys	Ser	Asn	His	435	440	445
Asn	Asn	Met	Tyr	Trp	Leu	Thr	Ile	Pro	Pro	Met	Lys	Asn	Leu	Ala	Leu	450	455	460
Gly	Val	Ile	Asn	Thr	Leu	Glu	Trp	Ile	Pro	Arg	Phe	Lys	Val	Ser	Pro	465	470	475
Asn	Leu	Phe	Thr	Val	Pro	Ile	Lys	Glu	Ala	Gly	Glu	Asp	Cys	His	Ala	485	490	495

-continued

Pro	Thr	Tyr	Leu	Pro	Ala	Glu	Val	Asp	Gly	Asp	Val	Lys	Leu	Ser	Ser
			500					505					510		
Asn	Leu	Val	Ile	Leu	Pro	Gly	Gln	Asp	Leu	Gln	Tyr	Val	Leu	Ala	Thr
		515					520					525			
Tyr	Asp	Thr	Ser	Arg	Val	Glu	His	Ala	Val	Val	Tyr	Tyr	Val	Tyr	Ser
	530					535					540				
Pro	Ser	Arg	Ser	Phe	Ser	Tyr	Phe	Tyr	Pro	Phe	Arg	Leu	Pro	Val	Arg
545					550					555					560
Gly	Val	Pro	Ile	Glu	Leu	Gln	Val	Glu	Cys	Phe	Thr	Trp	Asp	Gln	Lys
			565						570					575	
Leu	Trp	Cys	Arg	His	Phe	Cys	Val	Leu	Ala	Asp	Ser	Glu	Ser	Gly	Gly
			580					585					590		
His	Ile	Thr	His	Ser	Gly	Met	Val	Gly	Met	Gly	Val	Ser	Cys	Thr	Ala
		595					600					605			
Thr	Arg	Glu	Asp	Gly	Thr	Ser	Arg	Arg							
	610					615									

<210> SEQ ID NO 51

<211> LENGTH: 1729

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 51

tcaagctttt	ggaccctcgt	acagaagcta	atacgactca	ctatagggaa	ataagagaga	60
aaagaagagt	aagaagaaat	ataagagcca	ccatggcaca	agtcattaat	acaaacagcc	120
tgctcgtggt	gaccagaat	aacctgaaca	aatcccagtc	cgcactgggc	actgctatcg	180
agcgtttgtc	ttccggtctg	cgtatcaaca	gcgcgaaaga	cgatgcggca	ggacaggcga	240
ttgctaaccg	ttttaccgcg	aacatcaaag	gtctgactca	ggcttcccg	aacgctaacg	300
acggtatctc	cattgcgcag	accactgaag	gcgcgctgaa	cgaaatcaac	aacaacctgc	360
agcgtgtgcg	tgaactggcg	gttcagtctg	cgaatggtag	taactcccag	tctgacctcg	420
actccatcca	ggctgaaatc	accagcgcc	tgaacgaaat	cgaccgtgta	tccggccaga	480
ctcagttcaa	cggcgtgaaa	gtcctggcgc	aggacaacac	cctgaccatc	cagggttggtg	540
ccaacgacgg	tgaactatc	gatattgatt	taaaagaaat	cagctctaaa	acactgggac	600
ttgataagct	taatgtccaa	gatgcctaca	ccccgaaaga	aactgctgta	accgttgata	660
aaactaccta	taaaaatggt	acagatccta	ttacagccca	gagcaatact	gatatccaaa	720
ctgcaattgg	cgggtggtga	acgggggtta	ctggggctga	tatcaaattt	aaagatggtc	780
aatactat	agatgttaaa	ggcgggtgct	ctgctgggtg	ttataaagcc	acttatgatg	840
aaactacaaa	gaaagttaat	attgatacga	ctgataaaac	tccgttggca	actgcggaag	900
ctacagctat	tccgggaacg	gccactataa	cccacaacca	aattgctgaa	gtaacaaaag	960
aggggtgtga	tacgaccaca	gttgcggtc	aacttgcctc	agcaggggtt	actggcgccg	1020
ataaggacaa	tactagcctt	gtaaaactat	cgtttgagga	taaaaacggt	aagggtattg	1080
atgggtggcta	tgacgtgaaa	atgggcgacg	atttctatgc	cgctacatat	gatgagaaaa	1140
cagggtgcaat	tactgctaaa	accactactt	atacagatgg	tactggcggt	gtcctaaactg	1200
gagctgtgaa	atttggtggc	gcaaatggta	aatctgaagt	tggtactgct	accgatggta	1260

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agacttactt agcaagcgac cttgacaaac ataacttcag aacaggcggt gagcttaaag	1320
aggttaatac agataagact gaaaaccac tgcagaaaat tgatgctgcc ttggcacagg	1380
ttgatacact tcgttctgac ctgggtgctg ttcagaacgg tttcaactcc gctatcacca	1440
acctgggcaa taccgtaaata aacctgtctt ctgcccgtag ccgtatcgaa gattccgact	1500
acgcaaccga agtctccaac atgtctcgcg cgcagattct gcagcaggcc ggtacctccg	1560
ttctggcgca ggcgcaaccg gtcccgcaaa acgtcctctc tttactgcgt tgataatagg	1620
ctggagcctc ggtggccatg cttcttgccc ctggggcctc ccccgagccc ctctcccct	1680
tcctgcaccc gtacccccgt ggtctttgaa taaagtctga gtgggcggc	1729

<210> SEQ ID NO 52

<211> LENGTH: 1518

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 52

atggcacaag tcattaatac aaacagcctg tcgctgttga cccagaataa cctgaacaaa	60
tcccagtcgg cactgggac tgctatcgag cgtttgtctt ccggtctgcg tatcaacagc	120
gcgaaagacg atgcggcagg acaggcgatt gctaaccgtt ttaccgcgaa catcaaaggt	180
ctgactcagg cttcccgtaa cgtaacgcg ggtatctcca ttgcgcagac cactgaaggc	240
gcgctgaacg aaatcaacaa caacctgcag cgtgtgcgtg aactggcggt tcagtctgcg	300
aatggtacta actcccagtc tgacctcgac tccatccagg ctgaaatcac ccagcgctg	360
aacgaaatcg accgtgtatc cggccagact cagttcaacg gcgtgaaagt cctggcgag	420
gacaacaccc tgacctoca ggttgggtgc aacgacgggt aaactatcga tattgattta	480
aaagaaatca gctctaaac actgggactt gataagctta atgtccaaga tgctacacc	540
ccgaaagaaa ctgctgtaac cgttgataaa actacctata aaaatggtag agatcctatt	600
acagcccaga gcaatactga tatccaaact gcaattggcg gtggtgcaac ggggggttact	660
ggggctgata tcaaatttaa agatgggtcaa tactatttag atgttaaagg cgggtgctct	720
gctggtgttt ataaagccac ttatgatgaa actacaaaga aagttaatat tgatacgact	780
gataaaaact cgttggcaac tgccggaagc acagctatcc ggggaacggc cactataacc	840
cacaacaaaa ttgctgaagt aacaaaagag ggtgttgata cgaccacagt tgcggctcaa	900
cttgctgcag caggggttac tggcgccgat aaggacaata ctagccttgt aaaactatcg	960
tttgaggata aaaacggtaa ggttattgat ggtggctatg cagtgaaat gggcgacgat	1020
ttctatgcg ctacatatga tgagaaaaca ggtgcaatta ctgctaaac cactacttat	1080
acagatggta ctggcgttgc tcaaaactgga gctgtgaaat ttggtggcgc aaatggtaaa	1140
tctgaagttg ttactgtac cgatggtaag acttacttag caagcgacct tgacaaacat	1200
aacttcagaa caggcgggtg gcttaagag gttataacag ataagactga aaaccactg	1260
cagaaaattg atgctgcctt ggcacagggt gatacacttc gttctgacct ggggtgcggt	1320
cagaaccgtt tcaactccgc tatcaccac ctgggcaata ccgtaataa cctgtcttct	1380
gcccgtagcc gtatcgaaga ttcgactac gcaaccgaag tctccaatat gtctcgcgcg	1440
cagattctgc agcaggccgg tacctcgtt ctggcgagg cgaaccagg tccgcaaac	1500

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gtctctctctt tactgcgt 1518

<210> SEQ ID NO 53
 <211> LENGTH: 1790
 <212> TYPE: RNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 53

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ggggaaaaua gagagaaaag aagaguaaga agaaaauuaa gagccaccau ggcacaaguc    60
auuaauacaa acagccuguc gcuguugacc cagaauaacc ugaacaaauc ccaguccgca    120
cugggcacug cuaucgagcg uuugucuucc ggucugcgua ucaacagcgc gaaagacgau    180
gcggcaggac aggcgauugc uaaccguuuu accgcgaaca ucaaaggucu gacucaggcu    240
ucccguaacg cuaacgacgg uaucuccauu gcgcagacca cugaaggcgc gcugaacgaa    300
aucaacaaca accugcagcg ugugcgugaa cuggcgguuc agucugcgaa ugguacuaac    360
ucccagucug accucgacuc cauccaggcu gaaauacccc agcgccugaa cgaaaucgac    420
cguguauccg gccagacuca guucaacggc gugaagucc uggcgagga caacaccug    480
accauccagg uuggugccaa cgacggugaa acuaucgaa uugauuuuaa agaaucagc    540
ucuaaaacac ugggacuuga uaagcuuaa guccaagau ccuacacccc gaaagaaacu    600
gcuguaacgg uuguaaaaac uaccuuaaaa aaugguacag auccuauuac agcccagagc    660
aaucuguaa uccaaacugc aauggcggu ggugcaacgg ggguuacugg ggcugauauc    720
aaaauuaaag auggucaaua cuuuuagau guuaaaggcg gugcuucugc ugguguuuau    780
aaagccacu augaugaaac uacaaagaaa guuaauuug auacgacuga uaaaacuccg    840
uuggcaacug cgaagcuac agcuauucgg ggaacggcca cuuaaccca caaccaaau    900
gcugaaguaa caaaagagg uguugauacg accacaguug cggcucaacu ugcugcagca    960
gggguuacug gcgccguuaa ggacaauacu agccuuguaa aacuaucguu ugaggauaaa    1020
aacgguagg uuauugaugg ugguauagca gugaauaugg gcgacgauu cuaugccgcu    1080
acauaugaug agaaaacagg ugcauuuacu gcuaaaacca cuacuauuac agaugguacu    1140
ggcguugcuc aaacuggagc ugugaaaauu ggugcgcaa augguaaauc ugaaguuguu    1200
acugcuaccg augguaagac uuacuuaagc agcgaccuug acaaacauaa cuucagaaca    1260
ggcgguagc uuaaagaggu uaaucagau aagacugaaa acccacugca gaaaauugau    1320
gcugccuugg cacagguuga uacacuucgu ucugaccugg gugcgguuca gaaccguuuc    1380
aacuccgcu ucaccaaccu gggcaauacc guaaaauacc ugucuucugc ccguagccgu    1440
aucgaagauu ccgacuacgc aaccgaaguc uccaacaugu cucgcgcgca gauucugcag    1500
caggccggua ccuccguucu ggcgcaggcg aaccagguuc cgcaaacgu ccucucuua    1560
cugcgugau auuaggcugg agccucggug gccaugcuuc uugcccuug ggcuccccc    1620
cagccccucc ucccuuuccu gcaccguac ccccgugguc uuugaauaaa gucugagugg    1680
gcggcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa    1740
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaucua    1790

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<210> SEQ ID NO 54
 <211> LENGTH: 506
 <212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 54

```

Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Leu Thr Gln Asn
1          5          10          15

Asn Leu Asn Lys Ser Gln Ser Ala Leu Gly Thr Ala Ile Glu Arg Leu
20          25          30

Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Gln
35          40          45

Ala Ile Ala Asn Arg Phe Thr Ala Asn Ile Lys Gly Leu Thr Gln Ala
50          55          60

Ser Arg Asn Ala Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu Gly
65          70          75          80

Ala Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu Ala
85          90          95

Val Gln Ser Ala Asn Gly Thr Asn Ser Gln Ser Asp Leu Asp Ser Ile
100         105         110

Gln Ala Glu Ile Thr Gln Arg Leu Asn Glu Ile Asp Arg Val Ser Gly
115         120         125

Gln Thr Gln Phe Asn Gly Val Lys Val Leu Ala Gln Asp Asn Thr Leu
130         135         140

Thr Ile Gln Val Gly Ala Asn Asp Gly Glu Thr Ile Asp Ile Asp Leu
145         150         155         160

Lys Glu Ile Ser Ser Lys Thr Leu Gly Leu Asp Lys Leu Asn Val Gln
165         170         175

Asp Ala Tyr Thr Pro Lys Glu Thr Ala Val Thr Val Asp Lys Thr Thr
180         185         190

Tyr Lys Asn Gly Thr Asp Pro Ile Thr Ala Gln Ser Asn Thr Asp Ile
195         200         205

Gln Thr Ala Ile Gly Gly Gly Ala Thr Gly Val Thr Gly Ala Asp Ile
210         215         220

Lys Phe Lys Asp Gly Gln Tyr Tyr Leu Asp Val Lys Gly Gly Ala Ser
225         230         235         240

Ala Gly Val Tyr Lys Ala Thr Tyr Asp Glu Thr Thr Lys Lys Val Asn
245         250         255

Ile Asp Thr Thr Asp Lys Thr Pro Leu Ala Thr Ala Glu Ala Thr Ala
260         265         270

Ile Arg Gly Thr Ala Thr Ile Thr His Asn Gln Ile Ala Glu Val Thr
275         280         285

Lys Glu Gly Val Asp Thr Thr Thr Val Ala Ala Gln Leu Ala Ala Ala
290         295         300

Gly Val Thr Gly Ala Asp Lys Asp Asn Thr Ser Leu Val Lys Leu Ser
305         310         315         320

Phe Glu Asp Lys Asn Gly Lys Val Ile Asp Gly Gly Tyr Ala Val Lys
325         330         335

Met Gly Asp Asp Phe Tyr Ala Ala Thr Tyr Asp Glu Lys Thr Gly Ala
340         345         350

Ile Thr Ala Lys Thr Thr Thr Tyr Thr Asp Gly Thr Gly Val Ala Gln
355         360         365

Thr Gly Ala Val Lys Phe Gly Gly Ala Asn Gly Lys Ser Glu Val Val

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370	375	380
Thr Ala Thr Asp Gly Lys Thr Tyr Leu Ala Ser Asp Leu Asp Lys His		
385	390	395 400
Asn Phe Arg Thr Gly Gly Glu Leu Lys Glu Val Asn Thr Asp Lys Thr		
	405	410 415
Glu Asn Pro Leu Gln Lys Ile Asp Ala Ala Leu Ala Gln Val Asp Thr		
	420	425 430
Leu Arg Ser Asp Leu Gly Ala Val Gln Asn Arg Phe Asn Ser Ala Ile		
	435	440 445
Thr Asn Leu Gly Asn Thr Val Asn Asn Leu Ser Ser Ala Arg Ser Arg		
	450	455 460
Ile Glu Asp Ser Asp Tyr Ala Thr Glu Val Ser Asn Met Ser Arg Ala		
	465	470 475 480
Gln Ile Leu Gln Gln Ala Gly Thr Ser Val Leu Ala Gln Ala Asn Gln		
	485	490 495
Val Pro Gln Asn Val Leu Ser Leu Leu Arg		
	500	505
<210> SEQ ID NO 55		
<211> LENGTH: 698		
<212> TYPE: PRT		
<213> ORGANISM: Artificial Sequence		
<220> FEATURE:		
<223> OTHER INFORMATION: Synthetic Polypeptide		
<400> SEQUENCE: 55		
Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Leu Thr Gln Asn		
1	5	10 15
Asn Leu Asn Lys Ser Gln Ser Ala Leu Gly Thr Ala Ile Glu Arg Leu		
	20	25 30
Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Gln		
	35	40 45
Ala Ile Ala Asn Arg Phe Thr Ala Asn Ile Lys Gly Leu Thr Gln Ala		
	50	55 60
Ser Arg Asn Ala Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu Gly		
	65	70 75 80
Ala Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu Ala		
	85	90 95
Val Gln Ser Ala Asn Ser Thr Asn Ser Gln Ser Asp Leu Asp Ser Ile		
	100	105 110
Gln Ala Glu Ile Thr Gln Arg Leu Asn Glu Ile Asp Arg Val Ser Gly		
	115	120 125
Gln Thr Gln Phe Asn Gly Val Lys Val Leu Ala Gln Asp Asn Thr Leu		
	130	135 140
Thr Ile Gln Val Gly Ala Asn Asp Gly Glu Thr Ile Asp Ile Asp Leu		
	145	150 155 160
Lys Gln Ile Asn Ser Gln Thr Leu Gly Leu Asp Thr Leu Asn Val Gln		
	165	170 175
Gln Lys Tyr Lys Val Ser Asp Thr Ala Ala Thr Val Thr Gly Tyr Ala		
	180	185 190
Asp Thr Thr Ile Ala Leu Asp Asn Ser Thr Phe Lys Ala Ser Ala Thr		
	195	200 205
Gly Leu Gly Gly Thr Asp Gln Lys Ile Asp Gly Asp Leu Lys Phe Asp		

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210					215					220					
Asp 225	Thr	Thr	Gly	Lys	Tyr 230	Tyr	Ala	Lys	Val	Thr 235	Val	Thr	Gly	Gly	Thr 240
Gly	Lys	Asp	Gly	Tyr 245	Tyr	Glu	Val	Ser	Val 250	Asp	Lys	Thr	Asn	Gly	Glu 255
Val	Thr	Leu	Ala 260	Gly	Gly	Ala	Thr	Ser 265	Pro	Leu	Thr	Gly	Gly 270	Leu	Pro
Ala	Thr	Ala	Thr	Glu	Asp	Val	Lys 280	Asn	Val	Gln	Val	Ala 285	Asn	Ala	Asp
Leu	Thr 290	Glu	Ala	Lys	Ala	Ala 295	Leu	Thr	Ala	Ala	Gly 300	Val	Thr	Gly	Thr
Ala 305	Ser	Val	Val	Lys	Met 310	Ser	Tyr	Thr	Asp	Asn 315	Asn	Gly	Lys	Thr	Ile 320
Asp	Gly	Gly	Leu	Ala 325	Val	Lys	Val	Gly	Asp 330	Asp	Tyr	Tyr	Ser	Ala 335	Thr
Gln	Asn	Lys	Asp 340	Gly	Ser	Ile	Ser	Ile 345	Asn	Thr	Thr	Lys	Tyr 350	Thr	Ala
Asp	Asp	Gly 355	Thr	Ser	Lys	Thr	Ala 360	Leu	Asn	Lys	Leu	Gly 365	Gly	Ala	Asp
Gly	Lys 370	Thr	Glu	Val	Val	Ser 375	Ile	Gly	Gly	Lys	Thr 380	Tyr	Ala	Ala	Ser
Lys 385	Ala	Glu	Gly	His	Asn 390	Phe	Lys	Ala	Gln	Pro 395	Asp	Leu	Ala	Glu	Ala 400
Ala	Ala	Thr	Thr	Thr 405	Glu	Asn	Pro	Leu	Gln 410	Lys	Ile	Asp	Ala 415	Ala	Leu
Ala	Gln	Val	Asp 420	Thr	Leu	Arg	Ser	Asp 425	Leu	Gly	Ala	Val	Gln 430	Asn	Arg
Phe	Asn 435	Ser	Ala	Ile	Thr	Asn	Leu 440	Gly	Asn	Thr	Val	Asn 445	Asn	Leu	Thr
Ser	Ala 450	Arg	Ser	Arg	Ile 455	Glu	Asp	Ser	Asp	Tyr 460	Ala	Thr	Glu	Val	Ser
Asn 465	Met	Ser	Arg	Ala	Gln 470	Ile	Leu	Gln	Gln	Ala 475	Gly	Thr	Ser	Val	Leu 480
Ala	Gln	Ala	Asn 485	Gln	Val	Pro	Gln	Asn	Val 490	Leu	Ser	Leu	Leu 495	Arg	Gly
Gly	Gly	Gly	Ser 500	Gly	Gly	Gly	Gly	Ser 505	Met	Met	Ala	Pro 510	Asp	Pro	Asn
Ala	Asn 515	Pro	Asn	Ala	Asn	Pro	Asn 520	Ala	Asn	Pro	Asn	Ala 525	Asn	Pro	Asn
Ala	Asn 530	Pro	Asn	Ala	Asn	Pro 535	Asn	Ala	Asn	Pro 540	Asn	Ala	Asn	Pro	Asn
Ala 545	Asn	Pro	Asn	Ala	Asn 550	Pro	Asn	Ala	Asn	Pro 555	Asn	Ala	Asn	Pro	Asn 560
Ala	Asn	Pro	Asn 565	Ala	Asn	Pro	Asn	Ala	Asn 570	Pro	Asn	Ala	Asn	Pro 575	Asn
Ala	Asn	Pro	Asn 580	Ala	Asn	Pro	Asn	Ala 585	Asn	Pro	Asn	Lys	Asn 590	Asn	Gln
Gly	Asn 595	Gly	Gln	Gly	His	Asn 600	Met	Pro	Asn	Asp	Pro 605	Asn	Arg	Asn	Val
Asp	Glu 610	Asn	Ala	Asn	Ala	Asn 615	Asn	Ala	Val	Lys 620	Asn	Asn	Asn	Asn	Glu

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<210> SEQ ID NO 56
<211> LENGTH: 692
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 56
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Met 1	Met	Ala	Pro	Asp 5	Pro	Asn	Ala	Asn 10	Pro	Asn	Ala	Asn	Pro	Asn	Ala 15
Asn	Pro	Asn	Ala 20	Asn	Pro	Asn	Ala	Asn 25	Pro	Asn	Ala	Asn	Pro 30	Asn	Ala
Asn	Pro	Asn	Ala 35	Asn	Pro	Asn	Ala 40	Asn	Pro	Asn	Ala	Asn 45	Pro	Asn	Ala
Asn	Pro	Asn	Ala 50	Asn	Pro	Asn	Ala 55	Asn	Pro	Asn	Ala 60	Asn	Pro	Asn	Ala
Asn 65	Pro	Asn	Ala	Asn	Pro 70	Asn	Ala	Asn	Pro	Asn	Ala 75	Asn	Pro	Asn	Ala 80
Asn	Pro	Asn	Lys 85	Asn	Asn	Gln	Gly	Asn 90	Gly	Gln	Gly	His	Asn 95	Met	Pro
Asn	Asp	Pro	Asn 100	Arg	Asn	Val	Asp	Glu 105	Asn	Ala	Asn	Ala 110	Asn	Asn	Ala
Val	Lys	Asn	Asn 115	Asn	Asn	Glu	Glu 120	Pro	Ser	Asp	Lys	His 125	Ile	Glu	Gln
Tyr 130	Leu	Lys	Lys	Ile	Lys 135	Asn	Ser	Ile	Ser	Thr	Glu 140	Trp	Ser	Pro	Cys
Ser 145	Val	Thr	Cys	Gly	Asn 150	Gly	Ile	Gln	Val	Arg 155	Ile	Lys	Pro	Gly	Ser 160
Ala	Asn	Lys	Pro 165	Lys	Asp	Glu	Leu	Asp 170	Tyr	Glu	Asn	Asp 175	Ile	Glu	Lys
Lys	Ile	Cys	Lys 180	Met	Glu	Lys	Cys	Ser 185	Ser	Val	Phe	Asn 190	Val	Val	Asn
Ser	Arg	Pro 195	Val	Thr	Met	Ala	Gln 200	Val	Ile	Asn	Thr 205	Asn	Ser	Leu	Ser
Leu 210	Leu	Thr	Gln	Asn	Asn 215	Leu	Asn	Lys	Ser	Gln 220	Ser	Ala	Leu	Gly	Thr
Ala 225	Ile	Glu	Arg	Leu 230	Ser	Ser	Gly	Leu	Arg 235	Ile	Asn	Ser	Ala	Lys	Asp 240
Asp	Ala	Ala	Gly 245	Gln	Ala	Ile	Ala	Asn 250	Arg	Phe	Thr	Ala	Asn 255	Ile	Lys
Gly	Leu	Thr 260	Gln	Ala	Ser	Arg	Asn 265	Ala	Asn	Asp 270	Gly	Ile	Ser	Ile	Ala

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Gln Thr Thr Glu Gly Ala Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg	275	280	285	
Val Arg Glu Leu Ala Val Gln Ser Ala Asn Ser Thr Asn Ser Gln Ser	290	295	300	
Asp Leu Asp Ser Ile Gln Ala Glu Ile Thr Gln Arg Leu Asn Glu Ile	305	310	315	320
Asp Arg Val Ser Gly Gln Thr Gln Phe Asn Gly Val Lys Val Leu Ala	325	330	335	
Gln Asp Asn Thr Leu Thr Ile Gln Val Gly Ala Asn Asp Gly Glu Thr	340	345	350	
Ile Asp Ile Asp Leu Lys Gln Ile Asn Ser Gln Thr Leu Gly Leu Asp	355	360	365	
Thr Leu Asn Val Gln Gln Lys Tyr Lys Val Ser Asp Thr Ala Ala Thr	370	375	380	
Val Thr Gly Tyr Ala Asp Thr Thr Ile Ala Leu Asp Asn Ser Thr Phe	385	390	395	400
Lys Ala Ser Ala Thr Gly Leu Gly Gly Thr Asp Gln Lys Ile Asp Gly	405	410	415	
Asp Leu Lys Phe Asp Asp Thr Thr Gly Lys Tyr Tyr Ala Lys Val Thr	420	425	430	
Val Thr Gly Gly Thr Gly Lys Asp Gly Tyr Tyr Glu Val Ser Val Asp	435	440	445	
Lys Thr Asn Gly Glu Val Thr Leu Ala Gly Gly Ala Thr Ser Pro Leu	450	455	460	
Thr Gly Gly Leu Pro Ala Thr Ala Thr Glu Asp Val Lys Asn Val Gln	465	470	475	480
Val Ala Asn Ala Asp Leu Thr Glu Ala Lys Ala Ala Leu Thr Ala Ala	485	490	495	
Gly Val Thr Gly Thr Ala Ser Val Val Lys Met Ser Tyr Thr Asp Asn	500	505	510	
Asn Gly Lys Thr Ile Asp Gly Gly Leu Ala Val Lys Val Gly Asp Asp	515	520	525	
Tyr Tyr Ser Ala Thr Gln Asn Lys Asp Gly Ser Ile Ser Ile Asn Thr	530	535	540	
Thr Lys Tyr Thr Ala Asp Asp Gly Thr Ser Lys Thr Ala Leu Asn Lys	545	550	555	560
Leu Gly Gly Ala Asp Gly Lys Thr Glu Val Val Ser Ile Gly Gly Lys	565	570	575	
Thr Tyr Ala Ala Ser Lys Ala Glu Gly His Asn Phe Lys Ala Gln Pro	580	585	590	
Asp Leu Ala Glu Ala Ala Ala Thr Thr Thr Glu Asn Pro Leu Gln Lys	595	600	605	
Ile Asp Ala Ala Leu Ala Gln Val Asp Thr Leu Arg Ser Asp Leu Gly	610	615	620	
Ala Val Gln Asn Arg Phe Asn Ser Ala Ile Thr Asn Leu Gly Asn Thr	625	630	635	640
Val Asn Asn Leu Thr Ser Ala Arg Ser Arg Ile Glu Asp Ser Asp Tyr	645	650	655	
Ala Thr Glu Val Ser Asn Met Ser Arg Ala Gln Ile Leu Gln Gln Ala	660	665	670	

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Gly	Thr	Ser	Val	Leu	Ala	Gln	Ala	Asn	Gln	Val	Pro	Gln	Asn	Val	Leu
		675					680					685			

Ser	Leu	Leu	Arg
	690		

<210> SEQ ID NO 57
 <211> LENGTH: 1620
 <212> TYPE: RNA
 <213> ORGANISM: Human metapneumovirus

<400> SEQUENCE: 57

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augagcugga agggugggau uaucuucagc cugcugauua caccucaaca cggccugaag      60
gagagcuacc uggaagagag cugcuccacc aucaccgagg gcuaccugag cgugcugcgg      120
accggcuggu acaccaacgu guucacccug gaggugggagc acguggagaa ccugaccugc      180
agcgacggcc cuagccgau caagaccgag cuggaccuga ccaagagcgc ucugagagag      240
cugaagaccg uguccgccga ccagcuggcc agagaggaac agaucgagaa ccucggcgag      300
agcagauucg ugcuggggcg caucgcucug ggagucgccc cugccgcugc agugacagcu      360
ggaguggcca uugcuaagac caucagacug gaaagcggag ugacagccau caacaaugcc      420
cugaagaaga ccaacgaggc cgugagcacc cugggcaaug gagugagagu gcuggccaca      480
gccgugcggg agcugaagga cuucgugagc aagaaccuga ccagagccau caacaagaac      540
aagugcgaca ucgaugaccu gaagauggcc gugagcuucu ccaguucaa cagacgguuc      600
cugaacgugg ugagacaguu cuccgacaac gcuggaauca caccugccau uagccuggac      660
cugaugaccg acgccgagcu ggcuagagcc gugcccaaca ugcccaccag cgcuggccag      720
aucaagcuga ugcuggagaa cagagccaug gugcggagaa agggcuucgg cauccugauu      780
gggguguaug gaagcuccgu gaucuacaug gugcagcugc ccaucucggg cgugaucgac      840
acaccucgcu ggauccugaa ggccgcuccu agcugcuccg agaagaaagg aaacuaugcc      900
ugucugcuga gagaggacca gggcugguac ugccagaacg ccggaagcac aguguacuau      960
cccaacgaga aggacugcga gaccagaggc gaccacgugu ucugcgacac cgcugccgga     1020
aucaacgugg ccgagcagag caaggagugc aacaucaaca ucagcacaac caacuacccc     1080
ugcaagguga gcaccggagc gcaccccauc agcauggugg cucugagccc ucugggcgcu     1140
cuggguggccu gcuauaaggg cguguccugu agcaucggca gcaaucgggu gggcaucauc     1200
aagcagcuga acaagggaug cuccuacauc accaaccagg acgccgacac cgugaccauc     1260
gacaacaccg uguaccagcu gagcaaggug gagggcgagc agcacgugau caagggcaga     1320
cccgugagcu ccagcuuca ccccaucaag uucccugagg accaguucaa cguggcccug     1380
gaccaggugu uugagaacau cgagaacagc caggcccugg uggaccagag caacagaau     1440
cuguccagcg cugagaaggg caacaccggc uucaucauug ugaucuuuc gaucgccgug     1500
cugggcagcu ccaugauccu ggugagcauc uucaucauuu ucaagaagac caagaaacc     1560
accggagccc cuccugagcu gagcggcgug accaacaauug gcuucauucc ccacaacuga     1620

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<210> SEQ ID NO 58
 <211> LENGTH: 1620
 <212> TYPE: RNA
 <213> ORGANISM: Human metapneumovirus

<400> SEQUENCE: 58

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augucuugga aagugaugau caucauuucg uuacucauaa caccuccagca cgggcuaaaag	60
gagaguuuuu uggaagaauuc auguaguacu auaacugagg gauaccucag uguuuuaaga	120
acaggcuggu acacuaaugu cuucacauua gaaguuggug auguugaaaa ucuuacaugu	180
acugauggac cuagcuuaau caaaacagaa cuugaucuaa caaaaagugc uuuuagggaa	240
cucaaaacag ucucugcuga ucaguuggcg agagaggagc aaauugaaaa ucccagacaa	300
ucaagauuug ucuuaggugc gauagcucuc ggaguugcua cagcagcagc agucacagca	360
ggcauugcaa uagccaaaac cauuaaggcu gagagugagg ugaauugcau uaaaggugcu	420
cucaaaacaa cuaauaagc aguauccaca uuagggaug gugugcgguu ccuagccacu	480
gcagugagag agcuuaaaga auuugugagc aaaaaccuga cuagugcau caacaggaa	540
aaauugaca uugcugaucu gaagauggcu gucagcuua gucauuucaa cagaagauuu	600
cuaaauguug ugccgagcuu uucagacaa gcagggaaua caccagcau aucauuggac	660
cugaugacug augcugagu ggccagagcu guaucuaca ugccaacauc ugcaggcgag	720
auaaaacuga uguuggagaa ccgcgcaaug guaaaggagaa aaggauuugg aaucugaua	780
ggggucucg gaagcucugu gauuuacaug guucaauugc cgaucuuugg ugucauagau	840
acaccuuguu ggaucaucaa ggcagucucc ucuugcucag aaaaaacgg gaauuauugc	900
ugccuccuaa gagaggauca agggugguau uguaaaaug caggaucuac uguuuacuac	960
ccaaugaaa aagacugcga aacaagaggu gaucauguuu uuugugacac agcagcagg	1020
aucaauugug cugagcauuc aagagaauuc aacaucaca uaucuacuac caacuacca	1080
ugcaauuca gcacaggaag acaccuaua agcauugguu cacuauacc ucucggugcu	1140
uuggugguu gcuuaaaagg gguuagcugc ucgaauugca gcaauugggu uggaaucauc	1200
aaacaauuac ccaaggcug cucauacaua accaaccagg augcagacac uguuacaauu	1260
gacaauaccg uguaucaacu aagcaaguu gaaggugaac agcauguaa aaaagggaga	1320
ccaguuucaa gcaguuuuga uccaaucaag uuuccgagg aucaguuaa uguugcgcu	1380
gaucaugcu ucgaagcau ugagaacagu caggcacuag uggaccaguc aaacaaaau	1440
cuaaacagug cagaaaaagg aaacacuggu uucauuuucg uaguauuuu gguugcuguu	1500
cuuggucuaa ccaugauuuc agugagcauc aucaucaua ucaagaaaac aaggagccc	1560
acaggagcac cuccagagcu gaaugguguc accaacggcg guuucuuacc acauaguua	1620

<210> SEQ ID NO 59

<211> LENGTH: 1620

<212> TYPE: RNA

<213> ORGANISM: Human metapneumovirus

<400> SEQUENCE: 59

augucuugga aagugaugau uucauuucg uuacucauaa caccucagca uggacuaaaa	60
gaaaguuuuu uagaagaauuc auguaguacu auaacugaag gauaucucag uguuuuaaga	120
acaggguuggu acaccaauugu cuuuacauua gaaguuggug auguugaaaa ucuuacaugu	180
acugauggac cuagcuuaau caaaacagaa cuugaccuaa ccaaaagugc uuuuagagaa	240
cucaaaacag uuucugcuga ucaguuagcg agagaagaac aaauugaaaa ucccagacaa	300
ucaagguuug uccuaggugc aaugcucuu ggaguugcca cagcagcagc agucacagca	360
ggcauugcaa uagccaaaac uauaaggcu gagagugaag ugaauugcau caaaggugcu	420

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cucaaaacaa ccaaugaggc aguaucacaa cuaggaaaug gagugcgggu ccuagccacu	480
gcaguaagag agcugaaaga auuugugagc aaaaaccuga cuagugcgau caacaagaac	540
aagugugaca uugcugauuu gaagauggcu gucagcuuca gucaguucac cagaagauuc	600
cuaaauguug ugcggcaguu uucagacaa gucagggaaua caccagcaau aucauuggac	660
cugaugaauug augcugagcu ggccagagcu guaucuauaca ugccaacauc ugcaggacag	720
auaaaaacuaa uguuagagaa ccgugcaaug gugaggagaa aaggauuugg aaucugaua	780
ggggucuaag gaagcucugu gauuuacauug guccagcugc cgaucuuugg ugucuaaaau	840
acaccuuguu ggauaaucac ggccagcucc ucuuguucag aaaaagaugg aaauuagcu	900
ugccuccuaa gagaggauca agggugguau uguaaaaaug caggauccac uguuuacuac	960
ccaaaugaaa aagacugcga aacaagaggu gaucauguuu uuugugacac agcagcaggg	1020
aucaauguug cugagcaauc aagagaauug aacaucacaa uaucuaccac caacuaccca	1080
ugcaaaugca gcacaggaag acaccuauac agcaugguug cacuaucacc ucucggugcu	1140
uugguagcuu gcuacaaagg gguuagcugc ucgacuggca guaaucaggu uggaauaau	1200
aaacaacuac cuaaaggcug cucauacaua acuaaccagg acgcagacac uguacaauu	1260
gacaacacug uguaucaacu aagcaaaguu gagggugaac agcauguaau aaaagggaga	1320
ccaguuucaa gcaguuuuga uccaaucagg uuuccugagg aucaguucac uguugcguu	1380
gaucaagucu uugaaagcau ugaaaacagu caagcacuag uggaccaguc aaacaaaau	1440
cugaacagug cagaaaaagg aaacacuggu uucauuuug uauuuuuuu gauugcuguu	1500
cuuggguuaa ccaugauuuc agugagcauc aucaucauaa ucaaaaaaac aaggagccc	1560
acaggggcac cuccggagcu gaaugguguu accaacggcg guuucuuacc gcauaguua	1620

<210> SEQ ID NO 60

<211> LENGTH: 1725

<212> TYPE: RNA

<213> ORGANISM: Human respiratory syncytial virus

<400> SEQUENCE: 60

auggaguugc caauccucaa aacaaugca auuaccacaa uccuugcugc agucacacuc	60
uguuucgcuu ccagucacaa caucacugaa gaauuuuauc aaucacauug cagugcaguu	120
agcaaaggcu aucuuagugc ucuaagaacu gguugguaua cuaguguuau aacuuagaa	180
uuaguuaua ucaaggaaaa uaguguaau ggaacagauu cuaagguaaa auugauaaaa	240
caagaauuag auuuuuuuu aaauugcugua acagaauugc aguugcucac gcaagcaca	300
ccagcagcca acauucgagc cagaagagaa cuaccaaggu uuaugaauu uacacucaau	360
aaucacaaa auaccuauu aacuuuagc aagaaaagga aaagaagauu ucuuggcuuu	420
uuguuaggug uuggaucugc aaucggcagu ggcauugcug uaucauaggu ccugcaccua	480
gaaggggaag ugaacacaa caaaagugcu cuacuaucca caaacaggc uguagucagc	540
uuaucaauug gaguuagugu cuuaccagc aaaguguuag accuacaaa cuuuuagau	600
aaacaguugu uaccuauuug gaacaagcaa agcugcagca uaucaacau ugaaacugug	660
auagaguucc aacaaaagaa caacagacua cuagagauua ccagggaauu uaguguuaau	720
gcagguguua cuacaccugu aagcacuuau auguuacua auagugaauu auuaucauu	780
aucaaugaua ugccuuuac aaauagucag aaaaaguuaa uguccaacaa uguuacaaa	840

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guuagacagc aaaguacuc uaucaugucc auaauaaagg aggaagucuu agcauaugua	900
guacaauuac cacauauagg uguauuagau acaccucguu ggaaacugca cacauccccc	960
cuauguacaa ccaacacaaa ggaagggucc aacaucugcu uaacaagaac cgacagagga	1020
ugguauugug acaaugcagg aucaguauc uucuucccac aagcugaaac auguaaaguu	1080
caaucgauc ggguaauuug ugacacaaug aacaguuaa cauuaccaag ugaaguaaa	1140
cucugcaaca uugacauau caaccccaaa uaugauugca aaauuugac uucaaaaaca	1200
gauguaagca gcuccguuau cacaucucua ggagccauug ugucaugcua uggcaaaacu	1260
aaauguacag cauccaauaa aaucguggg aucauaaaga cauuuucuaa cgggugugau	1320
uauguaucaa auaagggggu ggauacugug ucuguaggua auacauuaa uuauguaaa	1380
aagcaagaag gcaaaagucu cuauguaaaa ggugaaccaa uaauaaauuu cuaugacca	1440
uuaguguucc ccucugauga auuugaugca ucaauaucuc aagucaauga gaagauuaac	1500
cagagccuag cauuuuuugc uaaauccgau gaauuuuac auaauguaaa ugcugguaaa	1560
uccaccacaa auaucaugau aacuaucua auuauaguga uuauaguau auuguuauc	1620
uuauuugcag uuggacugcu ccuauacugc aaggccagaa gcacaccagu cacacuaagu	1680
aaggaucaac ugagugguau aaauaaauuu gcauuuagua acuga	1725

<210> SEQ ID NO 61

<211> LENGTH: 1617

<212> TYPE: RNA

<213> ORGANISM: Human parainfluenza virus

<400> SEQUENCE: 61

augccaauuu caauacuguu aaauuuuaca accaugauca uggcaucaca cugccaaaua	60
gacauacaaa aacucagca uguaggugua ugggucaaca gucccaaagg gaugaagaua	120
ucacaaaacu ucgaacaag auaucuauc cugagucua uacaaaaau agaagauucu	180
aacucuugug gugaccaaca gaucaagcaa uacaagaggu uauuggauag acugaucau	240
ccuuuuauug auggacuaag auuacagaag gaugugauug ugacuaauca agaauccaau	300
gaaaacacug auccagaac agaacgauuc uuuggagggg uauuugaac uauugcucua	360
ggaguagcaa ccucagcaca aaauacagca gcaguugcuc ugguuagaag caagcaggca	420
agaucagaca uugaaaaacu caaggaagca aucagggaca caaauaaagc agugcaguca	480
guucagagcu cuguaggaaa uuuguauagua gcauuuuau caguccagga uuaugucaac	540
aaagaaucg ugccaucgau ugcgagacua gguugugaag cagcaggacu ucaguaggg	600
auugcauuua cacagcaua cucagaauua acaauuuau uuggugauaa cauaggauug	660
uuacaagaaa aaggauuaa auuacaaggu auagcaucau uauaccguac aaauaucaca	720
gaaauuuca caacaucaac aguugacaaa uaugauuuu augaucuaa auuuacagaa	780
ucaauaaagg ugagaguuau agauguugau uugaaugau acucaauaac ccuccaaguc	840
agacucccuu uauugaccag acugcugaac acucuuuacu acaaguaga uuccauauca	900
uacaauaucc aaauagaga augguauuac ccucuuccca gccauaucau gacgaaaggg	960
gcauuucuaug guggagcaga ugucaaagaa ugcauagaag cauucagcag uuauuuuugc	1020
ccuucugauc caggauuuu acuaaaaccu gaaauugaga gcugucuauc aggaaacaua	1080
ucccaauguc caagaaccac agucacauca gacauaguuc cuagguaugc auuugucaau	1140

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ggaggagugg uugcgaauug uauaacaacu acauguacau gcaaugguau cgguauuaga	1200
aucaaccaac caccugauca aggagucaaa auuauaacac auaaagaauug uauuacaaua	1260
gguaucacag gaauvcuauu caacacaaaac aaagaaggaa cucuugcauu cuacacacca	1320
gacgacauaa cauuaaacia uucuguugca cuugauccga uugacauauc aaucgagcuc	1380
aacaaggcca aaucagauuc ugaggaauc aaagaauuga uaagaagguc aaaucaaaag	1440
cuagaauucua uuggaaguug gcaucaauuc agcacuacaa ucauaguauu uuugauuauug	1500
augauuuauu uguuuuauu uauuauaaca auauuuacaa uugcauuuaa guuuuacaga	1560
auucaaaaaga gaaucgagu ggaucaaaau gaaagccgu augauuuuac aaacaag	1617

<210> SEQ ID NO 62

<211> LENGTH: 1716

<212> TYPE: RNA

<213> ORGANISM: Human parainfluenza virus 3

<400> SEQUENCE: 62

auggaauacu ggaagcacac caaccacgga aaggauvcug guauugagcu ggagacaucc	60
acagccacuc auggcaacaa gvcaccaac aagauaacau auauuuugug gacgauuacc	120
cuggguuuau uaucaauagu cuucauacua gugcuacua auuccauca aagugaaaag	180
gcccgcgaau cauvcuaca agacauaaau aaugauuuu uggaaguuc agaaaagau	240
caaguggcau cggauauuac uauugauuc auacagucag gagugaauac aaggcuucuu	300
acauuucaga gucaugucca gaauuuauu ccaauaucau ugacacacaa auuauvcgau	360
cuuaggaaau ucauuaguga auuacauuu agaaugaua aucaagaagu gccaccacaa	420
agauuacac augauguggg uauuuuaccu uuuuuuccag augauuucug gagauvcag	480
ucugguucuc caucuuugau gaaauucua auuuuagau uauugcggg accaggauu	540
uuagcuauvc caacgacug ugaugvcug gucagaaccc cguccuuagu gauuuuagau	600
cugauuuuug cuuacaccuc auuacuuuu acucgagguu gccaggauu agggauuau	660
uaucaaguau uacagauagg gauuuuacu guuauucag auuugguacc ugauuuuuu	720
ccuaggauuc cucauaccuu caacauuuu gacauuagaa agucauguc ucuagcacuc	780
cuuuuacag auguauuau acuguguuu acccaaaag uugauuagag aucagauuu	840
gcaucaucag gcauagaaga uauugauuc gauuuugua auuauagug cucauucug	900
acaacaagau uuaagaaua uauuuuaguu uuugauuac cauauvcggc auuuuaccca	960
ucugugggac caggguuuu cuuacaaaggc auuuuuuuu uucvcggguu ugaggguuu	1020
gaacauccaa uuuuagagaa ugcauucug aacacacug gguguccug gaaacacag	1080
agagacugua aucaagcuc ucauugucc ugguuuucag auagaaggau ggucacuc	1140
auuuuugug uugacaaggg cuugaacua guuccaaaa ugaagguaug gacgauuuc	1200
augagacaaa auuacuggg gucagaagg agauuucuc ucuagguaa caagauuc	1260
auuacacaa gauuacaaug uuggcacagc aguuuacau uaggauuuu ugacuuuac	1320
gacacagug auuuuaggau auuuugga ugguuuuug ugcuaucag accaggaaac	1380
auuauuguc auugggaca uucaugucc gaugaugua uauvcggag auuaccgau	1440
gcauuccac ucauuccac aggaagcau guuauucug ucauuuuga cucacaaaa	1500
ucgagagua accagucuu auuuuacua acagcaaccg auuggguuu cgagcuggu	1560

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auccgaaaca aaacacucuc agcuggguac acaacaacaa gcugcauuac acacuauaac	1620
aaaggguaau guuuucauau aguagaaaua aaucuaaaaa gcuuaaacac auuucaaccc	1680
auguuguuca aaacagagau uccaaaaagc ugcagu	1716

<210> SEQ ID NO 63
 <211> LENGTH: 1716
 <212> TYPE: RNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 63

auggaauacu ggaagcacac caaccacggc aaggacgccc gcaacgagcu ggaaaccagc	60
acagccacac acggcaacaa gcugaccaac aagaucaccu acauccugug gaccaucacc	120
cuggugcugc ugagcaucgu guucaucauc gugcugacca auagcaucac gagcgagaag	180
gccagagaga gccugcugca ggacaucaac aacgaguuca uggaagugac cgagaagauc	240
cagguggcca gcgacaacac caacgaccug auccagagcg gcgugaacac ccggcugcug	300
accauccaga gccacgugca gaacuacauc cccaucagcc ugacccagca gaucagcgac	360
cugcggaagu ucaucagcga gaucaccauc cggaacgaca accaggaagu gccccccag	420
agaauacccc acgacguggg caucaagccc cugaacccc acgaauucug gcgguguaca	480
agcgccugc ccagccugau gaagaccccc aagaucggc ugaugccug ccuggacug	540
cuggccaugc cuaccacagu ggauggcugu gugcggaccc ccagccugcu gaucacgau	600
cugaucuacg ccuacaccag caaccugauc acccggggcu gccaggauau cggaagagc	660
uaccaggugc ugcagaucgg caucaucacc gugaacuccg accugugcc cgaccugaac	720
ccucggauca gccacaccuu caacaucaac gacaacagaa agagcugcag ccuggcucug	780
cugaacaccg acguguacca gcugugcagc acccccaggc uggacgagag aagcgacuac	840
gccagcagcg gcaucgagga uaucgugcug gacaucguga acuaacgagg cagcaucagc	900
accacccggg ucaagaacaa caacaucaac uucgaccagc ccuacggcgc ccuguacccu	960
ucugugggcc cuggcaucua cuacaagggc aagaucacu uccugggcu cgggggccug	1020
gaacacccca ucaacgagaa cgccaucugc aacaccaccg gcugcccgug caagaccag	1080
agagacugca aucaggccag ccacagcccc ugguucagcg accgcagaau ggucaacucu	1140
aucaucgugg uggacaaggg ccugaacagc gugcccaagc ugaagugug gacaauacg	1200
augcgccaga acuaucgggg cagcgagggc agacuucugc ugcugggaaa caagaucuac	1260
aucuacaccc gguccaccag cuggcacagc aaacugcagc ugggaaucau cgacaucacc	1320
gacuacagcg acauccggau caaguggacc uggcacaacg ugcugagcag acccggaac	1380
aaugagugcc cuuggggcca cagcugcccc gauggaugua ucaccggcgu guacaccgac	1440
gccuaccccc ugaauccuac cgguccauac guguccagcg ugaucugga cagccagaaa	1500
agcagaguga accccgugau cacauacagc accgccaccg agagagugaa cgaacuggcc	1560
aucagaaaca agaccugag cgccggcuac accaccacaa gcugcaucac acacuacaac	1620
aagggcuacu gcuuccacau cguggaaauc aaccacaagu ccugaacac cuuccagccc	1680
augcuguuca agaccgagau cccaagagc ugcucc	1716

<210> SEQ ID NO 64

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<211> LENGTH: 1617
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 64
augcccauca gcauccugcu gaucaucacc acaaugauca uggccagcca cugccagauc      60
gacaucacca agcugcagca cgugggcgug cucgugaaca gcccgaagg caugaagauc      120
agccagaacu ucgagacacg cuaccugauc cugagccuga uccccaagau cgaggacagc      180
aacagcugcg gcgaccagca gaucaagcag uacaagcgcg ugcuggacag acugaucauc      240
ccccuguacg acggccugcg gcugcagaaa gacgugaucg ugaccaacca ggaaagcaac      300
gagaacaccg acccccggac cgagagauuc uucggcgcgcg ugaucggcac aaucgcccug      360
ggaguggcca caagcgccca gauuacagcc gcuguggccc ugguggaagc caagcaggcc      420
agaagcgaca ucgagaagcu gaaagaggcc auccgggaca ccaacaaggc cgugcagagc      480
gugcagucca gcgugggcaa ucugaucgug gccaucaagu ccgugcagga cuacgugaac      540
aaagaaucg ugcuccuauu cgcccggcug ggcugugaag cugccggacu gcagcugggc      600
auugcccuga cacagcacua cagcgagcug accaacaucu ucggcgacaa caucggcagc      660
cugcaggaaa agggcauuua gcugcaggga aucgccagcc uguaccgcac caacaucacc      720
gagaucuuca ccaccagcac cguggauaag uacgacaucu acgaccugcu guuacccgag      780
agcaucaaag ugcgcgugau cgacguggac cugaacgacu acagcaucac ccugcaagug      840
cggcugcccc ugcugaccag acugcugaac acccagaucu acaaggugga cagcaucucc      900
uacaacaucc agaaccgcca gugguacauc ccucugccca gccacauuau gaccaagggc      960
gccuuucugg gcggaagcga cgugaaagag ugcaucgagg ccuucagcag cuacaucugc     1020
cccagcgacc cuggcuucgu gcugaaccac gagauggaaa gcugccugag cggaacauc     1080
agccagugcc ccagaaccac cgugaccucc gacaucgugc ccagauacgc cuucgugaau     1140
ggcgcguggg uggccaacug cauccaccac accuguaccu gcaacggcau cggcaaccgg     1200
aucaaccagc cucccgauca gggcgugaag auuauacccc acaagagug uaacaccauc     1260
ggcaucaacg gcaucguguu caauaccaac aaagagggca ccugggccuu cuacaccccc     1320
gacgauauca ccugaaaca cuccguggcu cuggacccca ucgacaucuc caucgagcug     1380
aacaaggcca agagcgaccu ggaagagucc aaagagugga uccggcgag caaccagaag     1440
cuggacucua ucggcagcug gcaccagagc agcaccacca ucaucgugau ccugauuau     1500
augauuaucc uguucaucau caacauuacc aucaucacua ucgccaauaa guacuaccgg     1560
auccagaaac ggaaccgggu ggaccagaau gacaagcccu acgugcugac aaacaag      1617

<210> SEQ ID NO 65
<211> LENGTH: 4062
<212> TYPE: RNA
<213> ORGANISM: Middle East respiratory syndrome coronavirus

<400> SEQUENCE: 65
augauacacu caguguuucu acugauguuc uuguuaacac cuacagaaaag uuacguugau      60
guagggccag auucuguuaa gucugcuugu auugagguug auauacaaca gaccuucuuu     120
gauaaaaauu ggccuaggcc aaauauguuu ucuaaggcug acgguaauuu auaccucaa     180

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ggccguacau	auucuaacau	aacuaucacu	uaucagguc	uuuuuccua	ucaggagac	240
cauggugaua	uguauuuua	cucugcagga	caugcuacag	gcacaacucc	acaaaaguug	300
uuuguagcua	acuaauucua	ggacgucaaa	caguuuugcua	auggguuugu	cguccguaua	360
ggagcagcug	ccaauuccac	uggcacuguu	auuuuuagcc	caucuaccag	cgcuacuaua	420
cgaaaaauuu	accucugcuu	uauugcgggu	ucuucaguug	guaaauucuc	agaugguaaa	480
augggccgcu	ucuucaauca	uacucuguu	cuuuugcccg	auggaugug	cacuuuacuu	540
agagcuuuuu	auuguauucu	agagccucgc	ucuggaauc	auuguccugc	uggcaauucc	600
uauacuucuu	uugccacuua	ucacacuccu	gcaacagauu	guucugaugg	caauuacaau	660
cguaaugcca	gucugaacuc	uuuuaggag	uauuuuauu	uacguaacug	caccuuuau	720
uacacuuaua	acauuaccga	agaugagauu	uuagaguggu	uuggcuuuac	acaaacugcu	780
caagguguuc	accucucuc	aucucggau	guugauuugu	acggcggcaa	uauuuucaa	840
uuugccaccu	ugccuguuu	ugauacuau	aaguauuau	cuaucuuucc	ucacaguauu	900
cguucuauc	aaagugauag	aaaagcuug	gcugccuuc	acguauaua	acuucaaccg	960
uuaacuuucc	uguuggauu	uucuguugau	gguuauauac	gcagagcuau	agacuguggu	1020
uuuaaugauu	ugucacaacu	ccacugcuca	uauuauuccu	ucgauguuga	aucuggaguu	1080
uauucaguuu	cgucuuucga	agcaaaaccu	ucuggcucag	uuguggaaca	ggcugaaggu	1140
guugaaugug	auuuuucacc	ucucugucu	ggcacaccuc	cucagguuuu	uaauuucag	1200
cguuugguuu	uuaccaauug	cauuuauau	cuuaccuuu	ugcuuucacu	uuuuucugug	1260
aaugauuuuu	cuuguaguca	aaauucucca	gcagcaauug	cuagcaacug	uuauucuuca	1320
cugauuuugg	auuuuuuuc	auaccacuu	aguauuauu	ccgaucucag	uguuaguucu	1380
gcugguccaa	uauccaguu	uauuuuaua	caguuccuuu	cuaauccac	auguuugauc	1440
uuagcgacug	uuccucauaa	ccuuacuacu	auuacuaagc	cucuuaagua	cagcuauuu	1500
aacaagugcu	cucgucuuu	uucugaugau	cguacugaag	uaccucaguu	agugaacgcu	1560
aaucuuuacu	caccucugug	auccauuguc	ccaucacug	uguggggaaga	cgugauuuu	1620
uauaggaaac	aacuaucucc	acuugaaggu	gguggcuggc	uuguugcuag	uggcucaacu	1680
guugccauga	cugagcauuu	acagaugggc	uuugguauu	caguucaaua	ugguacagac	1740
accaauaugug	uuugccccaa	gcuugaauu	gcuauugaca	caaaaauugc	cucucauuu	1800
ggcaauugcg	uggauuauuc	cccuauuggu	guuucgggc	gugguuguuu	ucagaauugc	1860
acagcugug	guguucgaca	gcagcgcuu	guuuauugug	cguaccagaa	uuuauuggc	1920
uauuuuucug	augauggcaa	cuacuacug	cugcgugcuu	guguuagugu	uccuguuucu	1980
gucaucuaug	auaaagaaac	uaaaaccac	gcuacucua	uugguagugu	ugcaugugaa	2040
cacauuucuu	cuaccauguc	ucaauucucc	cguucucagc	gaucaaugcu	uaaacggcga	2100
gauucuaacu	auggccccu	ucagacaccu	guugguugug	uccuaggacu	uguuauuucc	2160
ucuuuguuug	uagaggacug	caaguugcu	cucggucaau	cucucuguc	ucuuccugac	2220
acaccuagua	cucucacacc	ucgcagugug	cgucucuguc	caggugaaau	gcgcuuugca	2280
uccauugcuu	uuauucaucc	cauucagguu	gaucaacuua	auaguaguua	uuuuuuuuu	2340
aguauacca	cuaauuuuuc	cuuugugug	acucaggagu	acauucagac	aaccauucag	2400
aaaguucug	uugauuguaa	acaguacguu	ugcaaugguu	uccagaagug	ugagcauuu	2460

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cugcgcgagu	auggccaguu	uuguuccaaa	auaaaccagg	cucuccaugg	ugccaauuuu	2520
cgccaggau	auucuguacg	uaauuuguuu	gcgagcguga	aaagcucuca	aucaucuccu	2580
aucauaccag	guuuuggagg	ugacuuuuau	uugacacuuc	uagaaccugu	uucuauaucu	2640
acuggcaguc	guagugcacg	uagugcuauu	gaggauuugc	uauuugacaa	agucacuaua	2700
gcugauccug	guuauaugca	agguuacgau	gauuguaugc	agcaaggucc	agcaucagcu	2760
cgugaucuuu	uuugugcuca	auauguggcu	gguuauaaag	uauuaccucc	ucuuauaggau	2820
guuauauagg	aagccgcgua	uacuucacuc	uugcuuggca	gcuaagcagg	uguuggcugg	2880
acugcuggcu	uauccuccuu	ugcugcuauu	ccauuugcac	agaguauyuu	uuauaggguu	2940
aacggugug	gcuuuacuca	acagguucuu	ucagagaacc	aaaagcuuuu	ugccaauaag	3000
uuuauucagg	cucugggagc	uagcaaaaca	ggcuucacua	caacuaauga	agcuuuucgg	3060
aagguucagg	augcugugaa	caacaauugca	caggcucua	ccaaauuagc	uagcgagcu	3120
ucuaauacuu	uugggugcu	uuccgccucu	auuggagaca	ucauacaacg	ucuugauguu	3180
cucgaacagg	acgccc aaau	agacagacuu	auuaauggcc	guuugacaac	acuaaaugcu	3240
uuuguugcac	agcagcuugu	ucguuuccgaa	ucagcugcuc	uuuccgcuca	auuggcuaaa	3300
gauaaaguca	augagugugu	caaggcaca	uccaagcguu	cuggauuuug	cggucaaggc	3360
acacauauag	uguccuuugu	uguaaaugcc	ccuaauggcc	uuuacuuuuu	gcauguuggu	3420
uauuaccua	gcaaccacau	ugagguuguu	ucugcuuau	gucuuuugcg	ugcagcuaac	3480
ccuacuaauu	guauagcccc	uguuaauggc	uacuuuuuu	aaacuaauaa	cacuaggauu	3540
guugaugagu	ggucauauac	uggcucguc	uucuaugcac	cugagcccau	caccucucuu	3600
aaucuaagu	auguugcacc	acaggugaca	uaccaaaca	uuucuaauaa	ccuccuccu	3660
ccucucucg	gcaauuccac	cgguuugac	uuccaagau	aguuggauga	guuuuucaaa	3720
aauguuagca	ccaguauacc	uaauuuuggu	ucucuaacac	agaauauuac	uacauuacuc	3780
gaucuuaccu	acgagauguu	gucucuuaa	caaguuguua	aagcccuuaa	ugagcuuac	3840
auagaccuaa	aagagcuugg	caauuauacu	uauuacaaca	aauggccgug	guacauuugg	3900
cuugguuuca	uugcugggcu	uguugccuuu	gcucuaugcg	ucuuuucuu	acugugcugc	3960
acugguugug	gcacaaacug	uauugggaaa	cuuaagugua	aucguuugug	ugauagauac	4020
gaggauuacg	accucgagcc	gcuaaagguu	cauguucacu	aa		4062

<210> SEQ ID NO 66

<211> LENGTH: 4062

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 66

augauacacu	caguguuucu	acugauguuc	uuguuaacac	cuacagaaag	uuacguugau	60
guagggccag	auucuguuua	gucugcuugu	auugagguug	auauacaaca	gacuuucuuu	120
gauaaaacuu	ggccuaggcc	aaugauguu	ucuaaggcug	acggauuuau	auaccucaa	180
ggccguacau	auucuaacau	aacuaucacu	uaucaagguc	uuuuucccu	ucaggagagc	240
cauggugaua	uguauuguua	cucugcagga	caugcuacag	gcacaacucc	acaaaaguug	300
uuuguagcu	acuaauucua	ggacgucaaa	caguuuugcu	auggguuugu	cguccguaua	360

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ggagcagcug	ccaauuccac	uggcacuguu	auuuuuagcc	caucuaccag	cgcuaauua	420
cgaaaaauuu	accugcguu	uauugcgggu	ucuucaguug	guauuuucuc	agaugguaaa	480
augggccgcu	ucuucaauca	uacucuaguu	cuuuugcccg	auggaugugg	cacuuuacuu	540
agagcuuuuu	auuguauucu	ggagccucgc	ucuggaauc	auuguccugc	uggcaauucc	600
uauacuucuu	uugccacuua	ucacacuccu	gcaacagauu	guucugaugg	caauuacaau	660
cguaaugcca	gucugaacuc	uuuuuaggag	uauuuuuuu	uacguaacug	caccuuuau	720
uacacuuaua	acauuaccga	agaugagauu	uuagaguggu	uuggcuuuac	acaaucugcu	780
caagguguuc	accucuucuc	aucucggau	guugauuugu	acggcggcaa	uauuuucaa	840
uuugccaccu	ugccguuuu	ugauacuauu	aaguauuuu	cuaucauucc	ucacaguauu	900
cguucuauc	aaagugauag	aaaagcuugg	gcugccuucu	acguauauaa	acuucaaccg	960
uuuacuuucc	uguuggauuu	uucuguugau	gguuauauac	gcagagcuau	agacuguggu	1020
uuuaaugauu	ugucacaacu	ccacugcuca	uauuauuccu	ucgauguuga	aucuggaguu	1080
uauucaguuu	cgucuuucga	agcaaaaccu	ucuggcucag	uuguggaaca	ggcugaaggu	1140
guugaaugug	auuuuucacc	ucucugucu	ggcacaccuc	cucagguuuu	uauuuucaag	1200
cguuugguuu	uuaccaauug	cauuuauauu	cuuaccaaau	ugcuuucacu	uuuuucugug	1260
aaugauuuuu	cuuguaguca	aaauucucca	gcagcaauug	cuagcaacug	uuauucuuca	1320
cugauuuugg	auuacuuuuc	auaccacuuu	aguauuauuu	ccgaucucag	uguuaguucu	1380
gcugguccaa	uauccaguuu	uauuuuuuuu	caguccuuuu	cuaaucccac	auguuugauu	1440
uuagcgacug	uuccucauaa	ccuuacuacu	auuacuaagc	cucuuuagua	cagcuauuuu	1500
aacaagugcu	cucgucuuuc	uucugaugau	cguacugaag	uaccucaguu	agugaacgcu	1560
aaucuuuacu	caccucugug	auccauuguc	ccauccacug	ugugggaaga	cggugauuuu	1620
uauaggaaac	aacuaucucc	acuugaaggu	gguggcuggc	uuguugcuag	uggcucaacu	1680
guugccauga	cugagcauuu	acagaugggc	uuugguuuu	caguucaaua	ugguacagac	1740
accaauaugug	uuugccccaa	gcuugaauuu	gcuaaugaca	caaaaauugc	cucucauuu	1800
ggcaauugcg	uggaauuuuc	ccucuauggu	guuucgggcc	gugguguuuu	ucagaauugc	1860
acagcuguag	guguucgaca	gcagcgcuuu	guuuuauaug	cguaccagaa	uuuauuggc	1920
uauuuuucug	augauggcaa	cuacuacugu	uugcgugcuu	guguuagugu	uccuguuuuc	1980
gucaucuaug	auaaagaaac	uaaaaccac	gcuaucuaau	uugguagugu	ugcaugugaa	2040
cacauuucuu	cuaccauguc	ucaauacucc	cguucuaagc	gaucaauugc	uaaacggcga	2100
gauucuaacu	auggcccccu	ucagacaccu	guugguugug	uccuaggacu	uguuaauucc	2160
ucuuuguucg	uagaggacug	caaguugccu	cuuggucaau	cucucugugc	ucuuuccugac	2220
acaccuagua	cucucacacc	ucgcagugug	cgcucuguuu	caggugaaau	gcgcuuuggca	2280
uccauugcuu	uuauuacucc	uauucagguu	gaucaacuua	auaguaguua	uuuuuuuuu	2340
aguauacca	cuaauuuuuu	cuuugguug	acucaggagu	acauucagac	aaccauucag	2400
aaaguuaucg	uugauuguaa	acaguacguu	ugcaaugguu	uccagaagug	ugagcauuu	2460
cugcgcgagu	auggccaguu	uuguuccaaa	auaaaccagg	cucuccaugg	ugccaauuu	2520
cgccaggau	auucuguacg	uauuuuguuu	gcgagcguga	aaagcucua	aucaucuccu	2580
aucauaccag	guuuuggagg	ugacuuaauu	uugacacuuc	uggaaccugu	uucuauaucu	2640

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acuggcaguc guagugcacg uagugcuauu gaggauuugc uauuugacaa agucacuaua	2700
gcugauccug guuauaugca agguuacgau gauugcaugc agcaaggucc agcaucagcu	2760
cgugaucuua uuugugcuca auauguggcu gguuacaaag uauuaccucc ucuuauggau	2820
guuaauaugg aagccgcgua uacuucacuc uugcuuggca gcuaugcagg uguuggcugg	2880
acugcuggcu uauccuccuu ugcugcuauu ccuuuugcac agaguauuuu uuauagguaa	2940
aacggugugug gcauuacuca acagguucuu ucagagaacc aaaagcuuau ugccaauaag	3000
uuuaaucagg cucugggagc uaugcaaaca ggcuuacuca caacuaauga agcuuuucag	3060
aagguucagg augcugugaa caacaugca caggcucuaa ccaauuagc uagcgagcua	3120
ucuaauacuu uugggucuaa uuccgccucu auuggagaca ucauacaacg ucuugauguu	3180
cucgaacagg acgcccacuu agacagacuu auuaauggcc guuugacaac acuaaaugcu	3240
uuuguugcac agcagcuugu ucguuuccga ucagcugcuc uuuccgcuca auuggcuaaa	3300
gauaaaguca augagugugu caaggcacia uccaagcguu cuggauuuug cggucaaggc	3360
acacauauag uguccuuugu uguaaaugcc ccuaauggcc uuuaacuaua gcauguuggu	3420
uauuaccuaa gcaaccacau ugagguuguu ucugcuuauu gucuuuugcg ugcagcuac	3480
ccuacuaauu guauagcccc uguuaauggc uacuuuuuaa aaacuaaua cacuaggauu	3540
guugaugagu ggucuuauac uggcucgucc uucuaugcac cugagcccau uaccuccuu	3600
aaucuaaagu auguugcacc acaggugaca uaccaaaca uuucuaaua ccuccuccu	3660
ccucuuucug gcauuuccac cgggaugac uuccaagau aguuggauga guuuuucaaa	3720
aauguuagca ccaguauacc uauuuuuggu ucccuaacac agauuaauac uacauuacuc	3780
gaucuuaccu acgagauguu gucucuuaa caaguuguua aagcccuua ugagcuuac	3840
auagaccuaa aagagcuugg caauuauacu uauuacaaca aauggccgug guacuuuug	3900
cuugguuua uugcugggcu uguugccua gcucuaugcg ucuucuaua acugugcugc	3960
acugguugug gcacaaacug uauugggaaa cuuaagugua aucguuguug ugauagauac	4020
gaggauuacg accucgagcc gcauaagguu cauguucacu aa	4062

<210> SEQ ID NO 67

<211> LENGTH: 1845

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 67

augauccacu ccguguuccu ccuauuguu cuguugaccc ccacugaguc agacugcaag	60
cucccgucug gacagucccu gugugcgug ccugacacuc cuagcacuc gacccacgc	120
uccgugcggu cggugccug cgaaaugcg cuggccucca ucgcuucaa ucaccaauc	180
caaguggauc agcugaauag cucguuuuuc aagcugucca uccccacgaa cuucucguu	240
ggggucaccc aggaguacau ccagaccaca auucagaagg ucaccgucga uugcaagcaa	300
uacgugugca acggcuucca gaagugcgag cagcugcuga gagaauacgg gcaguuuugc	360
agcaagauc accaggcgcu gcauggagcu aacuugcgcc aggacgacuc cgugcgcaac	420
cucuugccu cugugaaguc auccagucc ucccaaua uccgggaau cgaggaggac	480
uuaaccuga ccucucgga gcccgugug aucagcacg guagcagauc ggcgcgcua	540

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gccauugaag aucuucuguu cgacaagguc accaucgccg auccgggcua caugcagggg	600
uacgacgacu guaugcagca gggaccagcc uccgcgaggg accucaucug cgcgcaauac	660
guggccgggu acaaaugcu gccuccucug auggauguga acauggaggc cgcuaauacu	720
ucguccucug ucggcucuaug cgcgcggcug ggguggagcg ccggccuguc cuccuucgcc	780
gcuaucuccu uugcacaauu cauuuucua cggcucaacg gcgugggcau uacucaacaa	840
guccugucgg agaaccagaa guugaucgca aacaaguua aucaggcccu gggggccaug	900
cagacuggau ucacucagac uaacgaagcg uuccagaagg uccaggagcg ugugaacaac	960
aacgcccagg cgcucuaaaa gcuggccucc gaacucagca acaccuucgg agccaucagc	1020
gcaucgaucg gugacauau ucagcggcug gacgugcug agcaggagcg ccagaucgac	1080
cgccucauca acggagcgcu gaccaccuug aaugccuucg uggcacaaca gcugguuccg	1140
agcgaauacg cggcacuuuc cgcaccauc gccaaggaca aagucaacga augcgugaag	1200
gcccagucca agaggucggg uuucugcggu caaggaaccc auauuguguc cuucgucgug	1260
aacgcgccc aacggucugua cuuuauagc gucggcuacu acccgagcaa ucauaucgaa	1320
guggugucgg ccuacggccu gugcgaucc gcuaacccca cuaacugua ugcuccugug	1380
aacggauauu uuauuaagac caacaacacc cgcuaugugg acgaauaggc auacaccggu	1440
ucguccuuc aacgcgcccga gcccuaucac ucacugaaca ccaauuacgu ggcuccgcaa	1500
gugaccuacc agaacaucuc caccauuug ccgcgcggc ugcucggaaa cagcaccgga	1560
auugauuucc aagaugaacu ggacgaauu ucuaagaacg uguccacuuc cauucccaac	1620
uucggaagcc ugacacagau caacaccacc cuucucgacc ugaccuacga gaugcugagc	1680
cuucaacaag uggucaaggc ccugaacgag agcuacaucg accugaagga gcugggcaac	1740
uauaccuacu acaacaagug gccggacaag auugaggaga uucugucgaa aaucuaacc	1800
auugaaaacg agaucgccag aaucagaag cuuaucggcg aagcc	1845

<210> SEQ ID NO 68

<211> LENGTH: 4071

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 68

auggaaacc cugcccagcu gcuguuccug cugcugcugu ggcugccuga uaccaccggc	60
agcuauuggg acgugggccc cgauagcgug aaguccgccu guaucgaagu ggacauccag	120
cagaccuuuu ucgacaagac cuggcccaga cccaucgacg uguccaaggc cgacggcauc	180
aucuauccac aaggccggac cuacagcaac aucaccaua ccuaccaggc ccuguuccca	240
uaucaaggcg accacggcga uauguacgug uacucugcg gccacgccac cggcaccaca	300
ccccagaaac uguucguggc caacuacagc caggacguga agcaguucgc caacggcuuc	360
gucgugcgga uuggcgccgc ugccaauagc accggcacag ugaucaucag ccccagcacc	420
agcgcaccac uccggaagau cuaccccgcc uucaugcug gcagcuccgu gggcauuuuc	480
agcgacggca agaugggccc guucuucaac cacaccuagg ugcugcugcc cgauggcugu	540
ggcacacugc ugagagccuu cuacugcauc cuggaaccca gaagcgga ccacugcccu	600
gccggcaaua gcuaaccag cuucgccacc uaccacacac ccgccaccga uugcuccgac	660

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ggcaacuaca	accggaacgc	cagccugaac	agcuucaaag	aguacucaa	ccugcggaac	720
ugcaccuua	uguacaccua	caauaucacc	gaggacgaga	uccuggaug	guucggcauc	780
accagacgg	cccagggcgu	gcaccuguuc	agcagcagau	acguggaccu	guacggcggc	840
aacauguucc	aguuggccac	ccugcccug	uacgacacca	ucaaguacua	cagcaucauc	900
ccccacagca	uccgguccau	ccagagcgac	agaaaagccu	gggcccguu	cuacguguac	960
aagcugcagc	cccugaccuu	ccugcuggac	uucagcgugg	acggcuacau	cagacgggcc	1020
aucgacugcg	gcuucaacga	ccugagccag	cugcacugcu	ccuacgagag	cuucgacgug	1080
gaaagcggcg	uguacagcgu	guccagcuuc	gaggccaagc	cuagcggcag	cgugguggaa	1140
caggcugagg	gcguggaaug	cgacuucagc	ccucugcuga	gcggcaccac	uccccaggug	1200
uacaacuua	agcggcuggu	guucaccaac	ugcaauuaca	accugaccaa	gcugcugagc	1260
cuguucucgg	ugaacgacuu	caccuguagc	cagaucagcc	cugcccgcuu	ugccagcaac	1320
ugcuacagca	gccugauccu	ggacuacuuc	agcuaccccc	ugagcaugaa	guccgaucug	1380
agcguguccu	ccgccggacc	caucagccag	uucacuaca	agcagagcuu	cagcaaccuu	1440
accugccuga	uucuggccac	cgugccccc	aaucugacca	ccaucaccaa	gccccugaag	1500
uacagcuaca	ucaacaagug	cagcagacug	cuguccgacg	accggaccga	agugcccag	1560
cucgugaacg	ccaaccagua	cagccccugc	guguccaucg	ugcccagcac	cgugugggag	1620
gacggcgacu	acuacagaaa	gcagcugagc	ccccuggaag	gcggcggaug	gcugguggcu	1680
ucuggaagca	caguggccau	gaccgagcag	cugcagaugg	gcuuuggcau	caccgugcag	1740
uacggcaccg	acaccaacag	cgugugcccc	aagcuggaau	ucgccaauga	caccaagauc	1800
gccagccagc	ugggaaacug	cguggaaauac	ucccuguaug	gcguguccgg	acggggcgug	1860
uuccagaauu	gcacagcagu	gggagugcgg	cagcagagau	ucguguacga	ugccuaccag	1920
aaccucgugg	gcuacuacag	cgacgacggc	aauuacuacu	gccugcgggc	cugugugucc	1980
gugcccugug	ccgugaucua	cgacaaagag	acaaagaccc	acgccacacu	guucggcucc	2040
guggccugcg	agcacauacg	cuccaccaug	agccaguacu	cccgcuccac	ccgguccaug	2100
cugaagcgga	gagauagcac	cuacggcccc	cugcagacac	cugugggaug	ugugcugggc	2160
cucgugaaca	gcucccuguu	uguggaagau	ugcaagcugc	cccugggcca	gagccugugu	2220
gcccugccag	auaccccuag	caccucgacc	ccuagaagcg	ugcgucucugu	gcccggcgaa	2280
augcggcugg	ccucuauccg	cuucauacac	cccauccagg	uggaccagcu	gaacuccagc	2340
uacuuaagc	ugagcauccc	caccaacuuc	agcuucggcg	ugaccacgga	guacauccag	2400
accacaaucc	agaaagugac	cguggacugc	aagcaguacg	ugugcaacgg	cuuucagaag	2460
ugcgaaacgc	ugcugcgcg	guacggccag	uucugcagca	agaucaacca	ggcccugcac	2520
ggcgccaacc	ugagacagga	ugacagcgug	cggaaccugu	ucgccagcgu	gaaaagcagc	2580
caguccagcc	ccaucauccc	uggcuucggc	ggcgacuuua	accugaccuu	gcuggaaccu	2640
guguccauca	gcaccggcuc	cagaagcgcc	agauccgcca	ucgaggaccu	gcuguucgac	2700
aaagugacca	uugccgaccc	cgguacuacg	cagggcuacg	acgauugcau	gcagcagggc	2760
ccagccagcg	ccagggauuc	gaucugugcc	caguaugugg	ccgcuacaa	ggugcugccc	2820
ccccugaugg	acgugaacau	ggaagccgcc	uacaccucca	gccugcuggg	cucuauugcu	2880
ggcgugggau	ggacagccgg	ccugucuagc	uuugccgcca	ucccuuucgc	ccagagcauc	2940

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uucuaaccggc	ugaacggcggu	gggcuaucaca	caacaggugc	ugagcgagaa	ccagaagcug	3000
aucgccaaca	aguuaaacca	ggcacugggc	gccaugcaga	ccggcuucac	caccaccaac	3060
gaggccuuca	gaaaggugca	ggacgcccug	aacaacaacg	cccaggcucu	gagcaagcug	3120
gccuccgagc	ugagcaauac	cuucggcgcc	aucagcgccu	ccaucggcga	caucauccag	3180
cggcuggagc	ugcuggaaca	ggacgcccag	aucgaccggc	ugaucaacgg	cagacugacc	3240
accugaaacg	ccuucguggc	acagcagcuc	gugcgaggcg	aaucugccgc	ucugucugcu	3300
cagcuggcca	aggacaaagu	gaacgagugc	gugaaggccc	aguccaagcg	gagcgguuu	3360
uguggccagg	gcaccacau	cguguccuuc	gucgugaaug	cccccaacgg	ccuguacuui	3420
augcacgugg	gcuuuuaccc	cagcaaccac	aucgaggugg	uguccgccua	uggccugugc	3480
gacgcccga	auccuaccaa	cuguaucgcc	cccguagaacg	gcuacuucuu	caagaccaac	3540
aacacccgga	ucguggacga	gugguccuac	acaggcagca	gcuucuacgc	ccccgagccc	3600
aucaccuccc	ugaacaccaa	auacguggcc	ccccaaaguga	cauaccagaa	cauccaccac	3660
aaccugcccc	cuccacugcu	gggaaauucc	accggcaucg	acuuccagga	cgagcuggac	3720
gaguucuuca	agaacguguc	caccuccauc	cccaacuucg	gcagccugac	ccagaauaac	3780
accacucugc	uggaccugac	cuacgagaug	cugucccugc	aacaggucgu	gaaagcccug	3840
aacgagagcu	acaucgaccu	gaaagagcug	gggaacuaca	ccuacuacaa	caaguggccu	3900
ugguacauuu	ggcugggcuu	uacgcccggc	cugguggccc	uggcccugug	cguguucuu	3960
auccugugcu	gcaccggcug	cggcaccaau	ugcaugggca	agcugaaaug	caaccggugc	4020
ugcgacagau	acgaggaaua	cgaccuggaa	ccucacaaaag	ugcaugugca	c	4071

<210> SEQ ID NO 69

<211> LENGTH: 1864

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 69

ucaagcuuuu	ggaccucgu	acagaagcua	auacgacua	cuauagggaa	auaagagaga	60
aaagaagagu	aagaagaaau	auaagagcca	ccaugggucu	caaggugaac	gucucugccg	120
uauucauggc	aguacuguaa	acucuccaaa	caccgcccgg	ucaaaaucau	uggggcaauc	180
ucucuaagau	agggguagua	ggaauaggaa	gugcaagcua	caaaguuaug	acucguucca	240
gccaucaauc	auuagucuaa	aaaauaaugc	ccaaauaaac	ucuccucaau	aacugcacga	300
ggguagagau	ugcagaauac	aggagacuac	uaagaacagu	uuuggaacca	auuagggau	360
cacuuaaugc	aaugacccag	aacauaaggc	cgguucagag	cguagcuuca	aguaggagac	420
acaagagauu	ugcgggagua	guccuggcag	gugcgggccu	agguguugcc	acagcugcuc	480
agauaacagc	cggcauugca	cuucaccggu	ccaugcugaa	cucucaggcc	aucgacaau	540
ugagagcgag	ccuggaaaau	acuaaucagg	caauugaggc	aaucagacaa	gcagggcagg	600
agaugauauu	ggcuguucag	gguguccaag	acuacaucaa	uaaugagcug	auaccgucua	660
ugaaccagcu	aucuugugau	cuaaucgguc	agaagcucgg	gcucaaaau	cuuagauacu	720
auacagaaa	ccugucuuua	uuuggcccca	gccuacggga	ccccauaucu	gcggagauau	780
cuauccaggc	uuugaguuau	gcacuuggag	gagauaucaa	uaagguguua	gaaaagcucg	840

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gauacagugg	aggcgauuua	cuaggcaucu	uagagagcag	aggaauaaag	gcucggauaa	900
cucacgucga	cacagagucc	uacuucauag	uccucaguau	agccuauccg	acgcuguccg	960
agauuaaggg	ggugauuguc	caccggcuag	aggggggucuc	guacaacaua	ggcucucaag	1020
agugguauac	cacugugccc	aaguauguug	caaccaaggg	guaccuuauc	ucgaauuuug	1080
augagucauc	auguacuuc	augccagagg	ggacugugug	cagccaaaau	gccuuguacc	1140
cgaugagucc	ucuguccaa	gaaugccucc	gggggguccac	caaguccugu	gcucguacac	1200
ucguauccgg	gucuuuuggg	aaccgguuca	uuuuuacaca	aggggaaccua	auagccaauu	1260
gugcaucaau	ucuuuguuag	uguuacacaa	cagguacgau	uauuaaucaa	gaccugaca	1320
agauccuaac	auacauugcu	gccgaucgcu	gcccgguagu	cgaggugaac	ggcgugacca	1380
uccaagucgg	gagcaggagg	uauccagacg	cuguguacuu	gcacagaauu	gaccucgguc	1440
cucccauauc	auuggagagg	uuggacguag	ggacaaaucu	ggggaauuca	auugccaaa	1500
uggaggaugc	caaggaaug	uuggaaucuu	cggaccagau	auugagaagu	augaaagguu	1560
uauagagcac	uagcauaguc	uacauccuga	uugcagugug	ucuuaggagg	uugauaggga	1620
uccccacuuu	aaauuguugc	ugcagggggc	guuguacaaa	aaagggagaa	caaguuggua	1680
ugucaagacc	aggccuaaag	ccugaccuua	caggaaacuc	aaaauccuau	guaagaucgc	1740
uuugaugaua	auaggcugga	gccucggugg	ccaagcuucu	ugccccuugg	gccucccccc	1800
agccccuccu	ccccuuccug	caccguacc	cccugggucu	ugaauaaaag	ucugaguggg	1860
cggc						1864

<210> SEQ ID NO 70

<211> LENGTH: 1653

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 70

augggucuca	aggugaacgu	cucugccgua	uucauggcag	uacuguaaac	ucuccaaaca	60
cccgccgguc	aaauucauug	gggcaaucuc	ucuaagauag	ggguaguagg	aaauaggaagu	120
gcaagcuaca	aaguuaugac	ucguuaccag	caucaaucau	uagucauaaa	auuaaugccc	180
aaauaaacuc	uccucaauaa	cugcacgagg	guagagauug	cagaauacag	gagacuacua	240
agaacaguuu	uggaaccaau	uagggauuca	cuuaaugcaa	ugaccagaa	cauaaggccg	300
guucagagcg	uagcuucaag	uaggagacac	aagagauuug	cgggaguagu	ccuggcaggu	360
gcccgcucag	guguugccac	agcugcucag	auaacagccc	gcauugcacu	ucaccggucc	420
augcugaacu	cucaggccau	cgacaauucg	agagcgagcc	uggaaacuac	uaaucaggca	480
auugaggcaa	ucagacaagc	agggcaggag	augauauugg	cuguucaggg	uguccaagac	540
uacaucaaua	augagcugau	accgcuauug	aaccagcuau	cuugugaucu	aaucggucag	600
aagcucgggc	ucaaaauugc	uagauacuau	acagaaaucc	ugucauuuuu	uggccccagc	660
cuacgggacc	ccauaucugc	ggagauaucu	auccaggcuu	ugaguuaugc	acuuggagga	720
gauaucaaua	agguguuaga	aaagcucgga	uacaguggag	gcauuuuacu	aggcaucuaa	780
gagagcagag	gaauaaaggc	ucggauaacu	cacgucgaca	cagaguccua	cuucauaguc	840
cucaguauag	ccuauccgac	gcuguccgag	auuaaggggg	ugaauugucca	ccggcuagag	900

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ggggucucgu acaacauagg cucucaagag ugguauacca cugugcccaa guauguugca	960
acccaagggg accuuaucuc gaauuuugau gagucaucau guacuuucau gccagagggg	1020
acugugugca gccaauaugc cuuguaccgg augaguccuc ugcuccaaga augccuccgg	1080
ggguccacca aguccugugc ucguacacuc guauccgggu cuuuugggaa ccgguucauu	1140
uuauacacaag ggaaccuaau agccaauugu gcaucaauuc uuuguaagug uuacacaaca	1200
gguacgauua uuaaucaaga ccugacaag auccuaacau acauugcugc cgaucgcugc	1260
ccgguagucg agggagaacgg cgugaccauc caagucggga gcaggaggua uccagacgcu	1320
guguacuugc acagaauuga ccucgguccu cccauaucau uggagagguu ggacguaggg	1380
acaaaucugg ggaauugcau ugccaaaug gaggaugcca aggaauuguu ggaaucaucg	1440
gaccagauau ugagaaguau gaaagguua ucgagcacia gcuaugucia cauccugauu	1500
gcaguguguc uuggaggggu gauagggauc cccacuuuaa uauguugcug cagggggcgcu	1560
uguaacaaaa agggagaaca aguugguau ucaagaccag gccuaagcc ugaccuuaca	1620
ggaacaucaa aauccuaugu aagaucgcuu uga	1653

<210> SEQ ID NO 71

<211> LENGTH: 1925

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 71

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gugaacgucu cugccguauu cauggcagua cuguuaacuc uccaaacacc cgccggucaa	120
auucauuggg gcaaucucuc uaagauaggg guaguaggaa uaggaaugc aagcuacaaa	180
guuaugacuc guuccagcca ucaucauua gucauaaaau uaaugcccaa uauaacucuc	240
cucauaaacu gcacgagggg agagauugca gaaucacgga gacuacuaag aacaguuuug	300
gaaccaauua gggaugcacu uaaugcaaug acccagaaca uaaggccggg ucagagcgua	360
gcuucaagua ggagacacaa gagauuugc ggaguagucc uggcaggugc ggcccuaggu	420
guugccacag cugcucagau aacagccggc auugcacuuc accgguccau gcugaacucu	480
caggccaucg acaaucugag agcagcccg gaaacuacua aucaggcaau ugaggcaauc	540
agacaagcag ggcaggagau gauauuggcu guucagggug uccaagacua caucauaau	600
gagcugauac cgucuaugaa ccagcuaucu ugugaucuaa ucgugacaga gcucggguc	660
aaauugcuua gauacuauac agaaaucug ucauuuuug gcccagccu acgggacccc	720
auaucugcgg agauaucuau ccaggcuuug aguuaugcac uuggaggaga uaucauaag	780
guguuagaaa agcucggaua caguggaggc gauuuacuag gcaucuuga gagcagagga	840
auaaaggcuc ggauaacuca cgucgacaca gaguccuacu ucauaguccu caguauagcc	900
uauccgacgc uguccagau uaagggggug auuguccacc ggcuaagagg gguucguac	960
aacauaggcu cucaagagug guauaccacu gugcccaagu auguugcaac ccaaggguac	1020
cuuauucga auuuugauga gucaucaugu acuuucaugc cagaggggac ugugugcagc	1080
caaaugccu uguacccgau gaguccucug cuccaagaau gccuccggg guccaccaag	1140
uccugugcuc guacacucgu auccgggucu uuugggaacc gguucauuu aucacaaggg	1200

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aaccuaauag	ccaauugugc	aucaauucuu	uguaaguguu	acacaacagg	uacgauuuuu	1260
aaucaagacc	cugacaagau	ccuaacauac	auugcugccg	aucgcugccc	ggugaucgag	1320
gugaacggcg	ugaccaucca	agucgggagc	aggagguauc	cagacgcugu	guacuugcac	1380
agaaugacc	ucgguccucc	cauaucauug	gagagguugg	acguagggac	aaaucugggg	1440
aaugcaauug	ccaaaugga	ggaugccaag	gaaugguugg	aaucaucgga	ccagauuuug	1500
agaaguauga	aagguuuuac	gagcacuagc	auagucuaca	uccugauugc	agugugucuu	1560
ggaggguuga	uagggaucce	cacuuuaaua	uguugcugca	gggggcuug	uaacaaaaag	1620
ggagaacaag	uugguauguc	aagaccaggc	cuaaagccug	accuuacagg	aacaucaaaa	1680
uccuauguaa	gaucgcuuug	augauauuag	gcuggagccu	cgguggccaa	gcuucugcc	1740
ccuugggccu	ccccccagcc	ccuccucccc	uuccugcacc	cguacccccg	uggucuuuga	1800
auaaagucug	aguggggggc	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1860
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1920
ucuag						1925

<210> SEQ ID NO 72

<211> LENGTH: 1864

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 72

ucaagcuuuu	ggaccucugu	acagaagcua	auacgacuca	cuauaggga	auaagagaga	60
aaagaagagu	aagaagaaau	auaagagcca	ccaugggucu	caaggugaac	gucucuguca	120
uauucauggc	aguacuguaa	acucucaaaa	caccaccgg	ucaaauccau	uggggcaauc	180
ucucuaagau	agggguggua	gggguaggaa	gugcaagcua	caaaguuaug	acucguucca	240
gccaucaauc	auuagucuaa	aaguuaaagc	ccaaauaac	ucuccucaac	aaugcacga	300
ggguaggguu	ugcagaauac	aggagacuac	ugagaacagu	ucuggaacca	auuagagaug	360
cacuuauagc	aaugacccag	aaauaaagac	cgguuacagag	uguagcuuca	aguaggagac	420
acaagagauu	ugcgggaguu	guccuggcag	gugcggcccu	aggcguugcc	acagcugcuc	480
aaauaacagc	cgguaauugca	cuucaccagu	ccaugcugaa	cucucaagcc	aucgacaauc	540
ugagagcgag	ccuagaaacu	acuaaucagg	caauugaggc	aaucagacaa	gcagggcagg	600
agaugauuuu	ggcguucag	gguguccaag	acuacaucaa	uaaugagcug	auaccgucua	660
ugaaucaacu	aucuugugau	uuauucggcc	agaagcuagg	gcucaauuug	cucagauacu	720
auacagaaau	ccugucauuu	uuugggccca	gcuuacggga	ccccauaucu	gcggagauau	780
cuaucaggcc	uuugagcuau	gcgcuuaggag	gagauaucaa	uaaggguuug	gaaaagcucg	840
gauacagugg	aggugaucua	cugggcaucu	uagagagcag	aggaaauaag	gcccggauaa	900
cucacgucga	cacagagucc	uacuucuuug	uacucaguau	agccuauccg	acgcuaucgg	960
agauuaaggg	ggugauuguc	caccggcuag	aggggggucuc	guacaacaua	ggcucucaag	1020
agugguauac	cacugugccc	aaguauguug	caaccaagg	guaccuuuuc	ucgaauuuug	1080
augagucauc	augcacuuuc	augccagagg	ggacugugug	cagccagaau	gccuuguacc	1140
cgaugagucc	ucugcuccaa	gaaugccucc	ggggguccac	uaaguccugu	gcucguacac	1200

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ucguauccgg gucuuucggg aaccgguuca uuuuauacaca ggggaaccua auagccaauu	1260
gugcaucaau ccuugcaag uguuacacaa caggaacaau cauuaaucaa gaccugaca	1320
agauccaauac auacauugcu gccgaucacu gcccguggu cgaggugaau ggcgugacca	1380
uccaagucgg gagcaggagg uauccggacg cuguguacuu gcacaggauu gaccucgguc	1440
cucccauauuc uuuggagagg uuggacguag ggacaaauuc ggggaauuca auugcuaagu	1500
uggaggauuc caaggaaug uuggagucuu cggaccagau auugaggagu augaaagguu	1560
uauagagcac uaguauagu uacauccuga uugcagugug ucuuggagga uugauaggga	1620
uccccgcuuu aaauuguuc ugcagggggc guuguaacaa gaagggagaa caaguuggua	1680
ugucaagacc aggcuaaag ccugaucuaa caggaacauc aaaauccuau guaaggucac	1740
ucugaugaua auaggcugga gccucggugg ccaagcuuc ugcuccuugg gccucccccc	1800
agccccuccu cccuuccug caccguacc cccgugguu ugaauaaaag ucugaguggg	1860
cggc	1864

<210> SEQ ID NO 73

<211> LENGTH: 1653

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 73

augggucuca aggugaacgu cucugucuaa uucauggcag uacuguaac ucuucaaaca	60
cccaccgguc aaauccauug gggcaaucuc ucuaagauag gggugguagg gguaggaagu	120
gcaagcuaca aaguuaugac ucuuuccagc caucauacau uagucuaaaa guuaaugccc	180
aaauaaacuc uccucaacaa uugcacagg guagggaug cagaauacag gagacuacug	240
agaacaguuc uggaaccau uagagaugca cuuaaugcaa ugaccagaa uauaagaccg	300
guucagagug uagcuuacag uaggagacac aagagauuug cgggaguugu ccuggcagg	360
gcccgcucag gcuugccac agcugcucaa auaacagccg guauugcacu ucaccagucc	420
augcugaacu cucaagccau cgacaauuc agagcgagcc uagaaacuac uauacaggca	480
auugaggcaa ucagacaagc agggcaggag augauauugg cuguucaggg uguccaagac	540
uacaucaaua augagcugau accgucuaug aaucacuaa cuugugauuu aaucggccag	600
aagcuagggc ucaauuugcu cagauacuau acagaaaucc ugucuuuuu uggccccagc	660
uuacgggacc ccauauucg ggagauaucu auccaggcuu ugagcuauuc gcuuggagga	720
gauaucaaua agguuguuga aaagcucgga uacaguggag gugaucuacu gggcaucuaa	780
gagagcagag gaauaaaggc ccggauaacu cagcugcaca cagaguccua cuucauugua	840
cucaguauag ccuauccgac gcuauccgag auuaagggg ugauugucca ccggcuagag	900
ggggucucgu acaacauagg cucucaagag ugguaauacca cugugcccaa guauguugca	960
acccaagggu accuuauuc gaauuuugau gagucauau gcacuuuau gccagagggg	1020
acugugugca gccagaauuc cuuguaaccg augaguccuc ugcuccaaga augccuccg	1080
ggguccacua aguccuguc ucguacacuc guauccgggu cuuucgggaa ccgguucauu	1140
uuaucacagg ggaaccuau agccaauug gcaucaaucc uuugcaagug uuacacaaca	1200
ggaacaauc uuaaucaaga ccugacaaag auccuacau acuuugcugc cgaucacugc	1260

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ccggugguccg agguagaugg cgugaccauc caagucggga gcaggaggua uccggacgcu	1320
guguacuugc acaggauuga ccucgguccu cccauaucuu uggagagguu ggacguaggg	1380
acaaaucugg ggaauugcau ugcuaaguug gaggaugcca aggaauuguu ggagucaucg	1440
gaccagauau ugaggaguuu gaaagguuuu ucgagcacua guauaguuuu cauccugauu	1500
gcaguguguc uuggaggauu gauagggauc cccgcuuuu uauguugcug cagggggcgu	1560
uguaacaaga agggagaaca aguugguau ucaagaccag gccuaagcc ugaucuuaca	1620
ggaacaucaa aauccuauu aaggucacuc uga	1653

<210> SEQ ID NO 74

<211> LENGTH: 1925

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 74

ggggaaauaa gagagaaaag aagaguaaga agaaauuaa gagccaccu gggucucaag	60
gugaacgucu cugucauuu cauggcagua cuguuaacuc uucaaacacc caccggucaa	120
auccauuggg gcaaucucuc uagauaggg gugguagggg uaggaagugc aagcuacaaa	180
guuauagacuc guuccagcca ucaucauuu gucauaaagu uaaugcccaa uauaacucuc	240
cucaacaauu gcacgagggg agggauugca gaaucacgga gacuacugag aacaguucug	300
gaaccaauua gagaugcacu uaaugcaaug acccagaaua uaagaccggg ucagagugua	360
gcuucaagua ggagacacaa gagauuugcg ggaguugucc uggcaggugc ggcccuaggc	420
guugccacag cugcucaauu aacagccggg auugcacuuc accaguccau gcugaacucu	480
caagccaucg acaaucugag agcgagccua gaaacuacua aucaggcaau ugaggcaauc	540
agacaagcag ggcaggagau gauauuggcu guucagggug uccaagacua caucauuau	600
gagcugauac cgucuaugaa ucaacuauc uugauuuua ucgccagaa gcuaagggcuc	660
aaauugcuca gauacuauac agaaauccug ucauuuuug gcccagcuu acgggacccc	720
auaucugcgg agauaucuau ccaggcuug agcuauugcg uggaggaga uaucauuag	780
guguuggaaa agcucggaua caguggaggu gaucuacug gcaucuuaga gagcagagga	840
auaaaggccc ggauaacuca cgucgacaca gaguccuacu ucauuguacu caguauagcc	900
uauccgacgc uauccgagau uaagggggug auuguccacc ggcuaagagg gguccguac	960
aacauaggcu cucaagagug guauaccacu gugcccaagu auguugcaac ccaagggua	1020
cuaucucga auuuugauga gucaucaugc acuuucaugc cagaggggac ugugugcagc	1080
cagaauccu uguaccggau gaguccucug cuccaagaau gccuccggg guccacuaag	1140
uccugugcuc guacacucgu auccgggguu uucgggaacc gguucauuu aucacagggg	1200
aaccuaauag ccaauugugc aucaauccu ugcaguguu acacaacagg aacaaucau	1260
aaucagacc cugacaagau ccuaacauac auugcugccg aucacugccc gguggucgag	1320
gugaauaggc ugaccaucca agucgggagc aggagguau cggacgcugu guacuugcac	1380
aggauugacc ucgguccuc cauaucuuug gagagguugg acguaggagc aaauucggg	1440
augcaauug cuaaguugga ggaugccaag gaauguugg agucaucgga ccagauauug	1500
aggaguauga aagguuuuac gagcacuagu auaguuuaca uccugauugc agugugucu	1560

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ggaggauuga uagggauccc cgcuuuaaua uguugcugca gggggcguug uaacaagaag	1620
ggagaacaag uugguauguc aagaccaggc cuaaagccug aucuuacagg aacaucaaaa	1680
uccuauguaa ggucacucug augauauag gcuggagccu cgguggccaa gcuuuugcc	1740
ccuugggccc cccccagcc ccuccucucc uuccugcacc cguacccccg uggucuuuga	1800
auaaagucug aguggggcgc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1860
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1920
ucuag	1925

<210> SEQ ID NO 75

<211> LENGTH: 2065

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 75

ucaagcuuuu ggaccucgu acagaagcua auacgacuca cuauaggga auaagagaga	60
aaagaagagu aagaagaaau auaagagcca ccaugucacc gcaacgagac cggauaaaug	120
ccuucuaaca agauaaccuu uaucccaagg gaaguaggau aguauuaac agagaacauc	180
uuaugauuga cagaccuau guucugcugg cuguucuguu cgucauguuu cugagcuuga	240
ucggauugcu ggcaauugca ggcauuagac uucaucgggc agccaucua accgcggaga	300
uccauaaaag ccucaguacc aaucuggaug ugacuaacuc caucgagcau caggucaagg	360
acgugcugac accacucuuu aaaaucaucg ggaugaagu gggccugaga acaccucaga	420
gauucacuga ccuagugaaa uucaucucgg acaagauuaa auuccuuaa cgggauaggg	480
aguacgacuu cagagaucuc acuuggugca ucaaccgcc agagaggauc aaacuagauu	540
augaucauaa cugugcagau guggcugcug aagagcucau gaaugcauug gugaacuaa	600
cucucugga gaccagaaca accacucagu uccuagcugu cucaaaggga aacugcucag	660
ggcccacuaa aaucagaggu caauucuaa acaugucgu guccuuguug gacuuguacu	720
uaggucgagg uuacaauug ucaucuauag ucacuaugac auccaggga auguauggg	780
gaaccuaccu aguugaaaag ccuaaucuga acagcaaagg gucagaguug ucacaacuga	840
gcauguaccg aguguuugaa guagguguga ucagaaacc cggguuuggg gcuccggugu	900
uccauaugac aaacuauuuu gagcaaccag ucaguaaug ucucggcaac uguauggugg	960
cuuuggggga gcuaaacuc gcagccuuu gucacgggga cgaauucauc auauuuccu	1020
aucagggauc agggaaaaggu gucagcuucc agcucgucaa gcuggguguc uggaaaucc	1080
caaccgacau gcaauccugg gucccuuau caacggauga uccaguggua gacaggcuuu	1140
accucuauc ucacagaggu gucaucgcug acaaucaagc aaaugggcu gucccgacaa	1200
cacgaacaga ugacaaguug cgaauaggaga caugcuuca gcaggcgugu aaagguaaaa	1260
uccaagcacu cugcgagaau cccgaguggg uaccuuugaa ggauaacagg auuccuucuu	1320
acgggggucc gucuguugau cugagucuga cgguugagcu uaaaaucua auugcuucgg	1380
gauucgggcc auugaucaca cacggcucag ggauggaccu auacaaaucc aacugcaaca	1440
auguguauug gcugacuaau ccgccaauga gaaucuaag cuuaggcgua aucaacacau	1500
uggaguggau accgagauc aagguuaguc ccaaccucu cacugucca auuaagggaag	1560

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caggcgaaga cugccaugcc ccaacauacc uaccugcgga gguggacggu gaugucaaac	1620
ucaguuccaa ccuggugauu cuaccugguc aagaucucca auauguuuug gcaaccuacg	1680
auaccuccag gguugagcau gcugugguuu auuacguuaa cagcccaagc cgcucauuuu	1740
cuuacuuuuu uccuuuuagg uugccuauaa aggggguccc aaucgaacua caaguggaau	1800
gcuuacauug ggaucacaaa cucuggugcc gucacuucug ugugcuugcg gacucagaau	1860
ccgguggacu uauacacucac ucuggggaug ugaggcaugg agucagcugc acagcuaccc	1920
gggaagaugg aaccaaucgc agauaauug aauaggcugg agccucggug gccaaagcuuc	1980
uugcccccug ggcucccccc cagccccucc ucccuuccu gcacccguac ccccgugguc	2040
uuugaauaaa gucugagugg gcggc	2065

<210> SEQ ID NO 76

<211> LENGTH: 1854

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 76

augucaccgc aacgagaccg gaaaaugcc uucuaaaaag auaacccua ucccaagga	60
aguaggauag uuauuaacag agaacaucuu augauugaca gaccuauug ucugcuggcu	120
guucuguucg ucauguuucu gagcuugauc ggauugcugg caauugcagg cauuagacuu	180
caucgggagc ccaucucacac cgcggagauc cauaaaagcc ucaguaccaa ucuggaugug	240
acuaacucca ucgagcauca ggucaggac gucugacac cacucuuaa aaucaucggg	300
gaugaagugg gccugagaac accucagaga uucacugacc uagugaaau caucucggac	360
aagauuaauu uccuuaaucc ggauagggag uacgacuua gagaucucac uuggugcauc	420
aaccgcgcag agaggaucaa acuagauuau gaucaauacu gugcagaugu ggcugcugaa	480
gagcucauga augcauuggu gaacucaacu cuacuggaga ccagaacaac cacucaguuc	540
cuagcugucu caaagggaaa cugcucaggc cccacuacaa ucagaggguca auucuaaac	600
augucgcugu ccuuguugga cuuguacuua ggucgagguu acaauguguc aucuauaguc	660
acuagacau cccagggaau guauggggga accuaccuag uugaaaagcc uaaucugaac	720
agcaaagggg cagaguuguc acaacugagc auguaccgag uguuugaagu aggugugauc	780
agaaacccgg guuugggggc uccgguguuc cauaugacaa acuaauuuga gcaaccaguc	840
aguaaugguc ucggaacug uagguggcu uggggggagc ucaaacucgc agcccuuugu	900
cacggggagc auucuaucuu aaucuccuau cagggaucag ggaaaggugu cagcuuccag	960
cucgucaagc ugggugucug gaaaaccca accgacaugc aaucuggggu ccccuuauca	1020
acggaugauc cagugguaga caggcuuuac cucucaucuc acagaggugu caucgcugac	1080
aaucaagcaa aaugggcugu cccgacaaca cgaacagaug acaaguugcg aauggagaca	1140
ugcuuccagc aggcguguaa agguaaaauc caagcacucu gcgagaaucc cgagugggua	1200
ccauugaagg auaacaggau uccuucuuac gggguccugu cuguugaucu gagucugacg	1260
guugagcuua aaaucaaaau ugcucgggga uucgggccau ugauacaca cggcucaggg	1320
auggaccuau acaaaucuaa cugcaacaau guguauggc ugacuauucc gccaaugaga	1380
aaucuaagcu uaggcguaau caacacauug gaguggauac cgagauucaa gguuaguccc	1440

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aaccucuua	cugucccaau	uaaggaagca	ggcgaagacu	gccaugcccc	aacauaccua	1500
ccugcggagg	uggacgguga	ugucaaacuc	aguuccaacc	uggugauucu	accuggucaa	1560
gaucuccaau	auguuuuggc	aaccuacgau	accuccaggg	uugagcaugc	ugugguuuau	1620
uacguuuaca	gccaagccg	cucauuuuc	uacuuuuau	cuuuuagguu	gccuauaaag	1680
ggggucccaa	ucgaacuaca	aguggaauuc	uucacauagg	aucaaaaaac	cuggugccgu	1740
cacuucugug	ugcuugcgga	cucagaaucc	gguggacuua	ucacucacuc	ugggauggug	1800
ggcaugggag	ucagcugcac	agcuaccggg	gaagauggaa	ccaaucgag	auaa	1854

<210> SEQ ID NO 77

<211> LENGTH: 2126

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 77

ggggaaauaa	gagagaaaag	aagaguaaga	agaaauuaa	gagccaccau	gucaccgcaa	60
cgagaccgga	uaaaugccuu	cuacaagau	aaccuuau	ccaagggag	uaggauaguu	120
auuaacagag	aacauuuau	gauugacaga	cccuauuuc	ugcuggcgug	ucuguucguc	180
auguuucuga	gcuugaucgg	auugcuggca	auugcaggca	uuagacuua	ucgggcagcc	240
aucuacaccg	cggagaucua	uaaaagccuc	aguaccaau	uggaugugac	uaacuccauc	300
gagcaucagg	ucaaggacgu	gcuagacaca	cucuuaaaa	ucaucgggga	ugaagugggc	360
cugagaacac	cucagagauu	cacugaccua	gugaaauua	ucucggacaa	gauuaaauc	420
cuuaauccgg	auaggggag	cgacuucaga	gaucucacuu	ggugcaucaa	cccgccagag	480
aggaucaaac	uagauuauga	ucaauacugu	gcagaugugg	cugcugaaga	gcucaugaau	540
gcauugguga	acucaacucu	acuggagacc	agaacaacca	cucaguuccu	agcugucua	600
aagggaacu	gcucagggcc	cacuacaau	agaggucaau	ucucacacau	gucgcugucc	660
uuguuggacu	uguacuuaag	ucgagguuac	aaugugucau	cuauagucac	uagacaucc	720
cagggaau	augggggaac	cuaccuaguu	gaaaagccua	aucugaacag	caaaggguca	780
gaguugucac	aacugagcau	guaccgagug	uuugaaguag	gugugaucag	aaaccgggu	840
uuggggguc	cgguguuucca	uagacaaaac	uaauuugagc	aaccagucag	uaauggucuc	900
ggcaacugua	ugguggcuuu	gggggagcuc	aaacucgag	cccuuugua	cggggacgau	960
ucuaucuaa	uucccuauca	gggaucaggg	aaagguguca	gcuuccagcu	cgucaagcug	1020
ggugucugga	aaucuccaac	cgacaugcaa	uccugggucc	ccuuaucaac	ggaugaucca	1080
gugguagaca	ggcuuuaccu	cucaucucac	agagguguca	ucgcugacaa	ucaagcaaaa	1140
ugggcugucc	cgacaacacg	aacagaugac	aaguugcgaa	uggagacaug	cuuccagcag	1200
gcguguaaag	guaaaauucca	agcacucugc	gagaaucccg	aguggguacc	auugaaggau	1260
aacaggauuc	cuucauacgg	gguccugucu	guugaucuga	gucugacggg	ugagcuuaaa	1320
aucaaaaau	cuucgggguu	cgggccauug	aucacacacg	gcucagggau	ggaccuauac	1380
aaauccaacu	gcaacaau	guauuggcug	acuaauccgc	caaugagaaa	ucuaagccua	1440
ggcguaauca	acacauugga	guggauaccg	agauucaagg	uuagucccaa	ccucuucacu	1500
gucccauuu	aggaagcagg	cgaagacugc	caugcccaaa	cauaccuacc	ugcggaggug	1560

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gacggugaug ucaaacucag uuccaaccug gugauucua	cuggucaaga ucuccaaau	1620
guuuuggcaa ccuacgauac cuccaggggu gagcaugcug	ugguuuauua cguuuacagc	1680
ccaagccgcu cauuuucua cuuuuauccu uuuaagguug	cuaaaaagg ggucccauc	1740
gaacuacaag uggaaugcu cacaugggau caaaaacuc	ggugccguca cuucugugug	1800
cuugcggacu cagaauccgg uggacuuauc acucacucug	ggaugguggg caugggaguc	1860
agcugcacag cuaccggga agauggaacc aaucgcagau	aaugauaaua ggcuggagcc	1920
ucgguggcca agcuucugc ccuuggggc uccccccagc	cccuccucc cuuccugcac	1980
ccguaccccc guggucuug auaaaagcu gaguggggc	caaaaaaa aaaaaaaa	2040
aaaaaaaa aaaaaaaa aaaaaaaa aaaaaaaa	aaaaaaaa aaaaaaaa	2100
aaaaaaaa aaaaaaaa aucuag		2126

<210> SEQ ID NO 78

<211> LENGTH: 2065

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 78

ucaagcuuu ggaccucgu acagaagcua auacgacua	cuaaaggga auaagagaga	60
aaagaagagu aagaagaa auaagagcca ccaugucacc	acaacgagac cggauaaug	120
ccuucuaa agacaacccc cauccuaagg gaaguaggau	aguuaauaac agagaacau	180
uuaugauuga uagaccuuu guuuugcugg cuguucuuu	cgucauuuu cugagcuuga	240
ucggguugcu agccauugca ggcauuagac uucaucggc	agccaucuac accgcagaga	300
uccauaaaag ccucagcacc aaucuggaug uaacuaacuc	aaucgagcau cagguaaagg	360
acgugcugac accacucuc aagaucucg gugaugaagu	ggcuugagg acaccucaga	420
gauucacuga ccuagugaag uucaucucug acaagauua	auuccuuau cgggacagg	480
aaucgacuu cagagaucuc acuuggugua ucaacccgc	agagagaauc aaauuggau	540
augaucaua cugucagau guggcugcug aagaacucau	gaaugcauug gugaacuaa	600
cucucugga gaccaggga accaaucagu uccuagcug	cucaaaggga aacugcug	660
ggcccacuac aaucagaggc caauucuaa acaugucgu	guccuguuug gacuuguuu	720
uaagucgagg uuacaauug ucaucuaug ucacuaugac	auccaggga auguacggg	780
gaacuuaccu aguggaaaag ccuaaucuga gcagcaaagg	gucagaguug ucacaacuga	840
gcaugcaccg aguuuugaa guagguguua ucagaaaucc	ggguuugggg gucccgguu	900
uccauaugac aaacuaucuu gagcaaccag ucaguauga	uuucagcaac ugcauggug	960
cuuuggggga gcucaaguuc gcagcccuc gucacaggga	agaaucauc acaauuccu	1020
aucagggauc agggaaaagg gucagcuucc agcuuguca	gcuagguguc uggaaaucc	1080
caaccgacau gcaauccugg guccccuau caacggauga	uccagugaua gacaggcuu	1140
accucucauc ucacagaggc guuaucgug acaaucaagc	aaaauuggcu gucccgaca	1200
cacggacaga ugacaaguug cgaauaggaga caugcuucca	gcaggcgugu aaggguaaa	1260
uccaagcacu uugcgagaau ccgagugga caccuugaa	ggauaacagg auuccuuc	1320
acggggucuu gucuguugau cugagucuga caguugagcu	uaaaaucaaa auuguuucag	1380

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gauucgggcc auugaucaca cacgguucag ggauggaccu auacaaaucc aaccacaaca	1440
auauguauug gcugacuauc ccgccaauga agaaccuggc cuuaggugua aucaacacau	1500
uggaguggau accgagauuc aagguuaguc ccaaccucu cacuguucca auuaagggaag	1560
caggcgagga cugccaugcc ccaacauacc uaccugcgga gguggauggu gaugucaaac	1620
ucaguuccaa ucuggugauu cuaccugguc aagaucucca auauguucug gcaaccuacg	1680
auacuuccag aguugaacau gcuguaguuu auuacguuaa cagcccaagc cgcucuuuuu	1740
cuuacuuuuu uccuuuuagg uugccuguaa ggggggucgc cauugaaua caaguggaau	1800
guucacauug ggacaaaaa cucuggugcc gucacuucug ugugcuugcg gacucagaau	1860
cugguggaca uaucacucac ucugggaug ugaggcaugg agucagcugc acagccacuc	1920
gggaagaugg aaccagccgc agauagugau aaugggcug agccucggug gccaaagcuuc	1980
uugcccccug ggcuccccc cagccccucc ucccuuccu gcacccguac ccccgugguc	2040
uuugaauaaa gucugagugg gcggc	2065

<210> SEQ ID NO 79

<211> LENGTH: 1854

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 79

augucaccac aacgagaccg gauaaaugcc uucuaaaaag acaaccccca uccuaagggg	60
aguaggauag uuauuaacag agaacaucuu augauugaua gaccuuauug uuugcuggcu	120
guucuaauucg ucauguuucu gagcuugauc gggguugcuag ccuugcagg cauugacuu	180
caucgggcag ccaucuaacac cgcagagau caaaaagcc ucagcaccaa ucuggaugua	240
acuaacucua ucgagcauca gguaaaggac gugcugacac cacucucaa gaucaucggu	300
gaugaagugg gcuagaggac accucagaga uucacugacc uagugaagu caucucugac	360
aagauuaaaa uccuuauucc ggacagggaa uacgacuua gagaucucac uugguguauc	420
aaccgcag agagaaucaa auuggauuau gaucauacu gucagaugu ggcugcugaa	480
gaacucauga augcauuggu gaacucaacu cuacuggaga ccagggcaac caaucaguuc	540
cuagcugucu caaagggaaa cugcucaggg cccacucaa ucagaggcca auucuaaac	600
augucgcugu cccguugga cuuguauua agucgagguu acaauguguc aucuauaguc	660
acuauagacu cccagggaau guacggggga acuuaccuag uggaaaagcc uaaucugagc	720
agcaaagggg cagaguuguc acaacugagc augcaccgag uguuugaagu agguguauc	780
agaaaucggg guuugggggc uccgguaau ccauagacaa acuaucuaa gcaaccaguc	840
aguauagauu ucagcaacug caugguggc uggggggagc ucaaguucgc agcccucugu	900
cacagggaag auucuaucac aaucuccuau cagggaucag ggaaaggugu cagcuuccag	960
cuugucaagc uaggugucug gaaaaccca accgacaugc aaucugggg ccccuauca	1020
acggauaguc cagugauaga caggcuuac cucucaucuc acagaggcgu uaucgcugac	1080
aaucagcaa auugggcugu cccgacaaca cggacagau acaaguugcg aauggagaca	1140
ugcuuccagc aggcguguaa ggguaaaauc caagcacuuu gcgagaaucc cgaguggaca	1200
ccauugaagg auaacaggau uccuucuauc ggggucuuu cuguugaucu gagucugaca	1260

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guugagcuua	aaaucaaaau	uguuucagga	uucggggccau	ugaucacaca	cgguucaggg	1320
auggaccuau	acaaauccaa	ccacaacaau	auguauuggc	ugacuaucce	gccaauagaag	1380
aaccuggccu	uagguguaau	caacacauug	gaguggauac	cgagauucaa	gguuaguccc	1440
aaccucuua	cuguuccaa	uaaggaagca	ggcgaggacu	gccaugcccc	aacauaccua	1500
ccugcggagg	uggaugguga	ugucaaacuc	aguuccaau	uggugauucu	accuggucaa	1560
gaucuccaa	auguucuggc	aaccuacgau	acuuccagag	ugaacaugc	uguaguuuau	1620
uacguuua	gccaagccg	cucuuuuu	uacuuuuu	cuuuuaggu	gccuguaagg	1680
ggggucccca	uugaauuua	aguggaau	uucacauagg	acaaaaacu	cuggugccgu	1740
cacuucugug	ugcuugcgga	cucagaau	gguggacaua	ucacucacuc	ugggauggug	1800
ggcaugggag	ucagcugcac	agccacucgg	gaagauggaa	ccagccgcag	auag	1854

<210> SEQ ID NO 80

<211> LENGTH: 2126

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 80

ggggaaaua	gagagaaaag	aagaguaaga	agaaauuaa	gagccaccu	gucaccacaa	60
cgagaccgga	uaauugccu	cuacaagac	aacccccau	cuaagggag	uaggauagu	120
auuaacagag	aacauuuu	gauugauaga	ccuuauuuu	ugcuggcgug	ucuuuucguc	180
auguuucuga	gcuugaucgg	guugcuagcc	auugcaggca	uuagacuua	ucgggcagcc	240
aucuacaccg	cagagaucca	uaaaagccuc	agcaccaau	uggauguaac	uaacucaau	300
gagcaucagg	uaaaggacgu	gcuagacacca	cucuuaaga	ucaucgguga	ugaagugggc	360
uugaggacac	cucagagauu	cacugaccua	gugaaguua	ucucugacaa	gauuaauu	420
cuuaauccgg	acaggggaau	cgacuucaga	gaucucacuu	gguguaucua	cccggccagag	480
agaaucaaa	uggauuauga	ucaauacugu	gcagaugugg	cugcugaaga	acucaugaau	540
gcauugguga	acucaacucu	acuggagacc	agggcaacca	aucaguuccu	agcugucua	600
aagggaacu	gcucagggcc	cacuacaau	agaggccau	ucucuaacau	gucgcugucc	660
cuguuggacu	uguauuuuag	ucgagguuac	aaugugucuu	cuauagucac	uaugacauc	720
cagggaau	acgggggaac	uuaccuagug	gaaaagccua	aucugagcag	caaaggguca	780
gaguugucac	aacugagcau	gcaccgagug	uuugaaguag	guguuaucag	aaaucgggu	840
uuggggguc	cggauuuuca	uaugacaaac	uauuugagc	aaccagucag	uaugauuu	900
agcaacugca	uggugggcuu	gggggagcuc	aaguucgcag	cccucugua	cagggaagau	960
ucuaucacaa	uucccuauca	gggaucaggg	aaaggguuca	gcuuccagcu	ugucaagcu	1020
ggugucugga	aaucuccaac	cgacauagca	uccugggucc	cccuauaac	ggaugauca	1080
gugauagaca	ggcuuuaccu	cucaucucac	agaggcgua	ucgugacaa	ucaagcaaaa	1140
ugggcugucc	cgacaacacg	gacagaugac	aaguugcgaa	uggagacaug	cuuccagcag	1200
gcguguaagg	guaaaaucca	agcacuuugc	gagaaucccg	aguggacacc	auugaaggau	1260
aacaggauuc	cuucauacgg	ggcuuugucu	guugaucuga	gucugacagu	ugagcuuaaa	1320
aucaaaaau	uuucaggauu	cgggccauug	aucacacacg	guucaggga	ggaccuauac	1380

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aaauccaacc	acaacaauau	guaauaggcug	acuaucgccg	caaugaagaa	ccuggccuua	1440
gguguaauca	acacauugga	guggauaccg	agauucaagg	uuagucccaa	ccucuucacu	1500
guuccaauua	aggaagcagg	cgaggacugc	caugccccaa	cauaccuacc	ugcggaggug	1560
gauggugaug	ucaaacucag	uuccaauucg	gugaauucac	cuggucaaga	ucuccaauau	1620
guucuggcaa	ccuacgauac	uuccagaguu	gaacaugcug	uaguuuauua	cguuuacagc	1680
ccaagccgcu	cauuuucuaa	cuuuuauccu	uuuagguugc	cuguaagggg	gguccccauu	1740
gaauuacaag	uggaauucuu	cacaugggac	caaaaacucu	ggugccguca	cuucugugug	1800
cuugcggacu	cagaauucgg	uggacauauc	acucacucug	ggaugguggg	caugggaguc	1860
agcugcacag	ccacucggga	agauggaacc	agccgcagau	agugauaua	ggcuggagcc	1920
ucgguggcca	agcuucucug	cccuuggggc	ucccccagc	cccuccuccc	cuuccugcac	1980
ccguaccccc	guggucuuug	aaauaagucu	gaguggggcg	caaaaaaaaa	aaaaaaaaa	2040
aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	2100
aaaaaaaaa	aaaaaaaaa	aucuag				2126

<210> SEQ ID NO 81

<211> LENGTH: 1729

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 81

ucaagcuuuu	ggaccucugu	acagaagcua	auacgacuca	cuauagggaa	auaagagaga	60
aaagaagagu	aagaagaaau	auaagagcca	ccauggcaca	agucuuauu	acaaacagcc	120
ugucgcuguu	gacccagaau	aaccugaaca	aaucacaguc	cgacucgggc	acugcuauug	180
agcguuuguc	uuccggucug	cguaucaaca	gcgcgaaaga	cgaugcggca	ggacaggcga	240
uugcuaacgg	uuuuaccgcg	aacaucaaag	gucugacuca	ggcuucccgu	aacgcuaacg	300
acgguaucuc	cauugcgag	accacugaag	gcgcgcugaa	cgaaaauaac	aacaaccugc	360
agcguugcgc	ugaacuggcg	guucagucug	cgaauuguac	uaacucccag	ucugaccucg	420
acuccaucca	ggcugaaau	accagcgcc	ugaacgaaau	cgaccgugua	uccggccaga	480
cucaguucua	cggcgugaaa	guccuggcgc	aggacaacac	ccugaccauc	cagguuggug	540
ccaacgacgg	ugaaacuau	gauauugauu	uaaaagaaau	cagcucuaaa	acacugggac	600
uugauaagcu	uaauugucca	gaugccuaca	ccccgaaaga	aacugcugua	accguugaua	660
aaacuaccua	uaaaaauggu	acagauccua	uuacagccca	gagcaauacu	gauauccaaa	720
cugcaauugg	cgguggugca	acggggguua	cuggggcuga	uaucaauuuu	aaagaugguc	780
aauacuauuu	agauguuaaa	ggcggugcuu	cugcuggugu	uuauaaagcc	acuuauaug	840
aaacuacaaa	gaaaguuaau	auugauacga	cugauaaaac	uccguuggca	acugcggaag	900
cuacagcuau	ucggggaaag	gccacuauaa	cccacaacca	aaaugcugaa	guaacaaaag	960
aggguguuga	uacgaccaca	guugcggcuc	aacuugcugc	agcagggguu	acuggcgccg	1020
auaaggacaa	uacuagccuu	guaaaacuau	cguuugagga	uaaaacgggu	aagguuauug	1080
augguggcua	ugcagugaaa	auggggcgag	auuucuaugc	cgcuacauau	gaugagaaaa	1140
caggugcaau	uacugcuaaa	accacuacuu	auacagaugg	uacuggcguu	gcuaaacug	1200

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gagcugugaa auuugguggc gcaaauggua aaucugaagu uguuacugcu accgauggua	1260
agacuuacuu agcaagcgac cuugacaaac auaacuucag aacaggcggu gagcuuaaag	1320
agguuaauac agauaagacu gaaaaccac ugcagaaaau ugaugcugcc uuggcacagg	1380
uugauacacu ucguucugac cugggugcgg uucagaaccg uuucaacucc gcuaucacca	1440
accugggcaa uaccguaaa uaccugucuu cugcccguag ccguaucgaa gauuccgacu	1500
acgcaaccga agucuccaac augucucgag cgagauucu gcagcaggcc gguaccuccg	1560
uucuggcgca ggcaaccag guuccgaaa acguccucuc uuucugcgu ugauauagg	1620
cuggagccuc gguggccaug cuucugccc cuugggccuc ccccagccc cuccucccu	1680
uccugcacc guaccccggu ggucuugaa uaaagucuga gugggcggc	1729

<210> SEQ ID NO 82

<211> LENGTH: 1518

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 82

auggcacaag ucauuauac aaacagccug ugcguguuga cccagaauaa ccugaacaaa	60
ucccaguccg cacugggcac ugcuaucgag cguuugucuu ccgucugcg uaucaacagc	120
gcgaagacg augcggcagg acaggcgauu gcuaaccguu uuaccgcgaa cauccaaaggu	180
cugacucagg cuucccguaa cgcuaacgac gguaucucca uugcgagac cacugaaggc	240
gcgcugaacg aaaucaacaa caaccugcag cgugugcgug aacuggcggu ucagucugcg	300
aaugguacua acucccaguc ugaccucgac uccauccagg cugaaaucac ccagcgccug	360
aacgaaaucg accguguauc cggccagacu caguucaacg gcgugaagu ccuggcgag	420
gacaacaccc ugaccaucca gguuggugcc aacgacggug aaacuaucga uauugauua	480
aaagaaauca gcucuaaaac acugggacuu gaaagcuua auguccaaga ugccuacacc	540
ccgaaagaaa cugcguuaac cguugauaaa acuaaccuaa aaaaugguac agauccuauu	600
acagcccaga gcaauacuga uauccaaacu gcaauuggcg guggugcaac ggggguuacu	660
ggggcugaua ucauuuuuaa agauggucaa uacuauuag auguuuaagg cggugcuucu	720
gcugguguuu auaaagccac uuaugaugaa acuaaaaaga aaguuauau ugauacgacu	780
gauaaaacuc cguuggaac ugcggaagcu acagcuuuc ggggaacggc cacuaaacc	840
cacaacccaa uugcugaagu aacaaaagag gguguugaua cgaccacagu ugcggcucaa	900
cuugcugcag cagggguuac uggcgcccga aaggacaaua cuagccuugu aaacuaucg	960
uuugaggaua aaaccguaa gguuuuugau ggugcuauug cagugaaaau gggcgacgau	1020
uucuaugccg cuacauauga ugagaaaaca ggugcauuu cugcuaaaac cacuacuauu	1080
acagauggua cuggcgguug ucaaacugga gcugugaaau uuggugcgcg aaauuguaa	1140
ucugaaguug uuacugcuac cgaugguaag acuuacuuaag caagcgaccu ugacaaacau	1200
aacuucagaa caggcgguaga gcuuuaagag guuaauacag auuagacuga aaaccacug	1260
cagaaaauug augcugccuu ggcacagguu gauacacuuc guucugaccu gggugcgguu	1320
cagaaccguu ucaacuccgc uauaccaac cugggcaaua ccguaaaaa ccugcuucu	1380
gcccguagcc guaucgaaga uuccgacuac gcaaccgaag ucuccaaca uucucgcgcg	1440

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cagauucugc agcaggccgg uaccuccguu cuggcgccagg cgaaccaggu uccgcaaaac	1500
guccucucuu uacugcgu	1518

<210> SEQ ID NO 83

<211> LENGTH: 1790

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 83

ggggaaaaua gagagaaaag aagaguaaga agaaaauaua gagccaccau ggcacaaguc	60
auuaauacaa acagccuguc gcuguugacc cagaauaacc ugaacaaauc ccaguccgca	120
cugggcacug cuaucgagcg uuugucuucc ggucugcgua ucaacagcgc gaaagacgau	180
gcggcaggac aggcgauugc uaaccguuuu accgcgaaca ucaaaggguu gacucaggcu	240
ucccguaacg cuaacgacgg uaucuccauu gcgcagacca cugaaggcgc gcugaacgaa	300
aucaacaaca accugcagcg ugugcgugaa cuggcggguu agucugcgaa ugguacuaac	360
ucccagucug accucgacuc cauccaggcu gaaaucaccc agcgccugaa cgaauucgac	420
cguguaucgg gccagacuca guucaacggc gugaagucc uggcgcagga caacaccucg	480
accauccagg uuggugccaa cgacggugaa acuaucgaua uugauuuuaa agaaucagc	540
ucuaaaacac ugggacuuga uaagcuuaau guccaagauu ccuacacccc gaaagaaacu	600
gcuguaacgg uugauaaaac uaccuauaaa aaugguacag auccuauuac agcccagagc	660
aaucugaua uccaaacugc aaugggcggu ggugcaacgg ggguuucugg ggucgauauc	720
aaauuuuag auggucaaua cuuuuagau guuaaaggcg gugcuucugc ugguguuuau	780
aaagccacu augaugaaac uacaaagaaa guuaauuug auacgacuga uaaaacuccg	840
uuggcaacug cggagcuac agcuauucgg ggaacggcca cuauaaccca caaccaaaau	900
gcugaaguaa caaagagggg uguugauacg accacaguug cggcucaacu ugcugcagca	960
gggguuacug gcgcccgaaua ggacaauacu agccuuguaa aacuaucguu ugaggauaaa	1020
aacgguaagg uuauugaugg uggucaugca gugaaaugg gcgacgauuu cuaugccgcu	1080
acauaugaug agaaaacagg ugcauuuacu gcuaaaacca cuacuauuac agaugguacu	1140
ggcguuuguc aaacuggagc ugugaaaauu gguggcgcaa augguaaauc ugaaguuguu	1200
acugcuaccg augguaagac uuacuuagca agcgaccuug acaaacauaa cuucagaaca	1260
ggcgugagc uuaaagaggu uauuacagau aagacugaaa acccagugca gaaaauugau	1320
gcugccuugg cacagguuga uacacuucgu ucugaccugg gugcgguuca gaaccguuuc	1380
aacuccgcu ucaccaaccu gggcaauacc guaaaaaacc ugucuucugc ccguagccgu	1440
aucgaagauu ccgacuacgc aaccgaaguc uccaacaugu cugcgcgca gauucugcag	1500
caggccggua ccuccguuu ggcgaggcg aaccaggguu cgcaaacgu ccucucuuu	1560
cugcguugau aaugggcugg agccucggug gccaugcuuc uugcccuug ggccuccccc	1620
cagcccccucc ucccuuccu gcccccguac ccccgugguc uuugaauaaa gucugagugg	1680
gcggcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1740
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaucua	1790

<210> SEQ ID NO 84

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<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Salmonella typhimurium

<400> SEQUENCE: 84

Leu Gln Arg Val Arg Glu Leu Ala Val Gln Ser Ala Asn
1 5 10

<210> SEQ ID NO 85
<211> LENGTH: 539
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 85

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1 5 10 15
His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
20 25 30
Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
35 40 45
Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
50 55 60
Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65 70 75 80
Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
85 90 95
Asn Pro Gly Ser Gly Ser Phe Val Leu Gly Ala Ile Ala Leu Gly Val
100 105 110
Ala Ala Ala Ala Ala Val Thr Ala Gly Val Ala Ile Cys Lys Thr Ile
115 120 125
Arg Leu Glu Ser Glu Val Thr Ala Ile Asn Asn Ala Leu Lys Lys Thr
130 135 140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Phe
145 150 155 160
Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
165 170 175
Leu Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser
180 185 190
Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
195 200 205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
210 215 220
Ala Glu Leu Ala Arg Ala Val Pro Asn Met Pro Thr Ser Ala Gly Gln
225 230 235 240
Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
245 250 255
Gly Ile Leu Cys Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
260 265 270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
275 280 285
Ala Pro Ser Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
290 295 300

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Glu	Asp	Gln	Gly	Trp	Tyr	Cys	Gln	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr	305	310	315	320
Pro	Asn	Glu	Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp	325	330	335	
Thr	Ala	Ala	Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Lys	Glu	Cys	Asn	Ile	340	345	350	
Asn	Ile	Ser	Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His	355	360	365	
Pro	Ile	Ser	Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys	370	375	380	
Tyr	Lys	Gly	Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile	385	390	395	400
Lys	Gln	Leu	Asn	Lys	Gly	Cys	Ser	Tyr	Ile	Thr	Asn	Gln	Asp	Ala	Asp	405	410	415	
Thr	Val	Thr	Ile	Asp	Asn	Thr	Val	Tyr	Gln	Leu	Ser	Lys	Val	Glu	Gly	420	425	430	
Glu	Gln	His	Val	Ile	Lys	Gly	Arg	Pro	Val	Ser	Ser	Ser	Phe	Asp	Pro	435	440	445	
Ile	Lys	Phe	Pro	Glu	Asp	Gln	Phe	Asn	Val	Ala	Leu	Asp	Gln	Val	Phe	450	455	460	
Glu	Asn	Ile	Glu	Asn	Ser	Gln	Ala	Leu	Val	Asp	Gln	Ser	Asn	Arg	Ile	465	470	475	480
Leu	Ser	Ser	Ala	Glu	Lys	Gly	Asn	Thr	Gly	Phe	Ile	Ile	Val	Ile	Ile	485	490	495	
Leu	Ile	Ala	Val	Leu	Gly	Ser	Ser	Met	Ile	Leu	Val	Ser	Ile	Phe	Ile	500	505	510	
Ile	Ile	Lys	Lys	Thr	Lys	Lys	Pro	Thr	Gly	Ala	Pro	Pro	Glu	Leu	Ser	515	520	525	
Gly	Val	Thr	Asn	Asn	Gly	Phe	Ile	Pro	His	Asn						530	535		

<210> SEQ ID NO 86

<211> LENGTH: 539

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 86

Met	Ser	Trp	Lys	Val	Val	Ile	Ile	Phe	Ser	Leu	Leu	Ile	Thr	Pro	Gln	1	5	10	15
His	Gly	Leu	Lys	Glu	Ser	Tyr	Leu	Glu	Glu	Ser	Cys	Ser	Thr	Ile	Thr	20	25	30	
Glu	Gly	Tyr	Leu	Ser	Val	Leu	Arg	Thr	Gly	Trp	Tyr	Thr	Asn	Val	Phe	35	40	45	
Thr	Leu	Glu	Val	Gly	Asp	Val	Glu	Asn	Leu	Thr	Cys	Ser	Asp	Gly	Pro	50	55	60	
Ser	Leu	Ile	Lys	Thr	Glu	Leu	Asp	Leu	Thr	Lys	Ser	Ala	Leu	Arg	Glu	65	70	75	80
Leu	Lys	Thr	Val	Ser	Ala	Asp	Gln	Leu	Ala	Arg	Glu	Glu	Gln	Ile	Glu	85	90	95	
Asn	Pro	Gly	Ser	Gly	Ser	Phe	Val	Leu	Gly	Ala	Ile	Ala	Leu	Gly	Val	100	105	110	

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Ala	Ala	Ala	Ala	Ala	Val	Thr	Ala	Gly	Val	Ala	Ile	Cys	Lys	Thr	Ile
		115						120				125			
Arg	Leu	Glu	Ser	Glu	Val	Thr	Ala	Ile	Asn	Asn	Ala	Leu	Lys	Lys	Thr
	130					135					140				
Asn	Glu	Ala	Val	Ser	Thr	Leu	Gly	Asn	Gly	Val	Arg	Val	Leu	Ala	Thr
145					150					155					160
Ala	Val	Arg	Glu	Leu	Lys	Asp	Phe	Val	Ser	Lys	Asn	Leu	Thr	Arg	Ala
			165						170					175	
Ile	Asn	Lys	Asn	Lys	Cys	Asp	Ile	Asp	Asp	Leu	Lys	Met	Ala	Val	Ser
			180					185					190		
Phe	Ser	Gln	Phe	Asn	Arg	Arg	Phe	Leu	Asn	Val	Val	Arg	Gln	Phe	Ser
		195					200					205			
Asp	Asn	Ala	Gly	Ile	Thr	Pro	Ala	Ile	Ser	Leu	Asp	Leu	Met	Thr	Asp
	210					215					220				
Ala	Glu	Leu	Ala	Arg	Ala	Val	Pro	Asn	Met	Pro	Thr	Ser	Ala	Gly	Gln
225					230					235					240
Ile	Lys	Leu	Met	Leu	Glu	Asn	Arg	Ala	Met	Val	Arg	Arg	Lys	Gly	Phe
			245						250					255	
Gly	Ile	Leu	Cys	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln
		260						265					270		
Leu	Pro	Ile	Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Val	Lys	Ala
		275					280					285			
Ala	Pro	Ser	Cys	Ser	Glu	Lys	Lys	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg
	290					295					300				
Glu	Asp	Gln	Gly	Trp	Tyr	Cys	Gln	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr
305					310					315					320
Pro	Asn	Glu	Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp
			325						330					335	
Thr	Ala	Ala	Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Lys	Glu	Cys	Asn	Ile
		340						345					350		
Asn	Ile	Ser	Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His
		355				360						365			
Pro	Ile	Ser	Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys
	370					375					380				
Tyr	Lys	Gly	Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile
385					390					395					400
Lys	Gln	Leu	Asn	Lys	Gly	Cys	Ser	Tyr	Ile	Thr	Asn	Gln	Asp	Ala	Asp
			405						410					415	
Thr	Val	Thr	Ile	Asp	Asn	Thr	Val	Tyr	Gln	Leu	Ser	Lys	Val	Glu	Gly
		420						425					430		
Glu	Gln	His	Val	Ile	Lys	Gly	Arg	Pro	Val	Ser	Ser	Ser	Phe	Asp	Pro
		435					440					445			
Ile	Lys	Phe	Pro	Glu	His	Gln	Trp	His	Val	Ala	Leu	Asp	Gln	Val	Phe
	450					455					460				
Glu	Asn	Ile	Glu	Asn	Ser	Gln	Ala	Leu	Val	Asp	Gln	Ser	Asn	Arg	Ile
465					470					475					480
Leu	Ser	Ser	Ala	Glu	Lys	Gly	Asn	Thr	Gly	Phe	Ile	Ile	Val	Ile	Ile
			485					490					495		
Leu	Ile	Ala	Val	Leu	Gly	Ser	Ser	Met	Ile	Leu	Val	Ser	Ile	Phe	Ile
		500						505					510		
Ile	Ile	Lys	Lys	Thr	Lys	Lys	Pro	Thr	Gly	Ala	Pro	Pro	Glu	Leu	Ser

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515	520	525
Gly Val Thr Asn Asn Gly Phe Ile Pro His Asn		
530	535	
<210> SEQ ID NO 87		
<211> LENGTH: 539		
<212> TYPE: PRT		
<213> ORGANISM: Artificial Sequence		
<220> FEATURE:		
<223> OTHER INFORMATION: Synthetic Polypeptide		
<400> SEQUENCE: 87		
Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln		
1	5	10 15
His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr		
	20	25 30
Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe		
	35	40 45
Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro		
	50	55 60
Ser Leu Ile Lys Thr Glu Leu Asp Leu Leu Lys Ser Ala Leu Arg Glu		
	65	70 75 80
Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu		
	85	90 95
Asn Pro Gly Ser Gly Ser Phe Val Leu Gly Ala Ile Ala Leu Gly Val		
	100	105 110
Ala Ala Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile		
	115	120 125
Arg Leu Glu Ser Glu Val Thr Ala Ile Asn Asn Ala Leu Lys Lys Thr		
	130	135 140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr		
	145	150 155 160
Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala		
	165	170 175
Ile Asn Lys Asn Lys Cys Asp Ile Pro Asp Leu Lys Met Ala Val Ser		
	180	185 190
Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser		
	195	200 205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp		
	210	215 220
Ala Glu Leu Ala Arg Ala Val Pro Asn Met Pro Thr Ser Ala Gly Gln		
	225	230 235 240
Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe		
	245	250 255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln		
	260	265 270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala		
	275	280 285
Ala Pro Ser Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg		
	290	295 300
Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr		
	305	310 315 320
Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp		

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325					330					335					
Thr	Ala	Ala	Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Lys	Glu	Cys	Asn	Ile
			340						345					350	
Asn	Ile	Ser	Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His
		355					360					365			
Pro	Ile	Ser	Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys
	370					375					380				
Tyr	Lys	Gly	Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile
385						390					395				400
Lys	Gln	Leu	Asn	Lys	Gly	Cys	Ser	Tyr	Ile	Thr	Asn	Gln	Asp	Ala	Asp
			405						410					415	
Thr	Val	Thr	Ile	Asp	Asn	Thr	Val	Tyr	Gln	Leu	Ser	Lys	Val	Glu	Gly
			420					425					430		
Glu	Gln	His	Val	Ile	Lys	Gly	Arg	Pro	Val	Ser	Ser	Ser	Phe	Asp	Pro
		435					440						445		
Ile	Lys	Phe	Pro	Glu	Asp	Gln	Phe	Gln	Val	Ala	Leu	Asp	Gln	Val	Phe
	450					455					460				
Glu	Asn	Ile	Glu	Asn	Ser	Gln	Ala	Leu	Val	Asp	Gln	Ser	Asn	Arg	Ile
465						470					475				480
Leu	Ser	Ser	Ala	Glu	Lys	Gly	Asn	Thr	Gly	Phe	Ile	Ile	Val	Ile	Ile
			485					490						495	
Leu	Ile	Ala	Val	Leu	Gly	Ser	Ser	Met	Ile	Leu	Val	Ser	Ile	Phe	Ile
		500						505					510		
Ile	Ile	Lys	Lys	Thr	Lys	Lys	Pro	Thr	Gly	Ala	Pro	Pro	Glu	Leu	Ser
		515					520						525		
Gly	Val	Thr	Asn	Asn	Gly	Phe	Ile	Pro	His	Asn					
	530					535									

<210> SEQ ID NO 88

<211> LENGTH: 539

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 88

Met	Ser	Trp	Lys	Val	Val	Ile	Ile	Phe	Ser	Leu	Leu	Ile	Thr	Pro	Gln
1			5						10					15	
His	Gly	Leu	Lys	Glu	Ser	Tyr	Leu	Glu	Glu	Ser	Cys	Ser	Thr	Ile	Thr
		20						25					30		
Glu	Gly	Tyr	Leu	Ser	Val	Leu	Arg	Thr	Gly	Trp	Tyr	Thr	Asn	Val	Phe
		35					40					45			
Thr	Leu	Glu	Val	Gly	Asp	Val	Glu	Asn	Leu	Thr	Cys	Ser	Asp	Gly	Pro
	50					55					60				
Ser	Leu	Ile	Lys	Thr	Glu	Leu	Asp	Leu	Leu	Lys	Ser	Ala	Leu	Arg	Glu
65				70					75					80	
Leu	Lys	Thr	Val	Ser	Ala	Asp	Gln	Leu	Ala	Arg	Glu	Glu	Gln	Ile	Glu
			85					90						95	
Asn	Pro	Gly	Ser	Gly	Ser	Phe	Val	Leu	Gly	Ala	Ile	Ala	Leu	Gly	Val
		100						105					110		
Ala	Ala	Ala	Ala	Ala	Val	Thr	Ala	Gly	Val	Ala	Ile	Ala	Lys	Thr	Ile
		115					120					125			
Arg	Leu	Glu	Ser	Glu	Val	Thr	Ala	Ile	Asn	Asn	Ala	Leu	Lys	Lys	Thr

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130					135					140						
Asn 145	Glu	Ala	Val	Ser	Thr	Leu	Gly	Asn	Gly	Val	Arg	Val	Leu	Ala	Thr	
					150						155					
Ala	Val	Arg	Glu	Leu	Lys	Asp	Phe	Val	Ser	Lys	Asn	Leu	Thr	Arg	Ala	
					165						170					
Ile	Asn	Lys	Asn	Lys	Cys	Asp	Ile	Pro	Asp	Leu	Lys	Met	Ala	Val	Ser	
					180						185					
Phe	Ser	Gln	Phe	Asn	Arg	Arg	Phe	Leu	Asn	Val	Val	Arg	Gln	Phe	Ser	
					195						200					
Asp	Asn	Ala	Gly	Ile	Thr	Pro	Ala	Ile	Ser	Leu	Asp	Leu	Met	Thr	Asp	
					210						215					
Ala	Glu	Leu	Ala	Arg	Ala	Val	Pro	Asn	Met	Pro	Thr	Ser	Ala	Gly	Gln	
					225						230					
Ile	Lys	Leu	Met	Leu	Glu	Asn	Arg	Ala	Met	Val	Arg	Arg	Lys	Gly	Phe	
					245						250					
Gly	Ile	Leu	Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln	
					260						265					
Leu	Pro	Ile	Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Val	Lys	Ala	
					275						280					
Ala	Pro	Ser	Cys	Ser	Glu	Lys	Lys	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg	
					290						295					
Glu	Asp	Gln	Gly	Trp	Tyr	Cys	Gln	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr	
					305						310					
Pro	Asn	Glu	Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp	
					325						330					
Thr	Ala	Ala	Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Lys	Glu	Cys	Asn	Ile	
					340						345					
Asn	Ile	Ser	Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His	
					355						360					
Pro	Ile	Ser	Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys	
					370						375					
Tyr	Lys	Gly	Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile	
					385						390					
Lys	Gln	Leu	Asn	Lys	Gly	Cys	Ser	Tyr	Ile	Thr	Asn	Gln	Asp	Ala	Asp	
					405						410					
Thr	Val	Thr	Ile	Asp	Asn	Thr	Val	Tyr	Gln	Leu	Ser	Lys	Val	Glu	Gly	
					420						425					
Glu	Gln	His	Val	Ile	Lys	Gly	Arg	Pro	Val	Ser	Ser	Ser	Phe	Asp	Pro	
					435						440					
Ile	Lys	Phe	Pro	Glu	Asn	Gln	Phe	Gln	Val	Ala	Leu	Asp	Gln	Val	Phe	
					450						455					
Glu	Asn	Ile	Glu	Asn	Ser	Gln	Ala	Leu	Val	Asp	Gln	Ser	Asn	Arg	Ile	
					465						470					
Leu	Ser	Ser	Ala	Glu	Lys	Gly	Asn	Thr	Gly	Phe	Ile	Ile	Val	Ile	Ile	
					485						490					
Leu	Ile	Ala	Val	Leu	Gly	Ser	Ser	Met	Ile	Leu	Val	Ser	Ile	Phe	Ile	
					500						505					
Ile	Ile	Lys	Lys	Thr	Lys	Lys	Pro	Thr	Gly	Ala	Pro	Pro	Glu	Leu	Ser	
					515						520					
Gly	Val	Thr	Asn	Asn	Gly	Phe	Ile	Pro	His	Asn						
					530						535					

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<210> SEQ ID NO 89
<211> LENGTH: 539
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 89

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1      5      10      15

His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
      20      25      30

Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
      35      40      45

Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
50      55      60

Ser Leu Ile Lys Thr Glu Leu Asp Leu Leu Lys Ser Ala Leu Arg Glu
65      70      75      80

Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
      85      90      95

Asn Pro Gly Ser Gly Ser Phe Val Leu Gly Ala Ile Ala Leu Gly Val
100     105     110

Ala Ala Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
115     120     125

Arg Leu Glu Ser Glu Val Thr Ala Ile Asn Asn Ala Leu Lys Lys Thr
130     135     140

Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
145     150     155     160

Ala Val Arg Glu Leu Lys Asp Phe Val Leu Lys Asn Leu Thr Arg Ala
165     170     175

Ile Asn Lys Asn Lys Cys Asp Ile Pro Asp Leu Lys Met Ala Val Ser
180     185     190

Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
195     200     205

Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
210     215     220

Ala Glu Leu Ala Arg Ala Val Pro Asn Met Pro Thr Ser Ala Gly Gln
225     230     235     240

Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
245     250     255

Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
260     265     270

Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
275     280     285

Ala Pro Ser Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
290     295     300

Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305     310     315     320

Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
325     330     335

Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
340     345     350

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Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
  355                      360                      365

Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
  370                      375                      380

Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
  385                      390                      395                      400

Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
                      405                      410                      415

Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
                      420                      425                      430

Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Ser Phe Asp Pro
                      435                      440                      445

Ile Lys Phe Pro Glu Asp Gln Phe Gln Val Ala Leu Asp Gln Val Phe
  450                      455                      460

Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
  465                      470                      475                      480

Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
                      485                      490                      495

Leu Ile Ala Val Leu Gly Ser Ser Met Ile Leu Val Ser Ile Phe Ile
                      500                      505                      510

Ile Ile Lys Lys Thr Lys Lys Pro Thr Gly Ala Pro Pro Glu Leu Ser
  515                      520                      525

Gly Val Thr Asn Asn Gly Phe Ile Pro His Asn
  530                      535

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<210> SEQ ID NO 90
<211> LENGTH: 539
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide

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<400> SEQUENCE: 90

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Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
  1           5           10           15

His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
  20           25           30

Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
  35           40           45

Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
  50           55           60

Ser Leu Ile Lys Thr Glu Leu Asp Leu Leu Lys Ser Ala Leu Arg Glu
  65           70           75           80

Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
  85           90           95

Asn Pro Gly Ser Gly Ser Phe Val Leu Gly Ala Ile Ala Leu Gly Val
  100          105          110

Ala Ala Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
  115          120          125

Arg Leu Glu Ser Glu Val Thr Ala Ile Asn Asn Ala Leu Lys Lys Thr
  130          135          140

Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
  145          150          155          160

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Ala	Val	Arg	Glu	Leu	Lys	Asp	Phe	Val	Leu	Lys	Asn	Leu	Thr	Arg	Ala	165	170	175
Ile	Asn	Lys	Asn	Lys	Cys	Asp	Ile	Pro	Asp	Leu	Lys	Met	Ala	Val	Ser	180	185	190
Phe	Ser	Gln	Phe	Asn	Arg	Arg	Phe	Leu	Asn	Val	Val	Arg	Gln	Phe	Ser	195	200	205
Asp	Asn	Ala	Gly	Ile	Thr	Pro	Ala	Ile	Ser	Leu	Asp	Leu	Met	Thr	Asp	210	215	220
Ala	Glu	Leu	Ala	Arg	Ala	Val	Pro	Asn	Met	Pro	Thr	Ser	Ala	Gly	Gln	225	230	235
Ile	Lys	Leu	Met	Leu	Glu	Asn	Arg	Ala	Met	Val	Arg	Arg	Lys	Gly	Phe	245	250	255
Gly	Ile	Leu	Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln	260	265	270
Leu	Pro	Ile	Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Val	Lys	Ala	275	280	285
Ala	Pro	Ser	Cys	Ser	Glu	Lys	Lys	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg	290	295	300
Glu	Asp	Gln	Gly	Trp	Tyr	Cys	Gln	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr	305	310	315
Pro	Asn	Glu	Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp	325	330	335
Thr	Ala	Ala	Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Lys	Glu	Cys	Asn	Ile	340	345	350
Asn	Ile	Ser	Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His	355	360	365
Pro	Ile	Ser	Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys	370	375	380
Tyr	Lys	Gly	Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile	385	390	395
Lys	Gln	Leu	Asn	Lys	Gly	Cys	Ser	Tyr	Ile	Thr	Asn	Gln	Asp	Ala	Asp	405	410	415
Thr	Val	Thr	Ile	Asp	Asn	Thr	Val	Tyr	Gln	Leu	Ser	Lys	Val	Glu	Gly	420	425	430
Glu	Gln	His	Val	Ile	Lys	Gly	Arg	Pro	Val	Ser	Ser	Ser	Phe	Asp	Pro	435	440	445
Ile	Lys	Phe	Pro	Glu	Asn	Gln	Phe	Gln	Val	Ala	Leu	Asp	Gln	Val	Phe	450	455	460
Glu	Asn	Ile	Glu	Asn	Ser	Gln	Ala	Leu	Val	Asp	Gln	Ser	Asn	Arg	Ile	465	470	475
Leu	Ser	Ser	Ala	Glu	Lys	Gly	Asn	Thr	Gly	Phe	Ile	Ile	Val	Ile	Ile	485	490	495
Leu	Ile	Ala	Val	Leu	Gly	Ser	Ser	Met	Ile	Leu	Val	Ser	Ile	Phe	Ile	500	505	510
Ile	Ile	Lys	Lys	Thr	Lys	Lys	Pro	Thr	Gly	Ala	Pro	Pro	Glu	Leu	Ser	515	520	525
Gly	Val	Thr	Asn	Asn	Gly	Phe	Ile	Pro	His	Asn						530	535	

<210> SEQ ID NO 91

<211> LENGTH: 539

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<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 91

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1 5 10 15
His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
20 25 30
Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
35 40 45
Thr Leu Pro Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
50 55 60
Ser Leu Ile Lys Thr Glu Leu Asp Leu Leu Lys Ser Ala Leu Arg Glu
65 70 75 80
Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
85 90 95
Asn Pro Gly Ser Gly Ser Phe Val Leu Gly Ala Ile Ala Leu Gly Val
100 105 110
Ala Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
115 120 125
Arg Leu Glu Ser Glu Val Thr Ala Ile Asn Asn Ala Leu Lys Lys Thr
130 135 140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
145 150 155 160
Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
165 170 175
Ile Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser
180 185 190
Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
195 200 205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
210 215 220
Ala Glu Leu Ala Arg Ala Val Pro Asn Met Pro Thr Ser Ala Gly Gln
225 230 235 240
Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
245 250 255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
260 265 270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
275 280 285
Ala Pro Ser Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
290 295 300
Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305 310 315 320
Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
325 330 335
Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
340 345 350
Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
355 360 365

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Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
 370          375          380

Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385          390          395          400

Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
          405          410          415

Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
          420          425          430

Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Ser Phe Asp Pro
          435          440          445

Ile Lys Phe Pro Glu Asp Gln Phe Gln Val Ala Leu Asp Gln Val Phe
450          455          460

Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
465          470          475          480

Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
          485          490          495

Leu Ile Ala Val Leu Gly Ser Ser Met Ile Leu Val Ser Ile Phe Ile
          500          505          510

Ile Ile Lys Lys Thr Lys Lys Pro Thr Gly Ala Pro Pro Glu Leu Ser
          515          520          525

Gly Val Thr Asn Asn Gly Phe Ile Pro His Asn
530          535

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<210> SEQ ID NO 92

<211> LENGTH: 539

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 92

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Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
 1          5          10          15

His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
          20          25          30

Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
          35          40          45

Thr Leu Pro Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
          50          55          60

Ser Leu Ile Lys Thr Glu Leu Asp Leu Leu Lys Ser Ala Leu Arg Glu
65          70          75          80

Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
          85          90          95

Asn Pro Gly Ser Gly Ser Phe Val Leu Gly Ala Ile Ala Leu Gly Val
          100          105          110

Ala Ala Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
          115          120          125

Arg Leu Glu Ser Glu Val Thr Ala Ile Asn Asn Ala Leu Lys Lys Thr
          130          135          140

Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
          145          150          155          160

Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
          165          170          175

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Ile	Asn	Lys	Asn	Lys	Cys	Asp	Ile	Asp	Asp	Leu	Lys	Met	Ala	Val	Ser	180	185	190
Phe	Ser	Gln	Phe	Asn	Arg	Arg	Phe	Leu	Asn	Val	Val	Arg	Gln	Phe	Ser	195	200	205
Asp	Asn	Ala	Gly	Ile	Thr	Pro	Ala	Ile	Ser	Leu	Asp	Leu	Met	Thr	Asp	210	215	220
Ala	Glu	Leu	Ala	Arg	Ala	Val	Pro	Asn	Met	Pro	Thr	Ser	Ala	Gly	Gln	225	230	240
Ile	Lys	Leu	Met	Leu	Glu	Asn	Arg	Ala	Met	Val	Arg	Arg	Lys	Gly	Phe	245	250	255
Gly	Ile	Leu	Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln	260	265	270
Leu	Pro	Ile	Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Val	Lys	Ala	275	280	285
Ala	Pro	Ser	Cys	Ser	Glu	Lys	Lys	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg	290	295	300
Glu	Asp	Gln	Gly	Trp	Tyr	Cys	Gln	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr	305	310	315
Pro	Asn	Glu	Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp	325	330	335
Thr	Ala	Ala	Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Lys	Glu	Cys	Asn	Ile	340	345	350
Asn	Ile	Ser	Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His	355	360	365
Pro	Ile	Ser	Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys	370	375	380
Tyr	Lys	Gly	Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile	385	390	395
Lys	Gln	Leu	Asn	Lys	Gly	Cys	Ser	Tyr	Ile	Thr	Asn	Gln	Asp	Ala	Asp	405	410	415
Thr	Val	Thr	Ile	Asp	Asn	Thr	Val	Tyr	Gln	Leu	Ser	Lys	Val	Glu	Gly	420	425	430
Glu	Gln	His	Val	Ile	Lys	Gly	Arg	Pro	Val	Ser	Ser	Ser	Phe	Asp	Pro	435	440	445
Ile	Lys	Phe	Pro	Glu	Asn	Gln	Phe	Gln	Val	Ala	Leu	Asp	Gln	Val	Phe	450	455	460
Glu	Asn	Ile	Glu	Asn	Ser	Gln	Ala	Leu	Val	Asp	Gln	Ser	Asn	Arg	Ile	465	470	475
Leu	Ser	Ser	Ala	Glu	Lys	Gly	Asn	Thr	Gly	Phe	Ile	Ile	Val	Ile	Ile	485	490	495
Leu	Ile	Ala	Val	Leu	Gly	Ser	Ser	Met	Ile	Leu	Val	Ser	Ile	Phe	Ile	500	505	510
Ile	Ile	Lys	Lys	Thr	Lys	Lys	Pro	Thr	Gly	Ala	Pro	Pro	Glu	Leu	Ser	515	520	525
Gly	Val	Thr	Asn	Asn	Gly	Phe	Ile	Pro	His	Asn						530	535	

<210> SEQ ID NO 93

<211> LENGTH: 539

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

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<400> SEQUENCE: 93

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Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1      5      10      15
His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
20      25      30
Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
35      40      45
Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
50      55      60
Ser Leu Ile Lys Thr Glu Leu Asp Leu Leu Lys Ser Ala Leu Arg Glu
65      70      75      80
Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
85      90      95
Asn Pro Gly Ser Gly Ser Phe Val Leu Gly Ala Ile Ala Leu Gly Val
100     105     110
Ala Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
115     120     125
Arg Leu Glu Ser Glu Val Thr Ala Ile Asn Asn Ala Leu Lys Lys Thr
130     135     140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
145     150     155     160
Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
165     170     175
Ile Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser
180     185     190
Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
195     200     205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
210     215     220
Ala Glu Leu Ala Arg Ala Val Pro Asn Met Pro Thr Ser Ala Gly Gln
225     230     235     240
Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
245     250     255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
260     265     270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
275     280     285
Ala Pro Ser Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
290     295     300
Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305     310     315     320
Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
325     330     335
Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
340     345     350
Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
355     360     365
Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
370     375     380
Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile

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385	390	395	400
Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp	405	410	415
Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly	420	425	430
Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Ser Phe Asp Pro	435	440	445
Ile Lys Phe Pro Glu Asp Gln Phe Gln Val Ala Leu Asp Gln Val Phe	450	455	460
Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile	465	470	475
Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile	485	490	495
Leu Ile Ala Val Leu Gly Ser Ser Met Ile Leu Val Ser Ile Phe Ile	500	505	510
Ile Ile Lys Lys Thr Lys Lys Pro Thr Gly Ala Pro Pro Glu Leu Ser	515	520	525
Gly Val Thr Asn Asn Gly Phe Ile Pro His Asn	530	535	

<210> SEQ ID NO 94
 <211> LENGTH: 539
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 94

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln	1	5	10	15
His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr	20	25	30	
Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe	35	40	45	
Thr Leu Glu Val Gly Asp Leu Glu Asn Leu Thr Cys Ser Asp Gly Pro	50	55	60	
Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu	65	70	75	80
Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu	85	90	95	
Asn Pro Gly Ser Gly Ser Phe Val Leu Gly Ala Ile Ala Leu Gly Val	100	105	110	
Ala Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile	115	120	125	
Arg Leu Glu Ser Glu Val Thr Ala Ile Asn Asn Ala Leu Lys Lys Thr	130	135	140	
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr	145	150	155	160
Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala	165	170	175	
Ile Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser	180	185	190	
Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser				

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195						200					205				
Asp	Asn	Ala	Gly	Ile	Thr	Pro	Ala	Ile	Ser	Leu	Asp	Leu	Met	Thr	Asp
	210					215					220				
Ala	Glu	Leu	Ala	Arg	Ala	Val	Pro	Asn	Met	Pro	Thr	Ser	Ala	Gly	Gln
225					230					235					240
Ile	Lys	Leu	Met	Leu	Glu	Asn	Arg	Ala	Met	Val	Arg	Arg	Lys	Gly	Phe
				245					250					255	
Gly	Ile	Leu	Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln
		260						265					270		
Leu	Pro	Ile	Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Val	Lys	Ala
		275					280					285			
Ala	Pro	Ser	Cys	Ser	Glu	Lys	Lys	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg
	290					295					300				
Glu	Asp	Gln	Gly	Trp	Tyr	Cys	Gln	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr
305					310					315					320
Pro	Asn	Glu	Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp
			325						330					335	
Thr	Ala	Ala	Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Lys	Glu	Cys	Asn	Ile
			340					345					350		
Asn	Ile	Ser	Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His
		355					360					365			
Pro	Ile	Ser	Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys
	370					375					380				
Tyr	Lys	Gly	Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile
385					390					395					400
Lys	Gln	Leu	Asn	Lys	Gly	Cys	Ser	Tyr	Ile	Thr	Asn	Gln	Asp	Ala	Asp
			405						410					415	
Thr	Val	Thr	Ile	Asp	Asn	Thr	Val	Tyr	Gln	Leu	Ser	Lys	Val	Glu	Gly
			420					425					430		
Glu	Gln	His	Val	Ile	Lys	Gly	Arg	Pro	Val	Ser	Ser	Ser	Phe	Asp	Pro
		435					440					445			
Ile	Lys	Phe	Pro	Glu	Asp	Gln	Phe	Gln	Val	Ala	Leu	Asp	Gln	Val	Phe
	450					455					460				
Glu	Asn	Ile	Glu	Asn	Ser	Gln	Ala	Leu	Val	Asp	Gln	Ser	Asn	Arg	Ile
465					470					475					480
Leu	Ser	Ser	Ala	Glu	Lys	Gly	Asn	Thr	Gly	Phe	Ile	Ile	Val	Ile	Ile
			485						490					495	
Leu	Ile	Ala	Val	Leu	Gly	Ser	Ser	Met	Ile	Leu	Val	Ser	Ile	Phe	Ile
		500						505					510		
Ile	Ile	Lys	Lys	Thr	Lys	Lys	Pro	Thr	Gly	Ala	Pro	Pro	Glu	Leu	Ser
		515					520					525			
Gly	Val	Thr	Asn	Asn	Gly	Phe	Ile	Pro	His	Asn					
	530					535									

<210> SEQ ID NO 95

<211> LENGTH: 539

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 95

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln

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1	5	10	15
His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr	20	25	30
Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe	35	40	45
Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro	50	55	60
Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu	65	70	75
Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu	85	90	95
Asn Pro Gly Ser Gly Ser Phe Val Leu Gly Ala Ile Ala Leu Gly Val	100	105	110
Ala Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile	115	120	125
Arg Leu Glu Ser Glu Val Thr Ala Ile Asn Asn Ala Leu Lys Lys Thr	130	135	140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr	145	150	155
Ala Val Arg Glu Leu Lys Asp Phe Val Leu Lys Asn Leu Thr Arg Ala	165	170	175
Ile Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser	180	185	190
Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser	195	200	205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp	210	215	220
Ala Glu Leu Ala Arg Ala Val Pro Asn Met Pro Thr Ser Ala Gly Gln	225	230	235
Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe	245	250	255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln	260	265	270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala	275	280	285
Ala Pro Ser Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg	290	295	300
Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr	305	310	315
Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp	325	330	335
Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile	340	345	350
Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His	355	360	365
Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys	370	375	380
Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile	385	390	395
Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp	405	410	415

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Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
420 425 430

Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Ser Phe Asp Pro
435 440 445

Ile Lys Phe Pro Glu Asp Gln Phe Gln Val Ala Leu Asp Gln Val Phe
450 455 460

Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
465 470 475 480

Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
485 490 495

Leu Ile Ala Val Leu Gly Ser Ser Met Ile Leu Val Ser Ile Phe Ile
500 505 510

Ile Ile Lys Lys Thr Lys Lys Pro Thr Gly Ala Pro Pro Glu Leu Ser
515 520 525

Gly Val Thr Asn Asn Gly Phe Ile Pro His Asn
530 535

<210> SEQ ID NO 96

<211> LENGTH: 539

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 96

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1 5 10 15

His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
20 25 30

Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
35 40 45

Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
50 55 60

Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65 70 75 80

Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
85 90 95

Asn Pro Gly Ser Gly Ser Phe Val Leu Gly Ala Ile Ala Leu Gly Val
100 105 110

Ala Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
115 120 125

Arg Leu Glu Ser Glu Val Thr Ala Ile Asn Asn Ala Leu Lys Lys Thr
130 135 140

Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
145 150 155 160

Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Trp Arg Ala
165 170 175

Ile Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser
180 185 190

Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
195 200 205

Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
210 215 220

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Ala Glu Leu Ala Arg Ala Val Pro Asn Met Pro Thr Ser Ala Gly Gln
 225 230 235 240
 Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
 245 250 255
 Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
 260 265 270
 Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
 275 280 285
 Ala Pro Ser Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
 290 295 300
 Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
 305 310 315 320
 Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
 325 330 335
 Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
 340 345 350
 Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
 355 360 365
 Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
 370 375 380
 Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
 385 390 395 400
 Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
 405 410 415
 Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
 420 425 430
 Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Ser Phe Asp Pro
 435 440 445
 Ile Lys Phe Pro Glu Asp Gln Phe Gln Val Ala Leu Asp Gln Val Phe
 450 455 460
 Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
 465 470 475 480
 Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
 485 490 495
 Leu Ile Ala Val Leu Gly Ser Ser Met Ile Leu Val Ser Ile Phe Ile
 500 505 510
 Ile Ile Lys Lys Thr Lys Lys Pro Thr Gly Ala Pro Pro Glu Leu Ser
 515 520 525
 Gly Val Thr Asn Asn Gly Phe Ile Pro His Asn
 530 535

<210> SEQ ID NO 97

<211> LENGTH: 539

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 97

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
 1 5 10 15
 His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
 20 25 30

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Glu	Gly	Tyr	Leu	Ser	Val	Leu	Arg	Thr	Gly	Trp	Tyr	Thr	Asn	Val	Phe
	35						40					45			
Thr	Leu	Glu	Val	Gly	Asp	Leu	Glu	Asn	Leu	Thr	Cys	Ser	Asp	Gly	Pro
	50					55					60				
Ser	Leu	Ile	Lys	Thr	Glu	Leu	Asp	Leu	Leu	Lys	Ser	Ala	Leu	Arg	Glu
65					70					75					80
Leu	Lys	Thr	Val	Ser	Ala	Asp	Gln	Leu	Ala	Arg	Glu	Glu	Gln	Ile	Glu
			85						90					95	
Asn	Pro	Gly	Ser	Gly	Ser	Phe	Val	Leu	Gly	Ala	Ile	Ala	Leu	Gly	Val
		100						105					110		
Ala	Ala	Ala	Ala	Ala	Val	Thr	Ala	Gly	Val	Ala	Ile	Ala	Lys	Thr	Ile
	115						120					125			
Arg	Leu	Glu	Ser	Glu	Val	Thr	Ala	Ile	Asn	Asn	Ala	Leu	Lys	Lys	Thr
	130					135					140				
Asn	Glu	Ala	Val	Ser	Thr	Leu	Gly	Asn	Gly	Val	Arg	Val	Leu	Ala	Thr
145					150					155					160
Ala	Val	Arg	Glu	Leu	Lys	Asp	Phe	Val	Leu	Lys	Asn	Leu	Trp	Arg	Ala
			165					170						175	
Ile	Asn	Lys	Asn	Lys	Cys	Asp	Ile	Asp	Asp	Leu	Lys	Met	Ala	Val	Ser
		180						185					190		
Phe	Ser	Gln	Phe	Asn	Arg	Arg	Phe	Leu	Asn	Val	Val	Arg	Gln	Phe	Ser
	195						200					205			
Asp	Asn	Ala	Gly	Ile	Thr	Pro	Ala	Ile	Ser	Leu	Asp	Leu	Met	Thr	Asp
	210					215					220				
Ala	Glu	Leu	Ala	Arg	Ala	Val	Pro	Asn	Met	Pro	Thr	Ser	Ala	Gly	Gln
225					230					235					240
Ile	Lys	Leu	Met	Leu	Glu	Asn	Arg	Ala	Met	Val	Arg	Arg	Lys	Gly	Phe
		245						250						255	
Gly	Ile	Leu	Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln
		260					265					270			
Leu	Pro	Ile	Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Val	Lys	Ala
	275					280						285			
Ala	Pro	Ser	Cys	Ser	Glu	Lys	Lys	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg
	290					295					300				
Glu	Asp	Gln	Gly	Trp	Tyr	Cys	Gln	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr
305					310					315					320
Pro	Asn	Glu	Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp
		325							330					335	
Thr	Ala	Ala	Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Lys	Glu	Cys	Asn	Ile
		340						345					350		
Asn	Ile	Ser	Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His
	355					360						365			
Pro	Ile	Ser	Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys
	370					375					380				
Tyr	Lys	Gly	Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile
385					390					395					400
Lys	Gln	Leu	Asn	Lys	Gly	Cys	Ser	Tyr	Ile	Thr	Asn	Gln	Asp	Ala	Asp
			405						410					415	
Thr	Val	Thr	Ile	Asp	Asn	Thr	Val	Tyr	Gln	Leu	Ser	Lys	Val	Glu	Gly
			420					425						430	

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Glu	Gln	His	Val	Ile	Lys	Gly	Arg	Pro	Val	Ser	Ser	Ser	Phe	Asp	Pro
		435					440					445			
Ile	Lys	Phe	Pro	Glu	Asp	Gln	Phe	Gln	Val	Ala	Leu	Asp	Gln	Val	Phe
	450					455					460				
Glu	Asn	Ile	Glu	Asn	Ser	Gln	Ala	Leu	Val	Asp	Gln	Ser	Asn	Arg	Ile
465					470					475					480
Leu	Ser	Ser	Ala	Glu	Lys	Gly	Asn	Thr	Gly	Phe	Ile	Ile	Val	Ile	Ile
			485						490					495	
Leu	Ile	Ala	Val	Leu	Gly	Ser	Ser	Met	Ile	Leu	Val	Ser	Ile	Phe	Ile
		500						505					510		
Ile	Ile	Lys	Lys	Thr	Lys	Lys	Pro	Thr	Gly	Ala	Pro	Pro	Glu	Leu	Ser
	515						520					525			
Gly	Val	Thr	Asn	Asn	Gly	Phe	Ile	Pro	His	Asn					
530					535										

<210> SEQ ID NO 98

<211> LENGTH: 539

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 98

Met	Ser	Trp	Lys	Val	Val	Ile	Ile	Phe	Ser	Leu	Leu	Ile	Thr	Pro	Gln
1			5					10					15		
His	Gly	Leu	Lys	Glu	Ser	Tyr	Leu	Glu	Glu	Ser	Cys	Ser	Thr	Ile	Thr
		20					25					30			
Glu	Gly	Tyr	Leu	Ser	Val	Leu	Arg	Thr	Gly	Trp	Tyr	Thr	Asn	Val	Phe
	35					40					45				
Thr	Leu	Pro	Val	Gly	Asp	Val	Glu	Asn	Leu	Thr	Cys	Ser	Asp	Gly	Pro
	50				55					60					
Ser	Leu	Ile	Lys	Thr	Glu	Leu	Asp	Leu	Thr	Lys	Ser	Ala	Leu	Arg	Glu
65			70					75					80		
Leu	Lys	Thr	Val	Ser	Ala	Asp	Gln	Leu	Ala	Arg	Glu	Glu	Gln	Ile	Glu
		85					90						95		
Asn	Pro	Gly	Ser	Gly	Ser	Phe	Val	Leu	Gly	Ala	Ile	Ala	Leu	Gly	Val
	100						105				110				
Ala	Ala	Ala	Ala	Ala	Val	Thr	Ala	Gly	Val	Ala	Ile	Ala	Lys	Thr	Ile
	115					120					125				
Arg	Leu	Glu	Ser	Glu	Val	Thr	Ala	Ile	Asn	Asn	Ala	Leu	Lys	Lys	Thr
	130				135					140					
Asn	Glu	Ala	Val	Ser	Thr	Leu	Gly	Asn	Gly	Val	Arg	Val	Leu	Ala	Thr
145			150					155					160		
Ala	Val	Arg	Glu	Leu	Lys	Asp	Phe	Val	Ser	Lys	Asn	Leu	Thr	Arg	Ala
	165				170						175				
Ile	Asn	Lys	Asn	Lys	Cys	Asp	Ile	Asp	Asp	Leu	Lys	Met	Ala	Val	Ser
	180					185						190			
Phe	Ser	Gln	Phe	Asn	Arg	Arg	Phe	Leu	Asn	Val	Val	Arg	Gln	Phe	Ser
	195					200					205				
Asp	Asn	Ala	Gly	Ile	Thr	Pro	Ala	Ile	Ser	Leu	Asp	Leu	Met	Thr	Asp
210					215						220				
Ala	Glu	Leu	Ala	Arg	Ala	Val	Pro	Asn	Met	Pro	Thr	Ser	Ala	Gly	Gln
225				230					235					240	

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Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
      245                      250          255

Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
      260                      265          270

Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
      275                      280          285

Ala Pro Ser Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
      290                      295          300

Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
      305                      310          315          320

Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
      325                      330          335

Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
      340                      345          350

Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
      355                      360          365

Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
      370                      375          380

Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
      385                      390          395          400

Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
      405                      410          415

Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
      420                      425          430

Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Ser Phe Asp Pro
      435                      440          445

Ile Lys Phe Pro Glu Asp Gln Phe Gln Val Ala Leu Asp Gln Val Phe
      450                      455          460

Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
      465                      470          475          480

Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
      485                      490          495

Leu Ile Ala Val Leu Gly Ser Ser Met Ile Leu Val Ser Ile Phe Ile
      500                      505          510

Ile Ile Lys Lys Thr Lys Lys Pro Thr Gly Ala Pro Pro Glu Leu Ser
      515                      520          525

Gly Val Thr Asn Asn Gly Phe Ile Pro His Asn
      530                      535

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<210> SEQ ID NO 99
<211> LENGTH: 539
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide

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<400> SEQUENCE: 99

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Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1          5          10          15

His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
      20          25          30

Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
      35          40          45

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Thr	Leu	Glu	Val	Gly	Asp	Val	Glu	Asn	Leu	Thr	Cys	Ser	Asp	Gly	Pro
50						55					60				
Ser	Leu	Ile	Lys	Thr	Glu	Leu	Asp	Leu	Thr	Lys	Ser	Ala	Leu	Arg	Glu
65					70					75					80
Leu	Lys	Thr	Val	Ser	Ala	Asp	Gln	Leu	Ala	Arg	Glu	Glu	Gln	Ile	Glu
				85					90					95	
Asn	Pro	Gly	Ser	Gly	Ser	Phe	Val	Leu	Gly	Ala	Ile	Ala	Leu	Gly	Val
			100						105				110		
Ala	Ala	Ala	Ala	Ala	Val	Thr	Ala	Gly	Val	Ala	Ile	Ala	Lys	Thr	Ile
			115					120					125		
Arg	Leu	Glu	Ser	Glu	Val	Thr	Ala	Ile	Asn	Asn	Ala	Leu	Lys	Lys	Thr
	130					135					140				
Asn	Glu	Ala	Val	Ser	Thr	Leu	Gly	Asn	Gly	Val	Arg	Val	Leu	Ala	Thr
	145				150					155					160
Ala	Val	Arg	Glu	Leu	Lys	Asp	Phe	Val	Ser	Lys	Asn	Leu	Thr	Arg	Ala
				165					170					175	
Ile	Asn	Lys	Asn	Lys	Cys	Asp	Ile	Pro	Asp	Leu	Lys	Met	Ala	Val	Ser
			180					185					190		
Phe	Ser	Gln	Phe	Asn	Arg	Arg	Phe	Leu	Asn	Val	Val	Arg	Gln	Phe	Ser
		195					200					205			
Asp	Asn	Ala	Gly	Ile	Thr	Pro	Ala	Ile	Ser	Leu	Asp	Leu	Met	Thr	Asp
	210					215					220				
Ala	Glu	Leu	Ala	Arg	Ala	Val	Pro	Asn	Met	Pro	Thr	Ser	Ala	Gly	Gln
	225				230					235					240
Ile	Lys	Leu	Met	Leu	Glu	Asn	Arg	Ala	Met	Val	Arg	Arg	Lys	Gly	Phe
				245					250					255	
Gly	Ile	Leu	Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln
		260						265					270		
Leu	Pro	Ile	Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Val	Lys	Ala
		275					280						285		
Ala	Pro	Ser	Cys	Ser	Glu	Lys	Lys	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg
	290					295					300				
Glu	Asp	Gln	Gly	Trp	Tyr	Cys	Gln	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr
	305				310					315					320
Pro	Asn	Glu	Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp
				325					330					335	
Thr	Ala	Ala	Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Lys	Glu	Cys	Asn	Ile
			340						345				350		
Asn	Ile	Ser	Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His
		355					360						365		
Pro	Ile	Ser	Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys
	370					375					380				
Tyr	Lys	Gly	Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile
	385				390					395					400
Lys	Gln	Leu	Asn	Lys	Gly	Cys	Ser	Tyr	Ile	Thr	Asn	Gln	Asp	Ala	Asp
				405					410					415	
Thr	Val	Thr	Ile	Asp	Asn	Thr	Val	Tyr	Gln	Leu	Ser	Lys	Val	Glu	Gly
			420					425					430		
Glu	Gln	His	Val	Ile	Lys	Gly	Arg	Pro	Val	Ser	Ser	Ser	Phe	Asp	Pro
		435					440						445		
Ile	Lys	Phe	Pro	Glu	Asp	Gln	Phe	Gln	Val	Ala	Leu	Asp	Gln	Val	Phe

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450	455	460
Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile		
465	470	475 480
Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile		
	485	490 495
Leu Ile Ala Val Leu Gly Ser Ser Met Ile Leu Val Ser Ile Phe Ile		
	500	505 510
Ile Ile Lys Lys Thr Lys Lys Pro Thr Gly Ala Pro Pro Glu Leu Ser		
	515	520 525
Gly Val Thr Asn Asn Gly Phe Ile Pro His Asn		
530	535	

<210> SEQ ID NO 100
 <211> LENGTH: 539
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 100

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1 5 10 15
His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
20 25 30
Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
35 40 45
Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
50 55 60
Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65 70 75 80
Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
85 90 95
Asn Pro Gly Ser Gly Ser Phe Val Leu Gly Ala Ile Ala Leu Gly Val
100 105 110
Ala Ala Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
115 120 125
Arg Leu Glu Ser Glu Val Thr Ala Ile Asn Asn Ala Leu Lys Lys Thr
130 135 140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
145 150 155 160
Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
165 170 175
Ile Asn Lys Asn Lys Cys Pro Ile Asp Asp Leu Lys Met Ala Val Ser
180 185 190
Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
195 200 205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
210 215 220
Ala Glu Leu Ala Arg Ala Val Pro Asn Met Pro Thr Ser Ala Gly Gln
225 230 235 240
Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
245 250 255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln

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260					265					270					
Leu	Pro	Ile	Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Val	Lys	Ala
	275						280					285			
Ala	Pro	Ser	Cys	Ser	Glu	Lys	Lys	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg
	290					295					300				
Glu	Asp	Gln	Gly	Trp	Tyr	Cys	Gln	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr
	305					310					315				320
Pro	Asn	Glu	Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp
			325						330					335	
Thr	Ala	Ala	Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Lys	Glu	Cys	Asn	Ile
			340					345					350		
Asn	Ile	Ser	Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His
		355					360					365			
Pro	Ile	Ser	Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys
	370					375					380				
Tyr	Lys	Gly	Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile
	385					390					395				400
Lys	Gln	Leu	Asn	Lys	Gly	Cys	Ser	Tyr	Ile	Thr	Asn	Gln	Asp	Ala	Asp
			405						410					415	
Thr	Val	Thr	Ile	Asp	Asn	Thr	Val	Tyr	Gln	Leu	Ser	Lys	Val	Glu	Gly
			420					425					430		
Glu	Gln	His	Val	Ile	Lys	Gly	Arg	Pro	Val	Ser	Ser	Ser	Phe	Asp	Pro
		435					440					445			
Ile	Lys	Phe	Pro	Glu	Asp	Gln	Phe	Gln	Val	Ala	Leu	Asp	Gln	Val	Phe
	450					455					460				
Glu	Asn	Ile	Glu	Asn	Ser	Gln	Ala	Leu	Val	Asp	Gln	Ser	Asn	Arg	Ile
	465					470					475				480
Leu	Ser	Ser	Ala	Glu	Lys	Gly	Asn	Thr	Gly	Phe	Ile	Ile	Val	Ile	Ile
			485					490						495	
Leu	Ile	Ala	Val	Leu	Gly	Ser	Ser	Met	Ile	Leu	Val	Ser	Ile	Phe	Ile
		500					505						510		
Ile	Ile	Lys	Lys	Thr	Lys	Lys	Pro	Thr	Gly	Ala	Pro	Pro	Glu	Leu	Ser
		515					520					525			
Gly	Val	Thr	Asn	Asn	Gly	Phe	Ile	Pro	His	Asn					
	530					535									

<210> SEQ ID NO 101

<211> LENGTH: 539

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 101

Met	Ser	Trp	Lys	Val	Val	Ile	Ile	Phe	Ser	Leu	Leu	Ile	Thr	Pro	Gln
1			5						10				15		
His	Gly	Leu	Lys	Glu	Ser	Tyr	Leu	Glu	Glu	Ser	Cys	Ser	Thr	Ile	Thr
		20					25					30			
Glu	Gly	Tyr	Leu	Ser	Val	Leu	Arg	Thr	Gly	Trp	Tyr	Thr	Asn	Val	Phe
	35						40				45				
Thr	Leu	Glu	Val	Gly	Asp	Val	Glu	Asn	Leu	Thr	Cys	Ser	Asp	Gly	Pro
	50					55				60					
Ser	Leu	Ile	Lys	Thr	Glu	Leu	Asp	Leu	Thr	Lys	Ser	Ala	Leu	Arg	Glu

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65	70	75	80
Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu	85	90	95
Asn Pro Gly Ser Gly Ser Phe Val Leu Gly Ala Ile Ala Leu Gly Val	100	105	110
Ala Ala Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile	115	120	125
Arg Leu Pro Ser Glu Val Thr Ala Ile Asn Asn Ala Leu Lys Lys Thr	130	135	140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr	145	150	155
Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala	165	170	175
Ile Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser	180	185	190
Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser	195	200	205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp	210	215	220
Ala Glu Leu Ala Arg Ala Val Pro Asn Met Pro Thr Ser Ala Gly Gln	225	230	235
Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe	245	250	255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln	260	265	270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala	275	280	285
Ala Pro Ser Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg	290	295	300
Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr	305	310	315
Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp	325	330	335
Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile	340	345	350
Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His	355	360	365
Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys	370	375	380
Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile	385	390	395
Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp	405	410	415
Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly	420	425	430
Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Ser Phe Asp Pro	435	440	445
Ile Lys Phe Pro Glu Asp Gln Phe Gln Val Ala Leu Asp Gln Val Phe	450	455	460
Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile	465	470	475
			480

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Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
 485 490 495

Leu Ile Ala Val Leu Gly Ser Ser Met Ile Leu Val Ser Ile Phe Ile
 500 505 510

Ile Ile Lys Lys Thr Lys Lys Pro Thr Gly Ala Pro Pro Glu Leu Ser
 515 520 525

Gly Val Thr Asn Asn Gly Phe Ile Pro His Asn
 530 535

<210> SEQ ID NO 102
 <211> LENGTH: 539
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 102

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
 1 5 10 15

His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
 20 25 30

Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
 35 40 45

Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
 50 55 60

Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
 65 70 75 80

Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
 85 90 95

Asn Pro Gly Ser Gly Ser Phe Val Leu Gly Ala Ile Ala Leu Gly Val
 100 105 110

Ala Ala Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
 115 120 125

Arg Leu Glu Ser Glu Val Thr Ala Ile Asn Asn Ala Leu Lys Lys Thr
 130 135 140

Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
 145 150 155 160

Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
 165 170 175

Ile Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser
 180 185 190

Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
 195 200 205

Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
 210 215 220

Ala Glu Leu Ala Arg Ala Val Pro Asn Met Pro Thr Ser Ala Gly Gln
 225 230 235 240

Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
 245 250 255

Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
 260 265 270

Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
 275 280 285

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Ala Pro Ser Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
 290 295 300
 Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
 305 310 315 320
 Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
 325 330 335
 Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
 340 345 350
 Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
 355 360 365
 Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
 370 375 380
 Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
 385 390 395 400
 Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
 405 410 415
 Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
 420 425 430
 Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Ser Phe Pro Pro
 435 440 445
 Ile Lys Phe Pro Glu Asp Gln Phe Gln Val Ala Leu Asp Gln Val Phe
 450 455 460
 Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
 465 470 475 480
 Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
 485 490 495
 Leu Ile Ala Val Leu Gly Ser Ser Met Ile Leu Val Ser Ile Phe Ile
 500 505 510
 Ile Ile Lys Lys Thr Lys Lys Pro Thr Gly Ala Pro Pro Glu Leu Ser
 515 520 525
 Gly Val Thr Asn Asn Gly Phe Ile Pro His Asn
 530 535

<210> SEQ ID NO 103

<211> LENGTH: 539

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 103

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
 1 5 10 15
 His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
 20 25 30
 Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
 35 40 45
 Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
 50 55 60
 Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
 65 70 75 80
 Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
 85 90 95

Asn	Pro	Gly	Ser	Gly	Ser	Phe	Val	Leu	Gly	Ala	Ile	Ala	Leu	Gly	Val	
			100				105						110			
Ala	Ala	Ala	Ala	Ala	Val	Thr	Ala	Gly	Val	Ala	Ile	Ala	Lys	Thr	Ile	
			115				120				125					
Arg	Leu	Glu	Ser	Glu	Val	Thr	Ala	Ile	Asn	Asn	Ala	Leu	Lys	Lys	Thr	
			130				135				140					
Asn	Glu	Ala	Val	Ser	Thr	Leu	Gly	Asn	Gly	Val	Arg	Val	Leu	Ala	Thr	
			145				150				155			160		
Ala	Val	Arg	Glu	Leu	Lys	Asp	Phe	Val	Ser	Lys	Asn	Leu	Thr	Arg	Ala	
			165							170			175			
Ile	Asn	Lys	Asn	Lys	Cys	Asp	Ile	Asp	Asp	Leu	Lys	Met	Ala	Val	Ser	
			180							185			190			
Phe	Ser	Gln	Phe	Asn	Arg	Arg	Phe	Leu	Asn	Val	Val	Arg	Gln	Phe	Ser	
			195				200				205					
Asp	Asn	Ala	Gly	Ile	Thr	Pro	Ala	Ile	Ser	Leu	Asp	Leu	Met	Thr	Asp	
			210				215				220					
Ala	Glu	Leu	Ala	Arg	Ala	Val	Pro	Asn	Met	Pro	Thr	Ser	Ala	Gly	Gln	
			225				230				235			240		
Ile	Lys	Leu	Met	Leu	Glu	Asn	Arg	Ala	Met	Val	Arg	Arg	Lys	Gly	Phe	
			245							250			255			
Gly	Ile	Leu	Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln	
			260				265				270					
Leu	Pro	Ile	Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Val	Lys	Ala	
			275				280				285					
Ala	Pro	Ser	Cys	Ser	Glu	Lys	Lys	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg	
			290				295				300					
Glu	Asp	Gln	Gly	Trp	Tyr	Cys	Gln	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr	
			305				310				315			320		
Pro	Asn	Glu	Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp	
			325							330			335			
Thr	Ala	Ala	Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Lys	Glu	Cys	Asn	Ile	
			340							345			350			
Asn	Ile	Ser	Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His	
			355				360				365					
Pro	Ile	Ser	Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys	
			370				375				380					
Tyr	Lys	Gly	Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile	
			385				390				395			400		
Lys	Gln	Leu	Asn	Lys	Gly	Cys	Ser	Tyr	Ile	Thr	Asn	Gln	Asp	Ala	Asp	
			405							410			415			
Thr	Val	Thr	Ile	Asp	Asn	Thr	Val	Tyr	Gln	Leu	Ser	Lys	Val	Glu	Gly	
			420							425			430			
Glu	Gln	His	Val	Ile	Lys	Gly	Arg	Pro	Val	Ser	Ser	Ser	Phe	Asp	Pro	
			435				440				445					
Ile	Lys	Phe	Pro	Glu	Asn	Gln	Phe	Gln	Val	Ala	Leu	Asp	Gln	Val	Phe	
			450				455				460					
Glu	Asn	Ile	Glu	Asn	Ser	Gln	Ala	Leu	Val	Asp	Gln	Ser	Asn	Arg	Ile	
			465				470				475			480		
Leu	Ser	Ser	Ala	Glu	Lys	Gly	Asn	Thr	Gly	Phe	Ile	Ile	Val	Ile	Ile	
			485							490			495			

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Leu Ile Ala Val Leu Gly Ser Ser Met Ile Leu Val Ser Ile Phe Ile
 500 505 510

Ile Ile Lys Lys Thr Lys Lys Pro Thr Gly Ala Pro Pro Glu Leu Ser
 515 520 525

Gly Val Thr Asn Asn Gly Phe Ile Pro His Asn
 530 535

<210> SEQ ID NO 104
 <211> LENGTH: 539
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 104

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
 1 5 10 15

His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
 20 25 30

Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
 35 40 45

Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
 50 55 60

Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
 65 70 75 80

Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
 85 90 95

Asn Pro Gly Ser Gly Ser Phe Val Leu Gly Ala Ile Ala Leu Gly Val
 100 105 110

Ala Ala Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
 115 120 125

Arg Leu Glu Ser Glu Val Thr Ala Ile Asn Asn Ala Leu Lys Lys Thr
 130 135 140

Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
 145 150 155 160

Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
 165 170 175

Ile Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser
 180 185 190

Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
 195 200 205

Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
 210 215 220

Ala Glu Leu Ala Arg Ala Val Pro Asn Met Pro Thr Ser Ala Gly Gln
 225 230 235 240

Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
 245 250 255

Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
 260 265 270

Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
 275 280 285

Ala Pro Ser Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
 290 295 300

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Glu	Asp	Gln	Gly	Trp	Tyr	Cys	Gln	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr	305	310	315	320
Pro	Asn	Glu	Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp	325	330	335	
Thr	Ala	Ala	Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Lys	Glu	Cys	Asn	Ile	340	345	350	
Asn	Ile	Ser	Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His	355	360	365	
Pro	Ile	Ser	Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys	370	375	380	
Tyr	Lys	Gly	Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile	385	390	395	400
Lys	Gln	Leu	Asn	Lys	Gly	Cys	Ser	Tyr	Ile	Thr	Asn	Gln	Asp	Ala	Asp	405	410	415	
Thr	Val	Thr	Ile	Asp	Asn	Thr	Val	Tyr	Gln	Leu	Ser	Lys	Val	Glu	Gly	420	425	430	
Glu	Gln	His	Val	Ile	Lys	Gly	Arg	Pro	Val	Ser	Ser	Ser	Phe	Asp	Pro	435	440	445	
Ile	Lys	Phe	Pro	Gln	Asp	Gln	Phe	Gln	Val	Ala	Leu	Asp	Gln	Val	Phe	450	455	460	
Glu	Asn	Ile	Glu	Asn	Ser	Gln	Ala	Leu	Val	Asp	Gln	Ser	Asn	Arg	Ile	465	470	475	480
Leu	Ser	Ser	Ala	Glu	Lys	Gly	Asn	Thr	Gly	Phe	Ile	Ile	Val	Ile	Ile	485	490	495	
Leu	Ile	Ala	Val	Leu	Gly	Ser	Ser	Met	Ile	Leu	Val	Ser	Ile	Phe	Ile	500	505	510	
Ile	Ile	Lys	Lys	Thr	Lys	Lys	Pro	Thr	Gly	Ala	Pro	Pro	Glu	Leu	Ser	515	520	525	
Gly	Val	Thr	Asn	Asn	Gly	Phe	Ile	Pro	His	Asn						530	535		

<210> SEQ ID NO 105

<211> LENGTH: 539

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<400> SEQUENCE: 105

Met	Ser	Trp	Lys	Val	Val	Ile	Ile	Phe	Ser	Leu	Leu	Ile	Thr	Pro	Gln	1	5	10	15
His	Gly	Leu	Lys	Glu	Ser	Tyr	Leu	Glu	Glu	Ser	Cys	Ser	Thr	Ile	Thr	20	25	30	
Glu	Gly	Tyr	Leu	Ser	Val	Leu	Arg	Thr	Gly	Trp	Tyr	Thr	Asn	Val	Phe	35	40	45	
Thr	Leu	Glu	Val	Gly	Asp	Val	Glu	Asn	Leu	Thr	Cys	Ser	Asp	Gly	Pro	50	55	60	
Ser	Leu	Ile	Lys	Thr	Glu	Leu	Asp	Leu	Thr	Lys	Ser	Ala	Leu	Arg	Glu	65	70	75	80
Leu	Lys	Thr	Val	Ser	Ala	Asp	Gln	Leu	Ala	Arg	Glu	Glu	Gln	Ile	Glu	85	90	95	
Asn	Pro	Gly	Ser	Gly	Ser	Phe	Val	Leu	Gly	Ala	Ile	Ala	Leu	Gly	Val	100	105	110	

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Ala	Ala	Ala	Ala	Ala	Val	Thr	Ala	Gly	Val	Ala	Ile	Ala	Lys	Thr	Ile
		115					120					125			
Arg	Leu	Glu	Ser	Glu	Val	Thr	Ala	Ile	Asn	Asn	Ala	Leu	Lys	Lys	Thr
	130					135					140				
Asn	Glu	Ala	Val	Ser	Thr	Leu	Gly	Asn	Gly	Val	Arg	Val	Leu	Ala	Thr
	145				150					155					160
Ala	Val	Arg	Glu	Leu	Lys	Asp	Phe	Val	Ser	Lys	Asn	Leu	Thr	Arg	Ala
			165						170					175	
Ile	Asn	Lys	Asn	Lys	Cys	Asp	Ile	Asp	Asp	Leu	Lys	Met	Ala	Val	Ser
			180					185					190		
Phe	Ser	Gln	Trp	Asn	Arg	Arg	Phe	Leu	Asn	Val	Val	Arg	Gln	Phe	Ser
		195					200					205			
Asp	Asn	Ala	Gly	Ile	Thr	Pro	Ala	Ile	Ser	Leu	Asp	Leu	Met	Thr	Asp
	210					215					220				
Ala	Glu	Leu	Ala	Arg	Ala	Val	Pro	Asn	Met	Pro	Thr	Ser	Ala	Gly	Gln
	225				230					235					240
Ile	Lys	Leu	Met	Leu	Glu	Asn	Arg	Ala	Met	Val	Arg	Arg	Lys	Gly	Phe
			245						250					255	
Gly	Ile	Leu	Ile	Gly	Val	Tyr	Gly	Ser	Ser	Val	Ile	Tyr	Met	Val	Gln
		260						265					270		
Leu	Pro	Ile	Phe	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Ile	Val	Lys	Ala
		275					280					285			
Ala	Pro	Ser	Cys	Ser	Glu	Lys	Lys	Gly	Asn	Tyr	Ala	Cys	Leu	Leu	Arg
	290					295					300				
Glu	Asp	Gln	Gly	Trp	Tyr	Cys	Gln	Asn	Ala	Gly	Ser	Thr	Val	Tyr	Tyr
	305				310					315					320
Pro	Asn	Glu	Lys	Asp	Cys	Glu	Thr	Arg	Gly	Asp	His	Val	Phe	Cys	Asp
			325						330					335	
Thr	Ala	Ala	Gly	Ile	Asn	Val	Ala	Glu	Gln	Ser	Lys	Glu	Cys	Asn	Ile
		340						345					350		
Asn	Ile	Ser	Thr	Thr	Asn	Tyr	Pro	Cys	Lys	Val	Ser	Thr	Gly	Arg	His
		355				360						365			
Pro	Ile	Ser	Met	Val	Ala	Leu	Ser	Pro	Leu	Gly	Ala	Leu	Val	Ala	Cys
	370					375					380				
Tyr	Lys	Gly	Val	Ser	Cys	Ser	Ile	Gly	Ser	Asn	Arg	Val	Gly	Ile	Ile
	385				390					395					400
Lys	Gln	Leu	Asn	Lys	Gly	Cys	Ser	Tyr	Ile	Thr	Asn	Gln	Asp	Ala	Asp
			405						410					415	
Thr	Val	Thr	Ile	Asp	Asn	Thr	Val	Tyr	Gln	Leu	Ser	Lys	Val	Glu	Gly
		420						425					430		
Glu	Gln	His	Val	Ile	Lys	Gly	Arg	Pro	Val	Ser	Ser	Ser	Phe	Asp	Pro
		435					440					445			
Ile	Lys	Phe	Pro	Glu	Asp	Gln	Phe	Gln	Val	Ala	Leu	Asp	Gln	Val	Phe
	450					455					460				
Glu	Asn	Ile	Glu	Asn	Ser	Gln	Ala	Leu	Val	Asp	Gln	Ser	Asn	Arg	Ile
	465				470					475					480
Leu	Ser	Ser	Ala	Glu	Lys	Gly	Asn	Thr	Gly	Phe	Ile	Ile	Val	Ile	Ile
			485					490					495		
Leu	Ile	Ala	Val	Leu	Gly	Ser	Ser	Met	Ile	Leu	Val	Ser	Ile	Phe	Ile
		500						505					510		
Ile	Ile	Lys	Lys	Thr	Lys	Lys	Pro	Thr	Gly	Ala	Pro	Pro	Glu	Leu	Ser

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515	520	525
Gly Val Thr Asn Asn Gly Phe Ile Pro His Asn		
530	535	

<210> SEQ ID NO 106
 <211> LENGTH: 1617
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 106

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atgagctgga aggtggatcat catcttcagc ctgctgatca cacctcagca cggcctgaaa    60
gagagctacc tggaaagatc ctgcagcacc atcacagagg gctacctgtc tgtgctgaga    120
accggctggt acaccaacgt gttcacactg gaagtgggag acgtcgagaa tctgacatgc    180
tctgatggcc ctgacctgat caagaccgag ctggatctga ccaagagcgc cctgagagaa    240
ctcaagaccg tgtctgcca tcaagctggc agagaggaac agatcgagaa tcctggcagc    300
ggcagctttg tgctgggagc cattgtcttt ggagtggctg ctgctgcagc tgttacagca    360
ggcgtggcca tctgcaagac catcagactg gaaagcgaag tgaccgccat caacaacgcc    420
ctgaagaaga caaacgaggg cgtcagcaca ctgcgcaatg gcgttagagt gctggccttt    480
gccgtgcgag agctgaagga ctctgtgtcc aagaacctga caccggccct gaacaagaac    540
aagtgcgaca tcgacgacct gaagatggcc gtgtccttta gccagttcaa ccggcggttt    600
ctgaacgtcg tgccgcagtt tagcgacaac gccggaatca caccagccat cagcctggac    660
ctgatgacag atgctgagct ggctagagcc gtgcctaaca tgctacatc tgccggccag    720
atcaagctga tgctcgagaa tagagccatg gtccgacgga aaggtctcgg cattctgtgt    780
ggcgtgtacg gcagcagcgt gatctatatg gtgcagctgc ctatcttcgg cgtgatcgac    840
acacctgctt ggattgtgaa ggccgctcct agctgtagcg agaagaaggg caattacgcc    900
tgctctgctg gagaggacca aggtgggtat tgtcagaacg ccggcagcac cgtgtactac    960
cctaacgaga aggactgcca gacaagaggg gaccacgtgt tctgtgatac cgcgctgga    1020
atcaatgtgg ccgagcagag caaagagtgc aacatcaaca tcagcaccac caactatccc    1080
tgcaaggtgt ccaccggcag gcaccctatt tctatggtgg ctctgtctcc tctgggagcc    1140
ctggtggcct gttataaggg cgtgtcctgt agcatcgcca gcaacagagt gggcatcatc    1200
aagcagctga acaagggctg cagctacatc accaaccagg acgcccatac cgtgaccatc    1260
gacaacaccg tgtatcagct gagcaagggt gaaggcgaac agcacgtgat caagggcaga    1320
cctgtgtcca gcagcttcca cctatcaag ttccctgagg atcagttcaa cgtggccctg    1380
gaccaggtgt tcgagaacat cgagaattcc caggctctgg tggaccagtc caacagaatc    1440
ctgtctagcg ccgagaaggg aaacaccggc ttcacatcgc tgatcaccct gatcgccgtg    1500
ctgggcagct ccatgatcct ggtgtccatc ttcacatta tcaagaagac caagaagccc    1560
accggcgctc ctccagaact gagcggagtg accaacaatg gcttcacccc tcacaac    1617
  
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<210> SEQ ID NO 107
 <211> LENGTH: 1617
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 107

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atgagctgga aggtggatcat catcttcagc ctgctgatca cacctcagca cggcctgaaa    60
gagagctacc tggaaagatc ctgcagcacc atcacagagg gctacctgtc tgtgctgaga    120
accggctggt acaccaacgt gttcacactg gaagtgggag acgtcgagaa tctgacatgc    180
tctgatggcc ctgacctgat caagaccgag ctggatctga ccaagagcgc cctgagagaa    240
ctcaagaccg tgtctgccga tcagctggcc agagaggaac agatcgagaa tcctggcagc    300
ggcagctttg tgctgggagc cattgtcttt ggagtggctg ctgctgcagc tgttacagca    360
ggcgtggcca tctgcaagac catcagactg gaaagcgaag tgaccgccat caacaacgcc    420
ctgaagaaga caaacgaggg cgtcagcaca ctccgcaatg gcgttagagt gctggccaca    480
gccgtgcgag agctgaagga ctctgtgtcc aagaacctga caccggccat taacaagaac    540
aagtgcgaca tcgacgacct gaagatggcc gtgtccttta gccagttcaa ccggcggttt    600
ctgaacgtcg tgcggcagtt tagcgacaac gccggaatca caccagccat cagcctggac    660
ctgatgacag atgctgagct ggctagagcc gtgcctaaca tgctacatc tgccggccag    720
atcaagctga tgctcgagaa tagagccatg gtccgacgga aaggcttcgg cattctgtgt    780
ggcgtgtacg gcagcagcgt gatctatatg gtgcagctgc ctatcttcgg cgtgatcgac    840
acacctgtct ggattgtgaa ggccgctcct agctgtagcg agaagaaggg caattacgcc    900
tgctctgtga gagaggacca aggtctggtat tgtcagaacg ccggcagcac cgtgtactac    960
cctaacgaga aggactgcga gacaagaggc gaccacgtgt tctgtgatac cgcgctgga    1020
atcaatgtgg ccgagcagag caaagagtgc aacatcaaca tcagaccac caactatccc    1080
tgcaaggtgt ccaccggcag gcacctatt tctatggtgg ctctgtctcc tctgggagcc    1140
ctggtggctt gttataaggg cgtgtcctgt agcatcgga gcaacagagt gggcatcatc    1200
aagcagctga acaagggctg cagctacatc accaaccagg acgcccatac cgtgaccatc    1260
gacaacaccg tgtatcagct gagcaagggt gaaggcgaac agcacgtgat caagggcaga    1320
cctgtgtcca gcagcttcga cctatcaag ttccctgagc accagtggca tgtggccctg    1380
gaccaggtgt tcgagaacat cgagaattcc caggctctgg tggaccagtc caacagaatc    1440
ctgtctagcg ccgagaaggg aaacaccggc ttcacatcgc tgatcatcct gatcgccgtg    1500
ctgggcagct ccatgatcct ggtgtccatc ttcacatta tcaagaagac caagaagccc    1560
accggcgctc ctccagaact gagcggagtg accaacaatg gcttcacccc tcacaac    1617

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<210> SEQ ID NO 108

<211> LENGTH: 1617

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 108

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atgagctgga aggtggatcat catcttcagc ctgctgatca cacctcagca cggcctgaaa    60
gagagctacc tggaaagatc ctgcagcacc atcacagagg gctacctgtc tgtgctgaga    120
accggctggt acaccaacgt gttcacactg gaagtgggag acgtcgagaa tctgacatgc    180
tctgatggcc ctgacctgat caagaccgag ctggatctgc tcaagagcgc cctgagagaa    240
ctcaagaccg tgtctgccga tcagctggcc agagaggaac agatcgagaa tcctggcagc    300

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ggcagctttg tgctgggagc cattgctctt ggagtggctg ctgctgcagc tgttacagca	360
ggcgtggcca tcgctaagac catcagactg gaaagcgaag tgaccgccat caacaacgcc	420
ctgaagaaga caaacgaggc cgtcagcaca ctcggaatg gcgttagagt gctggccaca	480
gccgtgcgcg agctgaagga ctctgtgtcc aagaacctga cacgggccat taacaagaac	540
aagtgcgaca tccctgacct gaagatggcc gtgtccttta gccagttcaa ccggcggttt	600
ctgaacgtcg tgcggcagtt tagcgacaac gccggaatca caccagccat cagcctggac	660
ctgatgacag atgctgagct ggctagagcc gtgcctaaca tgectacatc tgccggccag	720
atcaagctga tgctcgagaa tagagccatg gtccgacgga aaggttcgg cattctgatt	780
ggcgtgtacg gcagcagcgt gatctatatg gtgcagctgc ctatcttcgg cgtgatcgac	840
acaccctgct ggattgtgaa ggccgctcct agctgtagcg agaagaagg caattacgcc	900
tgctctgctga gagaggacca aggtcggtat tgtcagaacg ccggcagcac cgtgtactac	960
cctaacgaga aggactcgga gacaagaggc gaccacgtgt tctgtgatac cgcgctgga	1020
atcaatgtgg ccgagcagag caaagagtgc aacatcaaca tcagcaccac caactatccc	1080
tgcaaggtgt ccaccggcag gcaccctatt tctatggtgg ctctgtctcc tctgggagcc	1140
ctggtggcctt gttataaggg cgtgtcctgt agcatcgcca gcaacagagt gggcatcatc	1200
aagcagctga acaagggctg cagctacatc accaaccagg acgcccatac cgtgaccatc	1260
gacaacaccg tgtatcagct gagcaagggt gaaggcgaac agcacgtgat caagggcaga	1320
cctgtgtcca gcagcttcga cctatcaag ttccctgagg atcagttcca ggtggccctg	1380
gaccaggtgt tcgagaacat cgagaattcc caggctctgg tggaccagtc caacagaatc	1440
ctgtctagcg ccgagaaggg aaacaccggc ttcacatcgc tgatcatcct gatcgccgtg	1500
ctgggcagct ccatgatcct ggtgtccatc ttcacatta tcaagaagac caagaagccc	1560
accggcgctc ctccagaact gagcggagtg accaacaatg gcttcacccc tcacaac	1617

<210> SEQ ID NO 109

<211> LENGTH: 1617

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 109

atgagctgga aggtggctcat catcttcagc ctgctgatca cacctcagca cggcctgaaa	60
gagagctacc tggaagagtc ctgcagcacc atcacagagg gctacctgtc tgtgctgaga	120
accggctggt acaccaacgt gttcacactg gaagtgggcg acgtcgagaa tctgacatgc	180
tctgatggcc ctagcctgat caagaccgag ctggatctgc tcaagagcgc cctgagagaa	240
ctcaagaccg tgtctgccga tcagctggcc agagaggaaac agatcgagaa tcctggcagc	300
ggcagctttg tgctgggagc cattgctctt ggagtggctg ctgctgcagc tgttacagca	360
ggcgtggcca tcgctaagac catcagactg gaaagcgaag tgaccgccat caacaacgcc	420
ctgaagaaga caaacgaggc cgtcagcaca ctcggaatg gcgttagagt gctggccaca	480
gccgtgcgcg agctgaagga ctctgtgtcc aagaacctga cacgggccat taacaagaac	540
aagtgcgaca tccctgacct gaagatggcc gtgtccttta gccagttcaa ccggcggttt	600
ctgaacgtcg tgcggcagtt tagcgacaac gccggaatca caccagccat cagcctggac	660

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ctgatgacag atgctgagct ggctagagcc gtgcctaaca tgctacatc tgcggccag	720
atcaagctga tgctcgagaa tagagccatg gtccgacgga aaggtctcgg cattctgatt	780
ggcgtgtacg gcagcagcgt gatctatatg gtgcagctgc ctatcttcgg cgtgatcgac	840
acacctgct ggattgtgaa ggcgcctcct agctgtagcg agaagaagg caattacgcc	900
tgcttctga gagaggacca aggttggtat tgtcagaacg ccggcagcac cgtgtactac	960
cctaacgaga aggactgcga gacaagaggc gaccacgtgt tctgtgatac cgccgctgga	1020
atcaatgtgg ccgagcagag caaagagtgc aacatcaaca tcagaccac caactatccc	1080
tgcaaggtgt ccaccggcag gcacctatt tctatggtgg ctctgtctcc tctgggagcc	1140
ctggtggcctt gttataaggc cgtgtcctgt agcatcgcca gcaacagagt gggcatcatc	1200
aagcagctga acaagggtg cagctacatc accaaccagg acgcccatac cgtgaccatc	1260
gacaacaccg tgtatcagct gagcaagggt gaaggcgaac agcacgtgat caagggcaga	1320
cctgtgtcca gcagcttcga cctatcaag ttccctgaga accagttcca ggtggccctg	1380
gaccaggtgt tcgagaacat cgagaattcc caggctctgg tggaccagtc caacagaatc	1440
ctgtctagcg ccgagaagg aaacaccggc ttcacatcg tgatcatcct gatcgccgtg	1500
ctgggcagct ccatgatcct ggtgtccatc ttcacatta tcaagaagac caagaagccc	1560
accggcgctc ctccagaact gagcggagtg accaacaatg gcttcatccc tcacaac	1617

<210> SEQ ID NO 110

<211> LENGTH: 1617

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 110

atgagctgga aggtggtcat catcttcagc ctgctgatca cacctcagca cggcctgaaa	60
gagagctacc tggaagagtc ctgcagcacc atcacagagg gctacctgtc tgtgctgaga	120
accggctggt acaccaacgt gttcacactg gaagtgggcg acgtcgagaa tctgacatgc	180
tctgatggcc ctagcctgat caagaccgag ctggatctgc tcaagagcgc cctgagagaa	240
ctcaagaccg tgtctgcga tcagctggcc agagaggaac agatcgagaa tcctggcagc	300
ggcagctttg tgctgggagc cattgtcttt ggagtggctg ctgctgcagc tgttacagca	360
ggcgtggcca tcgctaagac catcagactg gaaagcgaag tgaccgccat caacaacgcc	420
ctgaagaaga caaacgaggc cgtcagcaca ctcgcaatg gcgttagagt gctggccaca	480
gccgtgcgcg agctgaagga ctctgtgctt aagaacctga caccggccat taacaagaac	540
aagtgcgaca tccttgacct gaagatggcc gtgtccttta gccagttcaa ccggcggttt	600
ctgaacgtcg tgcggcagtt tagcgacaac gccggaatca caccagccat cagcctggac	660
ctgatgacag atgctgagct ggctagagcc gtgcctaaca tgctacatc tgcggccag	720
atcaagctga tgctcgagaa tagagccatg gtccgacgga aaggtctcgg cattctgatt	780
ggcgtgtacg gcagcagcgt gatctatatg gtgcagctgc ctatcttcgg cgtgatcgac	840
acacctgct ggattgtgaa ggcgcctcct agctgtagcg agaagaagg caattacgcc	900
tgcttctga gagaggacca aggttggtat tgtcagaacg ccggcagcac cgtgtactac	960
cctaacgaga aggactgcga gacaagaggc gaccacgtgt tctgtgatac cgccgctgga	1020

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atcaatgtgg ccgagcagag caaagagtgc aacatcaaca tcagcaccac caactatccc	1080
tgcaaggtgt ccaccggcag gcaccctatt tctatggtgg ctctgtctcc tctgggagcc	1140
ctggtggcctt gttataaggg cgtgtcctgt agcatcgga gcaacagagt gggcatcatc	1200
aagcagctga acaagggctg cagctacatc accaaccagg acgccgatac cgtgaccatc	1260
gacaacaccg tgtatcagct gagcaagggt gaaggcgaac agcacgtgat caagggcaga	1320
cctgtgtcca gcagcttcga ccctatcaag ttccctgagg atcagttcca ggtggccctg	1380
gaccaggtgt tcgagaacat cgagaattcc caggtctctg tggaccagtc caacagaatc	1440
ctgtctagcg ccgagaaggg aaacaccggc ttcacatcgc tgatcatcct gatcgccgtg	1500
ctgggcagct ccatgatcct ggtgtccatc ttcacatta tcaagaagac caagaagccc	1560
accggcgctc ctccagaact gagcggagtg accaacaatg gcttcatccc tcacaac	1617

<210> SEQ ID NO 111

<211> LENGTH: 1617

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 111

atgagctgga aggtggtcat catcttcagc ctgctgatca cacctcagca cggcctgaaa	60
gagagctacc tggaagagtc ctgcagcacc atcacagagg gctacctgtc tgtgctgaga	120
accggctggt acaccaacgt gttcacactg gaagtgggag acgtcgagaa tctgacatgc	180
tctgatggcc ctgacctgat caagaccgag ctggatctgc tcaagagcgc cctgagagaa	240
ctcaagaccg tgtctgccga tcagctggcc agagaggaac agatcgagaa tcctggcagc	300
ggcagctttg tgctgggagc cattgtcttt ggagtggctg ctgctgcagc tgttacagca	360
ggcgtggcca tcgctaagac catcagactg gaaagcgaag tgaccgccat caacaacgcc	420
ctgaagaaga caaacgaggg cgtcagcaca ctcggaatg gcgttagagt gctggccaca	480
gccgtgcgag agctgaagga ctctgtgctt aagaacctga caccggccat taacaagaac	540
aagtgcgaca tccttgacct gaagatggcc gtgtccttta gccagttcaa ccggcggttt	600
ctgaacgtcg tgcggcagtt tagcgacaac gccggaatca caccagccat cagcctggac	660
ctgatgacag atgctgagct ggctagagcc gtgcctaaca tgacctacatc tgccggccag	720
atcaagctga tgctcgagaa tagagccatg gtccgacgga aaggcttcgg cattctgatt	780
ggcgtgtacg gcagcagcgt gatctatatg gtgcagctgc ctatcttcgg cgtgatcgac	840
acaccctgct ggattgtgaa ggccgctcct agctgtagcg agaagaaggg caattacgcc	900
tgctgtctga gagaggacca aggtgggtat tgtcagaacg ccggcagcac cgtgtactac	960
cctaacgaga aggactgcga gacaagaggg gaccacgtgt tctgtgatac cgccgctgga	1020
atcaatgtgg ccgagcagag caaagagtgc aacatcaaca tcagcaccac caactatccc	1080
tgcaaggtgt ccaccggcag gcaccctatt tctatggtgg ctctgtctcc tctgggagcc	1140
ctggtggcctt gttataaggg cgtgtcctgt agcatcgga gcaacagagt gggcatcatc	1200
aagcagctga acaagggctg cagctacatc accaaccagg acgccgatac cgtgaccatc	1260
gacaacaccg tgtatcagct gagcaagggt gaaggcgaac agcacgtgat caagggcaga	1320
cctgtgtcca gcagcttcga ccctatcaag ttccctgaga accagttcca ggtggccctg	1380

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gaccaggtgt tcgagaacat cgagaattcc caggctctgg tggaccagtc caacagaatc 1440
ctgtctagcg ccgagaaggg aaacaccggc ttcacatcgc tgatcaccct gatcgccgtg 1500
ctgggcagct ccatgatcct ggtgtccatc ttcacatta tcaagaagac caagaagccc 1560
accggcgctc ctccagaact gagcggagtg accaacaatg gcttcacccc tcacaac 1617

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<210> SEQ ID NO 112
<211> LENGTH: 1617
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 112

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atgagctgga aggtggtcat catcttcagc ctgtgatca cacctcagca cggcctgaaa 60
gagagctacc tggaagagtc ctgcagcacc atcacagagg gctacctgtc tgtgctgaga 120
accggctggt acaccaacgt gttcacactg cctgtgggag acgtcgagaa tctgacatgc 180
tctgatggcc ctagcctgat caagaccgag ctggatctgc tcaagagcgc cctgagagaa 240
ctcaagaccg tgtctgccga tcagctggcc agagaggaac agatcgagaa tcctggcagc 300
ggcagctttg tgctgggagc cattgtcttt ggagtggctg ctgctgcagc tgttacagca 360
ggcgtggcca tcgctaagac catcagactg gaaagcgaag tgaccgccat caacaacgcc 420
ctgaagaaga caaacgaggg cgtcagcaca ctcggaatg gcgttagagt gctggccaca 480
gccgtgcgcg agctgaagga ctctgtgtcc aagaacctga caccggccat taacaagaac 540
aagtgcgaca tcgacgacct gaagatggcc gtgtccttta gccagttcaa ccggcggttt 600
ctgaacgtcg tgcggcagtt tagcgacaac gccggaatca caccagccat cagcctggac 660
ctgatgacag atgctgagct ggctagagcc gtgcctaaca tgccacatc tgccggccag 720
atcaagctga tgctcgagaa tagagccatg gtccagcga aaggcttcgg cattctgatt 780
ggcgtgtacg gcagcagcgt gatctatatg gtgcagctgc ctatcttcgg cgtgatcgac 840
acaccctgct ggatttgtga ggccgctcct agctgtagcg agaagaaggg caattacgcc 900
tgccctgctg gagaggacca aggctgggtat tgtcagaacg ccggcagcac cgtgtactac 960
cctaacgaga aggactgcga gacaagaggg gaccacgtgt tctgtgatac cgccgctgga 1020
atcaatgtgg ccgagcagag caaagagtgc aacatcaaca tcagcaccac caactatccc 1080
tgcaaggtgt ccaccggcag gcacctatt tctatgggtg ctctgtctcc tctgggagcc 1140
ctggtggctt gttataaggg cgtgtcctgt agcatcggca gcaacagagt gggcatcatc 1200
aagcagctga acaagggctg cagctacatc accaaccagg acgccgatac cgtgaccatc 1260
gacaacaccg tgtatcagct gagcaaggtg gaaggcgaac agcacgtgat caagggcaga 1320
cctgtgtcca gcagcttcga ccctatcaag ttccctgagg atcagttcca ggtggccctg 1380
gaccaggtgt tcgagaacat cgagaattcc caggctctgg tggaccagtc caacagaatc 1440
ctgtctagcg ccgagaaggg aaacaccggc ttcacatcgc tgatcaccct gatcgccgtg 1500
ctgggcagct ccatgatcct ggtgtccatc ttcacatta tcaagaagac caagaagccc 1560
accggcgctc ctccagaact gagcggagtg accaacaatg gcttcacccc tcacaac 1617

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<210> SEQ ID NO 113
<211> LENGTH: 1617

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 113

atgagctgga aggtggtcat catcttcagc ctgctgatca cacctcagca cggcctgaaa      60
gagagctacc tggaagagtc ctgcagcacc atcacagagg gctacctgtc tgtgctgaga      120
accggctggt acaccaacgt gtccacactg cctgtgggcg acgtcgagaa tctgacatgc      180
tctgatggcc ctagcctgat caagaccgag ctggatctgc tcaagagcgc cctgagagaa      240
ctcaagaccg tgtctgccga tcagctggcc agagaggaac agatcgagaa tcctggcagc      300
ggcagctttg tgctgggagc cattgtctct ggagtggctg ctgctgcagc tgttacagca      360
ggcgtggcca tcgctaagac catcagactg gaaagcgaag tgaccgccat caacaacgcc      420
ctgaagaaga caaacgaggc cgtcagcaca ctcggaatg gcgttagagt gctggccaca      480
gccgtgcgcg agctgaagga ctctgtgtcc aagaacctga caccggccat taacaagaac      540
aagtgcgaca tcgacgacct gaagatggcc gtgtccttta gccagttcaa ccggcggttt      600
ctgaacgtcg tgcggcagtt tagcgacaac gccggaatca caccagccat cagcctggac      660
ctgatgacag atgctgagct ggctagagcc gtgcctaaca tgctacatc tgcggccag      720
atcaagctga tgctcgagaa tagagccatg gtccgacgga aaggcttcgg cattctgatt      780
ggcgtgtacg gcagcagcgt gatctatatg gtgcagctgc ctatcttcgg cgtgatcgac      840
acaccctgct ggatttgtga ggccgctcct agctgtagcg agaagaaggg caattacgcc      900
tgctctgctg gagaggacca aggctgggtat tgtcagaacg ccggcagcac cgtgtactac      960
cctaacgaga aggactgcga gacaagaggc gaccacgtgt tctgtgatac cgccgctgga     1020
atcaatgtgg ccgagcgag caaagagtgc aacatcaaca tcagcaccac caactatccc     1080
tgcaaggtgt ccaccggcag gcacctatt tctatgggtg ctctgtctcc tctgggagcc     1140
ctggtggctt gttataaggg cgtgtcctgt agcatcgcca gcaacagagt gggcatcatc     1200
aagcagctga acaagggtg cagctacatc accaaccagg acgccgatac cgtgaccatc     1260
gacaacaccg tgtatcagct gagcaaggtg gaaggcgaac agcacgtgat caagggcaga     1320
cctgtgtcca gcagcttoga ccctatcaag ttccctgaga accagttcca ggtggccctg     1380
gaccaggtgt tcgagaacat cgagaattcc caggctcttg tggaccagtc caacagaatc     1440
ctgtctagcg ccgagaaggg aaacaccggc ttcacatcgc tgatcactct gatcgccgtg     1500
ctgggcagct ccatgatcct ggtgtccatc ttcacatta tcaagaagac caagaagccc     1560
accggcgctc ctccagaact gagcggagtg accaacaatg gcttcacccc tcacaac      1617

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<210> SEQ ID NO 114
<211> LENGTH: 1617
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 114

atgagctgga aggtggtcat catcttcagc ctgctgatca cacctcagca cggcctgaaa      60
gagagctacc tggaagagtc ctgcagcacc atcacagagg gctacctgtc tgtgctgaga      120
accggctggt acaccaacgt gtccacactg gaagtgggcg acgtcgagaa tctgacatgc      180

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tctgatggcc ctagcctgat caagaccgag ctggatctgc tcaagagcgc cctgagagaa	240
ctcaagaccg tgtctgccga tcagctggcc agagaggaac agatcgagaa tcctggcagc	300
ggcagctttg tgctgggagc cattgtctct ggagtggctg ctgctgcagc tgttacagca	360
ggcgtggcca tcgctaagac catcagactg gaaagcgaag tgaccgccat caacaacgcc	420
ctgaagaaga caaacgaggc cgtcagcaca ctcggaatg gcgttagagt gctggccaca	480
gccgtgcgcg agctgaagga ctctgtgtcc aagaacctga caccggccat taacaagaac	540
aagtgcgaca tcgacgacct gaagatggcc gtgtccttta gccagttcaa ccggcggttt	600
ctgaacgtcg tgcggcagtt tagcgacaac gccggaatca caccagccat cagcctggac	660
ctgatgacag atgctgagct ggctagagcc gtgcctaaca tgcctacatc tgcggccag	720
atcaagctga tgctcgagaa tagagccatg gtccgacgga aaggcttcgg cattctgatt	780
ggcgtgtaag gcagcagcgt gatctatatg gtgcagctgc ctatcttcgg cgtgatcgac	840
acaccctgct ggatttgtga ggccgctcct agctgtagcg agaagaaggg caattacgcc	900
tgctgtctga gagaggacca aggctgggtat tgtcagaacg ccggcagcac cgtgtactac	960
cctaacgaga aggactgcga gacaagaggc gaccacgtgt tctgtgatac cgccgctgga	1020
atcaatgtgg ccgagcagag caaagagtgc aacatcaaca tcagcaccac caactatccc	1080
tgcaaggtgt ccaccggcag gcacctatt tctatgggtg ctctgtctcc tctgggagcc	1140
ctggtggctt gttataaggg cgtgtcctgt agcatcgcca gcaacagagt gggcatcatc	1200
aagcagctga acaagggtg cagctacatc accaaccagg acgccgatac cgtgaccatc	1260
gacaacaccg tgtatcagct gagcaaggtg gaaggcgaac agcacgtgat caagggcaga	1320
cctgtgtcca gcagcttcga ccctatcaag ttccctgagg atcagttcca ggtggcctg	1380
gaccaggtgt tcgagaacat cgagaattcc caggctctgg tggaccagtc caacagaatc	1440
ctgtctagcg ccgagaaggg aaacaccggc ttcacatcag tgatcactct gatcgccgtg	1500
ctgggcagct ccatgatcct ggtgtccatc ttcacatta tcaagaagac caagaagccc	1560
accggcgctc ctccagaact gagcggagtg accaacaatg gcttcacccc tcacaac	1617

<210> SEQ ID NO 115

<211> LENGTH: 1617

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 115

atgagctgga aggtggatcat catcttcagc ctgctgatca cacctcagca cggcctgaaa	60
gagagctacc tggaagagtc ctgcagcacc atcacagagg gctacctgtc tgtgctgaga	120
accggctggt acaccaacgt gttcacactg gaagtgggag acctcgagaa tctgacatgc	180
tctgatggcc ctagcctgat caagaccgag ctggatctga ccaagagcgc cctgagagaa	240
ctcaagaccg tgtctgccga tcagctggcc agagaggaac agatcgagaa tcctggcagc	300
ggcagctttg tgctgggagc cattgtctct ggagtggctg ctgctgcagc tgttacagca	360
ggcgtggcca tcgctaagac catcagactg gaaagcgaag tgaccgccat caacaacgcc	420
ctgaagaaga caaacgaggc cgtcagcaca ctcggaatg gcgttagagt gctggccaca	480
gccgtgcgcg agctgaagga ctctgtgtcc aagaacctga caccggccat taacaagaac	540

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aagtgcgaca tgcacgaact gaagatggcc gtgtccttta gccagttcaa cggcggttt	600
ctgaacgtcg tgcggcagtt tagcgacaac gccggaatca caccagccat cagcctggac	660
ctgatgacag atgctgagct ggctagagcc gtgcctaaca tgctacatc tgccggccag	720
atcaagctga tgcctgagaa tagagccatg gtccgacgga aaggcttcgg cattctgatt	780
ggcgtgtacg gcagcagcgt gatctatatg gtgcagctgc ctatcttcgg cgtgatcgac	840
acaccctgct ggatttgtga ggccgctcct agctgtagcg agaagaagg caattacgcc	900
tgctctgctga gagaggacca aggctgggtat tgtcagaacg ccggcagcac cgtgtactac	960
cctaacgaga aggactgcga gacaagaggc gaccacgtgt tctgtgatac cgccgctgga	1020
atcaatgtgg ccgagcagag caaagagtgc aacatcaaca tcagcaccac caactatccc	1080
tgcaaggtgt ccaccggcag gcacctatt tctatgggtg ctctgtctcc tctgggagcc	1140
ctggtggctt gttataaggc cgtgtcctgt agcatcgcca gcaacagagt gggcatcatc	1200
aagcagctga acaagggtcg cagctacatc accaaccagg acgcccatac cgtgaccatc	1260
gacaacaccg tgtatcagct gagcaaggtg gaaggcgaac agcacgtgat caagggcaga	1320
cctgtgtcca gcagcttcga ccctatcaag ttccctgagg atcagttcca ggtggcctg	1380
gaccaggtgt tcgagaacat cgagaattcc caggctctgg tggaccagtc caacagaatc	1440
ctgtctagcg ccgagaaggg aaacaccggc ttcacatcg tgatcactct gatcgccgtg	1500
ctgggcagct ccatgatcct ggtgtccatc ttcacatta tcaagaagac caagaagccc	1560
accggcgctc ctccagaact gagcggagtg accaacaatg gcttcacccc tcacaac	1617

<210> SEQ ID NO 116

<211> LENGTH: 1617

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 116

atgagctgga aggtggctcat catcttcagc ctgctgatca cacctcagca cggcctgaaa	60
gagagctacc tggaagagtc ctgcagcacc atcacagagg gctacctgtc tgtgctgaga	120
accggctggt acaccaacgt gttcacactg gaagtgggag acgtcgagaa tctgacatgc	180
tctgatggcc ctagcctgat caagaccgag ctggatctga ccaagagcgc cctgagagaa	240
ctcaagaccg tgtctgcgga tcagctggcc agagaggaac agatcgagaa tcttggcagc	300
ggcagctttg tgctgggagc cattgtctct ggagtggctg ctgctgcagc tgttacagca	360
ggcgtggcca tcgctaagac catcagactg gaaagcgaag tgaccgccat caacaacgcc	420
ctgaagaaga caaacgaggc cgtcagcaca ctcggaatg gcgttagagt gctggccaca	480
gccgtgcgag agctgaagga cttcgtgctt aagaacctga cacgggccat taacaagaac	540
aagtgcgaca tgcacgaact gaagatggcc gtgtccttta gccagttcaa cggcggttt	600
ctgaacgtcg tgcggcagtt tagcgacaac gccggaatca caccagccat cagcctggac	660
ctgatgacag atgctgagct ggctagagcc gtgcctaaca tgctacatc tgccggccag	720
atcaagctga tgcctgagaa tagagccatg gtccgacgga aaggcttcgg cattctgatt	780
ggcgtgtacg gcagcagcgt gatctatatg gtgcagctgc ctatcttcgg cgtgatcgac	840
acaccctgct ggatttgtga ggccgctcct agctgtagcg agaagaagg caattacgcc	900

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tgccctgctga gagaggacca aggctgggtat tgtcagaacg ccggcagcac cgtgtactac	960
cctaacgaga aggactgcga gacaagaggc gaccacgtgt tctgtgatac cgccgctgga	1020
atcaatgtgg ccgagcagag caaagagtgc aacatcaaca tcagcaccac caactatccc	1080
tgcaagggtg ccaccggcag gcacctatt tctatgggtg ctctgtctcc tctgggagcc	1140
ctggtggctt gttataaggg cgtgtcctgt agcatcggca gcaacagagt gggcatcatc	1200
aagcagctga acaagggctg cagctacatc accaaccagg acgccgatac cgtgaccatc	1260
gacaacaccg tgtatcagct gagcaagggt gaaggcgaac agcacgtgat caagggcaga	1320
cctgtgtcca gcagcttcga ccctatcaag ttccctgagg atcagttcca ggtggcctg	1380
gaccaggtgt tcgagaacat cgagaattcc caggctctgg tggaccagtc caacagaatc	1440
ctgtctagcg ccgagaaggg aaacaccggc ttcacatcgg tgatcactct gatcgccgtg	1500
ctgggcagct ccatgatcct ggtgtccatc ttcacatta tcaagaagac caagaagccc	1560
accggcgctc ctccagaact gagcggagtg accaacaatg gcttcacccc tcacaac	1617

<210> SEQ ID NO 117

<211> LENGTH: 1617

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 117

atgagctgga aggtgggtcat catcttcagc ctgctgatca cacctcagca cgccctgaaa	60
gagagctacc tggaagagtc ctgcagcacc atcacagagg gctacctgtc tgtgctgaga	120
accggctggt acaccaacgt gttcacactg gaagtgggag acgtcgagaa tctgacatgc	180
tctgatggcc ctagcctgat caagaccgag ctggatctga ccaagagcgc cctgagagaa	240
ctcaagaccg tgtctgcoga tcagctggcc agagaggaac agatcgagaa tcttggcagc	300
ggcagctttg tgctgggagc cattgtctct ggagtggctg ctgctgcagc tgttacagca	360
ggcgtggcca tcgctaagac catcagactg gaaagcgaag tgaccgccat caacaacgcc	420
ctgaagaaga caaacgaggc cgtcagcaca ctcggaatg gcgttagagt gctggccaca	480
gccgtgcgag agctgaagga cttcgtgtcc aagaacctgt ggccggccat taacaagaac	540
aagtgcgaca tcgacgacct gaagatggcc gtgtccttta gccagttcaa ccggcggttt	600
ctgaacgtcg tgcggcagtt tagcgacaac gccggaatca caccagccat cagcctggac	660
ctgatgacag atgctgagct ggctagagcc gtgcctaaca tgcctacatc tgcggccag	720
atcaagctga tgctcgagaa tagagccatg gtccgacgga aaggcttcgg cattctgatt	780
ggcgtgtacg gcagcagcgt gatctatatg gtgcagctgc ctatcttcgg cgtgatcgac	840
acaccctgct ggatttgtgaa ggccgctcct agctgtagcg agaagaaggg caattacgcc	900
tgccctgctga gagaggacca aggctgggtat tgtcagaacg ccggcagcac cgtgtactac	960
cctaacgaga aggactgcga gacaagaggc gaccacgtgt tctgtgatac cgccgctgga	1020
atcaatgtgg ccgagcagag caaagagtgc aacatcaaca tcagcaccac caactatccc	1080
tgcaagggtg ccaccggcag gcacctatt tctatgggtg ctctgtctcc tctgggagcc	1140
ctggtggctt gttataaggg cgtgtcctgt agcatcggca gcaacagagt gggcatcatc	1200
aagcagctga acaagggctg cagctacatc accaaccagg acgccgatac cgtgaccatc	1260

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gacaacacccg tgtatcagct gagcaagggtg gaaggcgaac agcacgtgat caagggcaga	1320
cctgtgtcca gcagcttoga ccctatcaag ttccctgagg atcagttcca ggtggccctg	1380
gaccaggtgt tcgagaacat cgagaattcc caggctctgg tggaccagtc caacagaatc	1440
ctgtctagcg ccgagaaggg aaacaccggc ttcacatcg tgatcatcct gatcgccgtg	1500
ctgggcagct ccatgatcct ggtgtccatc ttcacatta tcaagaagac caagaagccc	1560
accggcgctc ctccagaact gagcggagtg accaacaatg gcttcacccc tcacaac	1617

<210> SEQ ID NO 118

<211> LENGTH: 1617

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 118

atgagctgga aggtggctcat catcttcagc ctgctgatca cacctcagca cggcctgaaa	60
gagagctacc tggaagagtc ctgcagcacc atcacagagg gctacctgtc tgtgctgaga	120
accggctggt acaccaacgt gttcacactg gaagtgggag acctcgagaa tctgacatgc	180
tctgatggcc ctagcctgat caagaccgag ctggatctgc tcaagagcgc cctgagagaa	240
ctcaagaccg tgtctgccga tcagctggcc agagaggaa agatcgagaa tcttggcagc	300
ggcagctttg tgctgggagc cattgtctct ggagtggctg ctgctgcagc tgttacagca	360
ggcgtggcca tcgctaagac catcagactg gaaagcgaag tgaccgccat caacaacgcc	420
ctgaagaaga caaacgaggc cgtcagcaca ctggcgaatg gcgttagagt gctggccaca	480
gccgtgcgcg agctgaagga ctctgtgctt aagaacctgt ggcgggccat taacaagaac	540
aagtgcgaca tcgacgacct gaagatggcc gtgtccttta gccagttcaa ccggcggttt	600
ctgaacgtcg tgcggcagtt tagcgacaac gccggaatca caccagccat cagcctggac	660
ctgatgacag atgctgagct ggctagagcc gtgcctaaca tgcctacatc tgccggccag	720
atcaagctga tgctcgagaa tagagccatg gtccgacgga aaggcttcgg cattctgatt	780
ggcgtgtacg gcagcagcgt gatctatatg gtgcagctgc ctatcttcgg cgtgatcgac	840
acaccctgct ggattgtgaa ggcgcctcct agctgtagcg agaagaaggg caattacgcc	900
tgccctgtga gagaggacca aggctggtat tgtcagaacg ccggcagcac cgtgtactac	960
cctaacgaga aggactgcga gacaagaggc gaccacgtgt tctgtgatac cgcgcgtgga	1020
atcaatgtgg ccgagcagag caaagagtgc aacatcaaca tcagcaccac caactatccc	1080
tgcaaggtgt ccaccggcag gcaccctatt tctatgggtg ctctgtctcc tctgggagcc	1140
ctggtggcct gttataaggg cgtgtcctgt agcatcgga gcaacagagt gggcatcatc	1200
aagcagctga acaagggctg cagctacatc accaaccagg acgcccagac cgtgaccatc	1260
gacaacacccg tgtatcagct gagcaagggtg gaaggcgaac agcacgtgat caagggcaga	1320
cctgtgtcca gcagcttoga ccctatcaag ttccctgagg atcagttcca ggtggccctg	1380
gaccaggtgt tcgagaacat cgagaattcc caggctctgg tggaccagtc caacagaatc	1440
ctgtctagcg ccgagaaggg aaacaccggc ttcacatcg tgatcatcct gatcgccgtg	1500
ctgggcagct ccatgatcct ggtgtccatc ttcacatta tcaagaagac caagaagccc	1560
accggcgctc ctccagaact gagcggagtg accaacaatg gcttcacccc tcacaac	1617

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<210> SEQ ID NO 119

<211> LENGTH: 1617

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 119

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atgagctgga aggtggtcat catcttcagc ctgctgatca cacctcagca cggcctgaaa    60
gagagctacc tggaagagtc ctgcagcacc atcacagagg gctacctgtc tgtgctgaga    120
accggctggt acaccaacgt gttcacactg cctgtgggag acgtcgagaa tctgacatgc    180
tctgatggcc ctagcctgat caagaccgag ctggatctga ccaagagcgc cctgagagaa    240
ctcaagaccg tgtctgccga tcagctggcc agagaggaac agatcgagaa tcttggcagc    300
ggcagctttg tgctgggagc cattgtctct ggagtggctg ctgctgcagc tggtacagca    360
ggcgtggcca tcgctaagac catcagactg gaaagcgaag tgaccgccat caacaacgcc    420
ctgaagaaga caaacgaggc cgtcagcaca ctgcgcaatg gcgttagagt gctggccaca    480
gccgtgcgcg agctgaagga cttcgtgtcc aagaacctga cacgggccat taacaagaac    540
aagtgcgaca tcgacgacct gaagatggcc gtgtccttta gccagttcaa ccggcggttt    600
ctgaacgtcg tgccgcagtt tagcgacaac gccggaatca caccagccat cagcctggac    660
ctgatgacag atgctgagct ggctagagcc gtgcctaaca tgcctacatc tgccggccag    720
atcaagctga tgctcgagaa tagagccatg gtccgacgga aaggcttcgg cattctgatt    780
ggcgtgtacg gcagcagcgt gatctatatg gtgcagctgc ctatcttcgg cgtgatcgac    840
acaccctgct ggatttgtga ggccgctcct agctgtagcg agaagaaggg caattacgcc    900
tgccctgctga gagaggacca aggctggtat tgtcagaacg ccggcagcac cgtgtactac    960
cctaacgaga aggactgcga gacaagaggc gaccacgtgt tctgtgatac cggcgtgga    1020
atcaatgtgg ccgagcagag caaagagtgc aacatcaaca tcagcaccac caactatccc    1080
tgcaaggtgt ccaccggcag gcaccctatt tctatgggtg ctctgtctcc tctgggagcc    1140
ctggtggctt gttataaggg cgtgtcctgt agcatcgga gcaacagagt gggcatcatc    1200
aagcagctga acaagggtg cagctacatc accaaccagg acgccgatac cgtgaccatc    1260
gacaacaccg tgtatcagct gagcaagggt gaaggcgaac agcacgtgat caagggcaga    1320
cctgtgtcca gcagcttcga cctatcaag ttcctgagg atcagttcca ggtggccctg    1380
gaccaggtgt tcgagaacat cgagaattcc caggctctgg tggaccagtc caacagaatc    1440
ctgtctagcg ccgagaaggg aaacaccggc ttcacatcgt tgatcaccct gatcgccgtg    1500
ctgggcagct ccatgatcct ggtgtccatc ttcacatta tcaagaagac caagaagccc    1560
accggcgctc ctccagaact gagcggagtg accaacaatg gcttcacccc tcacaac    1617
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<210> SEQ ID NO 120

<211> LENGTH: 1617

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 120

```
atgagctgga aggtggtcat catcttcagc ctgctgatca cacctcagca cggcctgaaa    60
```


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gagagctacc	tggaagagtc	ctgcagcacc	atcacagagg	gctacctgtc	tgtgctgaga	120
accggctggt	acaccaacgt	gttcacactg	gaagtgggcg	acgtcgagaa	tctgacatgc	180
tctgatggcc	ctagcctgat	caagaccgag	ctggatctga	ccaagagcgc	cctgagagaa	240
ctcaagaccg	tgtctgccga	tcagctggcc	agagaggaac	agatcgagaa	tcctggcagc	300
ggcagctttg	tgctgggagc	cattgctctt	ggagtggctg	ctgctgcagc	tgttacagca	360
ggcgtggcca	tcgctaagac	catcagactg	gaaagcgaag	tgaccgccat	caacaacgcc	420
ctgaagaaga	caaacgaggc	cgtcagcaca	ctcggcaatg	gcgttagagt	gctggccaca	480
gccgtgcgcg	agctgaagga	cttcgtgtcc	aagaacctga	cacgggccat	taacaagaac	540
aagtgcgaca	tccctgacct	gaagatggcc	gtgtccttta	gccagttcaa	ccggcggttt	600
ctgaacgtcg	tgccgcagtt	tagcgacaac	gccggaatca	caccagccat	cagcctggac	660
ctgatgacag	atgctgagct	ggctagagcc	gtgcctaaca	tgcctacatc	tgccggccag	720
atcaagctga	tgctcgagaa	tagagccatg	gtccgacgga	aaggcttcgg	cattctgatt	780
ggcgtgtacg	gcagcagcgt	gatctatatg	gtgcagctgc	ctatcttcgg	cgtgatcgac	840
acaccctgct	ggatttgtga	ggccgctcct	agctgtagcg	agaagaaggg	caattacgcc	900
tgcctgctga	gagaggacca	aggctggtat	tgtcagaacg	ccggcagcac	cgtgtactac	960
cctaacgaga	aggactgcga	gacaagaggc	gaccacgtgt	tctgtgatac	cgccgctgga	1020
atcaatgtgg	ccgagcagag	caaagagtgc	aacatcaaca	tcagcaccac	caactatccc	1080
tgcaaggtgt	ccaccggcag	gcaccctatt	tctatgggtg	ctctgtctcc	tctgggagcc	1140
ctggtggctt	gttataaggg	cgtgtcctgt	agcatcggca	gcaacagagt	gggcatcctc	1200
aagcagctga	acaagggctg	cagctacatc	accaaccagg	acgccgatac	cgtgaccatc	1260
gacaacaccg	tgtatcagct	gagcaagggtg	gaaggcgaac	agcacgtgat	caagggcaga	1320
cctgtgtcca	gcagcttcga	ccctatcaag	ttccctgagg	atcagttcca	ggtggccctg	1380
gaccaggtgt	tcgagaacat	cgagaattcc	caggctctgg	tggaccagtc	caacagaatc	1440
ctgtctagcg	ccgagaaggg	aaacaccggc	ttcatcatcg	tgatcctcct	gatcgccgtg	1500
ctgggcagct	ccatgatcct	ggtgtccatc	ttcatcatta	tcaagaagac	caagaagccc	1560
accggcgctc	ctccagaact	gagcggagtg	accaacaatg	gcttcacccc	tcacaac	1617

<210> SEQ ID NO 121

<211> LENGTH: 1617

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 121

atgagctgga	agggtgtcat	catcttcagc	ctgctgatca	cacctcagca	cggcctgaaa	60
gagagctacc	tggaagagtc	ctgcagcacc	atcacagagg	gctacctgtc	tgtgctgaga	120
accggctggt	acaccaacgt	gttcacactg	gaagtgggcg	acgtcgagaa	tctgacatgc	180
tctgatggcc	ctagcctgat	caagaccgag	ctggatctga	ccaagagcgc	cctgagagaa	240
ctcaagaccg	tgtctgccga	tcagctggcc	agagaggaac	agatcgagaa	tcctggcagc	300
ggcagctttg	tgctgggagc	cattgctctt	ggagtggctg	ctgctgcagc	tgttacagca	360
ggcgtggcca	tcgctaagac	catcagactg	gaaagcgaag	tgaccgccat	caacaacgcc	420

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ctgaagaaga caaacgaggg cgtcagcaca ctcggcaatg gcgttagagt gctggccaca	480
gccgtgcgcg agctgaagga cttcgtgtcc aagaacctga cacgggcat taacaagaac	540
aagtgcccta tcgacgacct gaagatggcc gtgtccttta gccagttcaa ccggcggttt	600
ctgaacgtcg tgcggcagtt tagcgacaac gccggaatca caccagccat cagcctggac	660
ctgatgacag atgctgagct ggctagagcc gtgcctaaca tgctacatc tgccggccag	720
atcaagctga tgctcgagaa tagagccatg gtccgacgga aaggcttcgg cattctgatt	780
ggcgtgtacg gcagcagcgt gatctatatg gtgcagctgc ctatcttcgg cgtgatcgac	840
acacctgct ggatttgtga gcccgctcct agctgtagcg agaagaagg caattacgcc	900
tgccctgctga gagaggacca aggctggat tgtcagaacg ccggcagcac cgtgtactac	960
cctaacgaga aggactgcga gacaagaggg gaccacgtgt tctgtgatac cgcgctgga	1020
atcaatgtgg ccgagcagag caaagagtgc aacatcaaca tcagcaccac caactatccc	1080
tgcaaggtgt ccaccggcag gcaccctatt tctatggagg ctctgtctcc tctgggagcc	1140
ctggtggctt gttataaggg cgtgtcctgt agcatcgcca gcaacagagt gggcatcatc	1200
aagcagctga acaagggctg cagctacatc accaaccagg acgcccatac cgtgaccatc	1260
gacaacaccg tgtatcagct gagcaagggt gaaggcgaac agcacgtgat caagggcaga	1320
cctgtgtcca gcagcttcga cctatcaag ttccctgagg atcagttcca ggtggccctg	1380
gaccaggtgt tcgagaacat cgagaattcc caggctctgg tggaccagtc caacagaatc	1440
ctgtctagcg ccgagaaggg aaacaccggc ttcacatcgc tgatcaccct gatcgccgtg	1500
ctgggcagct ccatgatcct ggtgtccatc ttcacatta tcaagaagac caagaagccc	1560
accggcgctc ctccagaact gagcggagt accaacaatg gcttcacccc tcacaac	1617

<210> SEQ ID NO 122

<211> LENGTH: 1617

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 122

atgagctgga aggtggatcat catcttcagc ctgctgatca cacctcagca cggcctgaaa	60
gagagctacc tggaagagtc ctgcagcacc atcacagagg gctacctgtc tgtgctgaga	120
accggctggg acaccaacgt gttcacactg gaagtgggcy acgtcgagaa tctgacatgc	180
tctgatggcc ctagcctgat caagaccgag ctggatctga ccaagagcgc cctgagagaa	240
ctcaagaccg tgtctgccga tcagctggcc agagaggaac agatcgagaa tcttgccagc	300
ggcagctttg tgctgggagc cattgtctct ggagtggctg ctgctgcagc tgttacagca	360
ggcgtggcca tcgctaagac catcagactg cctagcgaag tgaccgccat caacaacgcc	420
ctgaagaaga caaacgaggg cgtcagcaca ctcggcaatg gcgttagagt gctggccaca	480
gccgtgcgcg agctgaagga cttcgtgtcc aagaacctga cacgggcat taacaagaac	540
aagtgcgaca tcgacgacct gaagatggcc gtgtccttta gccagttcaa ccggcggttt	600
ctgaacgtcg tgcggcagtt tagcgacaac gccggaatca caccagccat cagcctggac	660
ctgatgacag atgctgagct ggctagagcc gtgcctaaca tgctacatc tgccggccag	720
atcaagctga tgctcgagaa tagagccatg gtccgacgga aaggcttcgg cattctgatt	780

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ggcgtgtacg gcagcagcgt gatctatatg gtgcagctgc ctatcttcgg cgtgatcgac	840
acacctgct ggatttgtgaa ggccgctcct agctgtagcg agaagaagg caattacgcc	900
tgcctgtga gagaggacca aggctgggtat tgtcagaacg ccggcagcac cgtgtactac	960
cctaacgaga aggactgcga gacaagaggc gaccacgtgt tctgtgatac cgcgctgga	1020
atcaatgtgg ccgagcagag caaagagtgc aacatcaaca tcagcaccac caactatccc	1080
tgcaaggtgt ccaccggcag gcaccctatt tctatgggtg ctctgtctcc tctgggagcc	1140
ctgggtgctt gttataaggc cgtgtcctgt agcatcgga gcaacagagt gggcatcatc	1200
aagcagctga acaagggctg cagctacatc accaaccagg acgcccagac cgtgaccatc	1260
gacaacaccg tgtatcagct gagcaagggt gaaggcgaac agcacgtgat caagggcaga	1320
cctgtgtcca gcagcttcga cctatcaag ttccctgagg atcagttcca ggtggccctg	1380
gaccaggtgt tcgagaacat cgagaattcc caggctctgg tggaccagtc caacagaatc	1440
ctgtctagcg ccgagaaggg aaacaccggc ttcacatcgc tgatcatcct gatcgccgtg	1500
ctgggcagct ccattgatcct ggtgtccatc ttcacatta tcaagaagac caagaagccc	1560
accggcgctc ctccagaact gagcggagt accaacaatg gcttcacccc tcacaac	1617

<210> SEQ ID NO 123

<211> LENGTH: 1617

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 123

atgagctgga aggtggctcat catcttcagc ctgctgatca cacctcagca cggcctgaaa	60
gagagctacc tggaagagtc ctgcagcacc atcacagagg gctacctgtc tgtgctgaga	120
accggctggt acaccaacgt gttcacactg gaagtgggcy acgtcgagaa tctgacatgc	180
tctgatggcc ctagcctgat caagaccgag ctggatctga ccaagagcgc cctgagagaa	240
ctcaagaccg tgtctgccga tcagctggcc agagaggaa agatcgagaa tcttggcagc	300
ggcagctttg tgtggggagc cattgtctct ggagtggctg ctgctgcagc tgttacagca	360
ggcgtggcca tcgctaagac catcagactg gaaagcgaag tgaccgccat caacaacgcc	420
ctgaagaaga caaacgaggc cgtcagcaca ctccgcaatg gcgttagagt gctggccaca	480
gccgtgcgcy agctgaagga ctctgtgtcc aagaacctga caccggccat taacaagaac	540
aagtgcgaca tcgacgacct gaagatggcc gtgtccttta gccagttcaa ccggcggttt	600
ctgaacgtcg tgcggcagtt tagcgacaac gccggaatca caccagccat cagcctggac	660
ctgatgacag atgctgagct ggctagagcc gtgcctaaca tgccatcatc tgccggccag	720
atcaagctga tgctcgagaa tagagccatg gtccgacgga aaggcttcgg cattctgatt	780
ggcgtgtacg gcagcagcgt gatctatatg gtgcagctgc ctatcttcgg cgtgatcgac	840
acacctgct ggatttgtgaa ggccgctcct agctgtagcg agaagaagg caattacgcc	900
tgcctgtga gagaggacca aggctgggtat tgtcagaacg ccggcagcac cgtgtactac	960
cctaacgaga aggactgcga gacaagaggc gaccacgtgt tctgtgatac cgcgctgga	1020
atcaatgtgg ccgagcagag caaagagtgc aacatcaaca tcagcaccac caactatccc	1080
tgcaaggtgt ccaccggcag gcaccctatt tctatgggtg ctctgtctcc tctgggagcc	1140

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ctggtggctt gttataaggg cgtgtcctgt agcatcggca gcaacagagt gggcatcatc	1200
aagcagctga acaagggctg cagctacatc accaaccagg acgccgatac cgtgaccatc	1260
gacaacaccg tgtatcagct gagcaagggtg gaaggcgaac agcacgtgat caagggcaga	1320
cctgtgtcca gcagcttccc acctatcaag ttccctgagg atcagttcca ggtggccctg	1380
gaccagggtg tcgagaacat cgagaattcc caggctctgg tggaccagtc caacagaatc	1440
ctgtctagcg ccgagaaggg aaacaccggc ttcatcatcg tgatcatcct gatcgccgtg	1500
ctgggcagct ccatgatcct ggtgtccatc ttcattcatta tcaagaagac caagaagccc	1560
accggcgctc ctccagaact gagcggagtg accaacaatg gcttcatccc tcacaac	1617

<210> SEQ ID NO 124

<211> LENGTH: 1617

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 124

atgagctgga aggtggctcat catcttcagc ctgctgatca cacctcagca cggcctgaaa	60
gagagctacc tggaagagtc ctgcagcacc atcacagagg gctacctgtc tgtgctgaga	120
accggctggt acaccaacgt gttcacactg gaagtgggag acgtcgagaa tctgacatgc	180
tctgatggcc ctagcctgat caagaccgag ctggatctga ccaagagcgc cctgagagaa	240
ctcaagaccg tgtctgccga tcagctggcc agagaggaa agatcgagaa tcctggcagc	300
ggcagctttg tgctgggagc cattgtcttt ggagtggctg ctgctgcagc tgttacagca	360
ggcgtggcca tcgctaagac catcagactg gaaagcgaag tgaccgccat caacaacgcc	420
ctgaagaaga caaacgaggg cgtcagcaca ctccgcaatg gcgttagagt gctggccaca	480
gccgtgcgag agctgaagga ctctgtgtcc aagaacctga caccggccat taacaagaac	540
aagtgcgaca tcgacgacct gaagatggcc gtgtccttta gccagttcaa ccggcggttt	600
ctgaacgtcg tgcggcagtt tagcgacaac gccggaatca caccagccat cagcctggac	660
ctgatgacag atgtgtagct ggctagagcc gtgcctaaca tgctacatc tgcggccag	720
atcaagctga tgctcgagaa tagagccatg gtccgacgga aaggcttcgg cattctgatt	780
ggcgtgtacg gcagcagcgt gatctatatg gtgcagctgc ctatcttcgg cgtgatcgac	840
acacctgtct ggattgtgaa ggccgctcct agctgtagcg agaagaaggg caattacgcc	900
tgccctgtga gagaggacca aggtgggtat gtgcagaacg ccggcagcac cgtgtactac	960
cctaacgaga aggactgcga gacaagaggc gaccacgtgt tctgtgatac cgcgctgga	1020
atcaatgtgg ccgagcagag caaagagtgc aacatcaaca tcagcaccac caactatccc	1080
tgcaagggtg ccaccggcag gcacctatt tctatgggtg ctctgtctcc tctgggagcc	1140
ctggtggctt gttataaggg cgtgtcctgt agcatcggca gcaacagagt gggcatcatc	1200
aagcagctga acaagggctg cagctacatc accaaccagg acgccgatac cgtgaccatc	1260
gacaacaccg tgtatcagct gagcaagggtg gaaggcgaac agcacgtgat caagggcaga	1320
cctgtgtcca gcagcttcca cctatcaag ttccctgaga accagttcca ggtggccctg	1380
gaccagggtg tcgagaacat cgagaattcc caggctctgg tggaccagtc caacagaatc	1440
ctgtctagcg ccgagaaggg aaacaccggc ttcattcatc tgatcatcct gatcgccgtg	1500

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ctgggcagct ccatgatcct ggtgtccatc ttcattatta tcaagaagac caagaagccc 1560

accggcgctc ctccagaact gagcggagt accaacaatg gcttcattcc tcacaac 1617

<210> SEQ ID NO 125

<211> LENGTH: 1617

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 125

atgagctgga aggtggtcat catcttcagc ctgctgatca cacctcagca cggcctgaaa 60

gagagctacc tggaagagtc ctgcagcacc atcacagagg gctacctgtc tgtgctgaga 120

accggctggt acaccaacgt gttcacactg gaagtgggag acgtcgagaa tctgacatgc 180

tctgatggcc ctacgctgat caagaccgag ctggatctga ccaagagcgc cctgagagaa 240

ctcaagaccg tgtctgcca tcagctggcc agagaggaac agatcgagaa tcctggcagc 300

ggcagctttg tgctgggagc cattgtctct ggagtggctg ctgctgcagc tgttacagca 360

ggcgtggcca tcgctaagac catcagactg gaaagcgaag tgaccgccat caacaacgcc 420

ctgaagaaga caaacgaggc cgtcagcaca ctccgcaatg gcgttagagt gctggccaca 480

gccgtgcgag agctgaagga ctctgtgtcc aagaacctga caccggccat taacaagaac 540

aagtgcgaca tcgacgacct gaagatggcc gtgtccttta gccagttcaa ccggcggttt 600

ctgaacgtcg tgccgcagtt tagcgacaac gccggaatca caccagccat cagcctggac 660

ctgatgacag atgctgagct ggctagagcc gtgcctaaca tgctacatc tgccggccag 720

atcaagctga tgctcgagaa tagagccatg gtccgacgga aaggtctcgg cattctgatt 780

ggcgtgtacg gcagcagcgt gatctatatg gtgcagctgc ctatcttcgg cgtgatcgac 840

acacctgctt ggattgtgaa ggccgctcct agctgtagcg agaagaagg caattacgcc 900

tgctctgctg gagaggacca aggtgggtat tgtcagaacg ccggcagcac cgtgtactac 960

cctaacgaga aggactcgca gacaagaggc gaccacgtgt tctgtgatac cgcgctgga 1020

atcaatgtgg ccgagcagag caaagagtgc aacatcaaca tcagcaccac caactatccc 1080

tgcaaggtgt ccaccggcag gcacctatt tctatggtgg ctctgtctcc tctgggagcc 1140

ctggtggctt gttataaggg cgtgtcctgt agcatcgca gcaacagagt gggcatcatc 1200

aagcagctga acaagggctg cagctacatc accaaccagg acgcccatac cgtgaccatc 1260

gacaacaccg tgtatcagct gagcaagggt gaaggcgaac agcacgtgat caagggcaga 1320

cctgtgtcca gcagcttcga cctatcaag ttccctcagg atcagttcca ggtggccctg 1380

gaccaggtgt tcgagaacat cgagaattcc caggctctgg tggaccagtc caacagaatc 1440

ctgtctagcg ccgagaaggg aaacaccggc ttcattatcg tgatcattct gatcgccgtg 1500

ctgggcagct ccatgatcct ggtgtccatc ttcattatta tcaagaagac caagaagccc 1560

accggcgctc ctccagaact gagcggagt accaacaatg gcttcattcc tcacaac 1617

<210> SEQ ID NO 126

<211> LENGTH: 1617

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 126

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atgagctgga aggtggteat catcttcagc ctgctgatca cacctcagca cggectgaaa    60
gagagctacc tggaagagtc ctgcagcacc atcacagagg gctacctgtc tgtgctgaga    120
accggctggt acaccaacgt gttcacactg gaagtgggag acgtcgagaa tctgacatgc    180
tctgatggcc ctagcctgat caagaccgag ctggatctga ccaagagcgc cctgagagaa    240
ctcaagaccg tgtctgccga tcagctggcc agagaggaac agatcgagaa tcctggcagc    300
ggcagctttg tgctgggagc cattgtcttt ggagtggctg ctgctgcagc tgttacagca    360
ggcgtggcca tcgctaagac catcagactg gaaagcgaag tgaccgccat caacaacgcc    420
ctgaagaaga caaacgaggg cgctcagaca ctccgcaatg gcgttagagt gctggccaca    480
gccgtgcgag agctgaagga ctctgtgtcc aagaacctga caccggccat taacaagaac    540
aagtgcgaca tcgacgacct gaagatggcc gtgtccttta gccagtggaa ccggcggttt    600
ctgaacgtcg tgccgcagtt tagcgacaac gccggaatca caccagccat cagcctggac    660
ctgatgacag atgctgagct ggctagagcc gtgcctaaca tgctacatc tgccggccag    720
atcaagctga tgctcgagaa tagagccatg gtccgacgga aaggtctcgg cattctgatt    780
ggcgtgtacg gcagcagcgt gatctatatg gtgcagctgc ctatcttcgg cgtgatcgac    840
acacctgctt ggattgtgaa ggccgctcct agctgtagcg agaagaaggg caattacgcc    900
tgctctgctg gagaggacca aggtctggtat tgtcagaacg ccggcagcac cgtgtactac    960
cctaacgaga aggactgcga gacaagaggc gaccacgtgt tctgtgatac cgccgctgga   1020
atcaatgtgg ccgagcagag caaagagtgc aacatcaaca tcagaccac caactatccc   1080
tgcaaggtgt ccaccggcag gcacctatt tctatggtgg ctctgtctcc tctgggagcc   1140
ctggtggctt gttataaggg cgtgtcctgt agcatcgcca gcaacagagt gggcatcatc   1200
aagcagctga acaagggctg cagctacatc accaaccagg acgcccatac cgtgaccatc   1260
gacaacaccg tgtatcagct gagcaagggt gaaggcgaac agcacgtgat caagggcaga   1320
cctgtgtcca gcagcttcga cctatcaag ttccctgagg atcagttcca ggtggccctg   1380
gaccaggtgt tcgagaacat cgagaattcc caggctctgg tggaccagtc caacagaatc   1440
ctgtctagcg ccgagaaggg aaacaccggc ttcacatcgc tgatcatcct gatcgccgtg   1500
ctgggcagct ccatgatcct ggtgtccatc ttcacatta tcaagaagac caagaagccc   1560
accggcgctc ctccagaact gagcggagtg accaacaatg gcttcacccc tcacaac    1617

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<210> SEQ ID NO 127

<211> LENGTH: 1617

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 127

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augagcugga agguugucau caucuucagc cugcugauca caccucagca cgccugaaa    60
gagagcuacc uggaagaguc cugcagcacc aacacagagg gcuaccuguc ugugcugaga    120
accggcuggu acaccaacgu guucacacug gaagugggag acgucgagaa ucugacaugc    180
ucugauggcc cuagccugau caagaccgag cuggaucuga ccaagagcgc ccugagagaa    240
cucaagaccg ugucugccga ucagcuggcc agagaggaac agaucgagaa uccuggcagc    300

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ggcagcuuug	ugcugggagc	cauugcucu	ggaguggcug	cugcugcagc	uguuacagca	360
ggcguggcca	ucugcaagac	caucagacug	gaaagcgaag	ugaccgccau	caacaacgcc	420
cugaagaaga	caaacgaggc	cgucagcaca	cucggcaaug	gcguuagagu	gcuggccuuu	480
gccgugcgcg	agcugaagga	cuucgugucc	aagaaccuga	cacgggcccu	gaacaagaac	540
aagugcgaca	ucgacgaccu	gaagauggcc	guguccuuu	gccaguucua	ccggcgguuu	600
cugaacgucg	ugcggcaguu	uagcgacaac	gccggaauca	caccagccau	cagccuggac	660
cugaugacag	augcugagcu	ggcuagagcc	gugccuaaca	ugccuacauc	ugccggccag	720
aucaagcuga	ugcucgagaa	uagagccaug	guccgacgga	aaggcuucgg	cauucugugu	780
ggcguguaag	gcagcagcgu	gaucuauaug	gugcagcugc	cuauucucgg	cgugaucgac	840
acaccucgcu	ggauugugaa	ggccgcuccu	agcuguagcg	agaagaaggg	caauuacgcc	900
ugccugcuga	gagaggacca	aggcugguau	ugucagaacg	ccggcagcac	cguguacuac	960
ccuaacgaga	aggacugcga	gacaagaggc	gaccacgugu	ucugugauac	cgccgcugga	1020
aucaaugugg	ccgagcagag	caaagagugc	aacaucuaaca	ucagcaccac	caacuauccc	1080
ugcaaggugu	ccaccggcag	gcaccuauu	ucuauuggug	cucugucucc	ucugggagcc	1140
cuggguggcu	guuauaagg	cguguccugu	agcaucggca	gcaacagagu	gggcaucauc	1200
aagcagcuga	acaaggcgug	cagcuacauc	accaaccagg	acgccgauac	cgugaccauc	1260
gacaacaccg	uguaucagcu	gagcaaggug	gaaggcgaac	agcagugau	caagggcaga	1320
ccugugucca	gcagcuucga	cccuaucaag	uucccugagg	aucaguucua	cguggcccug	1380
gaccaggugu	ucgagaacau	cgagaauucc	caggcucugg	uggaccaguc	caacagaau	1440
cugucuagcg	ccgagaagg	aaacaccggc	uucaucaucg	ugaucuccu	gaucgcccug	1500
cugggcagcu	ccaugauccu	gguguccauc	uucaucuuu	ucaagaagac	caagaagccc	1560
accggcguc	cuccagaacu	gagcggagug	accaacaau	gcuucaucc	ucacaac	1617

<210> SEQ ID NO 128

<211> LENGTH: 1617

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 128

augagcugga	agguggucau	caucuucagc	cugcugauca	caccucagca	cgccugaaa	60
gagagcuacc	uggaagaguc	cugcagcacc	aucacagagg	gcuaccuguc	ugugcugaga	120
accggcuggu	acaccaacgu	guucacacug	gaaguggcg	acgucgagaa	ucugacaugc	180
ucugauggcc	cuagccugau	caagaccgag	cuggaucuga	ccaagagcgc	ccugagagaa	240
cucaagaccg	ugucugccga	ucagcuggcc	agagaggaa	agaucgagaa	uccuggcagc	300
ggcagcuuug	ugcugggagc	cauugcucu	ggaguggcug	cugcugcagc	uguuacagca	360
ggcguggcca	ucugcaagac	caucagacug	gaaagcgaag	ugaccgccau	caacaacgcc	420
cugaagaaga	caaacgaggc	cgucagcaca	cucggcaaug	gcguuagagu	gcuggccaca	480
gccgugcgcg	agcugaagga	cuucgugucc	aagaaccuga	cacgggccau	uaacaagaac	540
aagugcgaca	ucgacgaccu	gaagauggcc	guguccuuu	gccaguucua	ccggcgguuu	600
cugaacgucg	ugcggcaguu	uagcgacaac	gccggaauca	caccagccau	cagccuggac	660

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cugaugacag augcugagcu ggcuagagcc gugccuaaca ugccuacauc ugccggccag	720
aucaagcuga ugcucgagaa uagagccaug guccgacgga aaggcuucgg cauucugugu	780
ggcguguacg gcagcagcgu gaucuaauaug gugcagcugc cuaucuucgg cgugaucgac	840
acaccucgcu ggauugugaa ggccgcuccu agcuguagcg agaagaaggg caauuacgcc	900
ugccugcuga gagaggacca aggcugguau ugucagaacg ccggcagcac cguguacuac	960
ccuaacgaga aggacugcga gacaagaggc gaccacgugu ucugugauac cgccgcugga	1020
aucaaugugg ccgagcagag caaagagugc aacaucacaa ucagcaccac caacuauccc	1080
ugcaaggugu ccaccggcag gcaccuauu ucuauggugg cucugucucc ucugggagcc	1140
cugguggcuu guuauaaggg cguguccugu agcaucggca gcaacagagu gggcaucauc	1200
aagcagcuga acaaggcgug cagcuacauc accaaccagg acgcccgauc cgugaccauc	1260
gacaacaccg uguaucagcu gagcaaggug gaaggcgaac agcacgugau caagggcaga	1320
ccugugucca gcagcuucga ccuaucaag ucccugagc accaguggca uguggcccug	1380
gaccaggugu ucgagaacau cgagaauucc caggcucugg uggaccaguc caacagaau	1440
cugucuagcg ccgagaaggg aaacaccggc uucaucaucg ugaucuccu gaucgcccug	1500
cugggcagcu ccaugauccu gguguccauc uucaucauu ucaagaagac caagaagccc	1560
accggcguc cuccagaacu gagcggagug accaacaau gcuucauucc ucacaac	1617

<210> SEQ ID NO 129

<211> LENGTH: 1617

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 129

augagcugga agguggucau caucuacgc cugcugauca caccucagca cggccugaaa	60
gagagcuacc uggaagaguc cugcagcacc aucacagagg gcuaccuguc ugugcugaga	120
accggcuggu acaccaacgu guucacacug gaagugggcg acgucgagaa ucugacaugc	180
ucugauggcc cuagccugau caagaccgag cuggaucugc ucaagagcgc ccugagagaa	240
cucaagaccg ugucugccga ucagcuggcc agagaggaac agaucgagaa uccuggcagc	300
ggcagcuuug ugcugggagc cauugcucu ggaguggcug cugcugcagc uguuacagca	360
ggcguggcca ugcuaagac caucagacug gaaagcgaag ugaccgccau caacaacgcc	420
cugaagaaga caaacgaggc cgucagcaca cucggcaaug gcuuagagu gcuggccaca	480
gccgugcgcg agcugaagga cuucgugucc aagaaccuga cacgggccau uaacaagaac	540
aagugcgaca ucccugaccu gaagauggcc guguccuuu gccaguuaa ccggcgguuu	600
cugaacgucg ugcggcaguu uagcgacaac gccggaauca caccagccau cagccuggac	660
cugaugacag augcugagcu ggcuagagcc gugccuaaca ugccuacauc ugccggccag	720
aucaagcuga ugcucgagaa uagagccaug guccgacgga aaggcuucgg cauucugauu	780
ggcguguacg gcagcagcgu gaucuaauaug gugcagcugc cuaucuucgg cgugaucgac	840
acaccucgcu ggauugugaa ggccgcuccu agcuguagcg agaagaaggg caauuacgcc	900
ugccugcuga gagaggacca aggcugguau ugucagaacg ccggcagcac cguguacuac	960
ccuaacgaga aggacugcga gacaagaggc gaccacgugu ucugugauac cgccgcugga	1020

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aucaaugugg ccgagcagag caaagagugc aacaaucaaca ucagcaccac caacuauccc	1080
ugcaaggugu ccaccggcag gcaccuauu ucuauggugg cucugucucc ucugggagcc	1140
cugguggcuu guuaaaggcg cguguccugu agcaucggca gcaacagagu gggcaucauc	1200
aagcagcuga acaaggcgug cagcuacauc accaaccagg acgcccgauc cgugaccauc	1260
gacaacaccg uguauacagcu gagcaaggug gaaggcgaac agcacgugau caagggcaga	1320
ccugugucca gcagcuucga ccuaucaag uucccugagg aucaguucca gguggcccug	1380
gaccaggugu ucgagaacau cgagaauucc caggcucugg uggaccaguc caacagaau	1440
cugucuagcg ccgagaaggg aaacaccggc uucaucaucg ugaucuccu gaucgcccug	1500
cugggcagcu ccaugauccu gguguccauc uucaucauu ucaagaagac caagaagccc	1560
accgggcguc cuccagaacu gagcggagug accaacaau gcuucaucc ucacaac	1617

<210> SEQ ID NO 130

<211> LENGTH: 1617

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 130

augagcugga agguggucau caucuucagc cugcugauca caccucagca cggccugaaa	60
gagagcuacc uggaagaguc cugcagcacc aucacagagg gcuaccuguc ugugcugaga	120
accggcuggu acaccaacgu guucacacug gaagugggcg acgucgagaa ucugacaugc	180
ucugauggcc cuagccugau caagaccgag cuggaucugc ucaagagcgc ccugagagaa	240
cucaagaccg ugucugccga ucagcuggcc agagaggaac agaucgagaa uccuggcagc	300
ggcagcuuug ugcugggagc cauugcucu ggaguggcug cugcugcagc uguuacagca	360
ggcguggcca ucgcuagac caucagacug gaaagcgaag ugaccgccau caacaacgcc	420
cugaagaaga caaacgaggc cgucagcaca cucggcaaug gcuuagagu gcuggccaca	480
gccgugcgcg agcugaagga cuucgugucc aagaaccuga cacgggccau uaacaagaac	540
aagugcgaca ucccugaccu gaagauggcc guguccuuu gccaguuaa ccggcgguuu	600
cugaacgucg ugcggcaguu uagcgacaac gccggaauca caccagccau cagccuggac	660
cugaugacag augcugagcu ggcuaagacc gugccuaca ugccuacuc ugccggccag	720
aucaagcuga ugcucgagaa uagagccaug guccgacgga aaggcuucgg cauucugauu	780
ggcguguacg gcagcagcgu gaucuauaug gugcagcugc cuaucuucgg cgugaucgac	840
acaccucgcu ggaauugaa ggcgcuccu agcuguagcg agaagaaggg caauuacgcc	900
ugccugcuga gagaggacca aggcugguau ugucagaacg ccggcagcac cguguacuac	960
ccuaacgaga aggacugcga gacaagaggc gaccacgugu ucugugauac cgccgcugga	1020
aucaaugugg ccgagcagag caaagagugc aacaaucaaca ucagcaccac caacuauccc	1080
ugcaaggugu ccaccggcag gcaccuauu ucuauggugg cucugucucc ucugggagcc	1140
cugguggcuu guuaaaggcg cguguccugu agcaucggca gcaacagagu gggcaucauc	1200
aagcagcuga acaaggcgug cagcuacauc accaaccagg acgcccgauc cgugaccauc	1260
gacaacaccg uguauacagcu gagcaaggug gaaggcgaac agcacgugau caagggcaga	1320
ccugugucca gcagcuucga ccuaucaag uucccugaga accaguucca gguggcccug	1380

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gaccaggugu ucgagaacau cgagaauucc caggcucugg	uggaccaguc caacagaau	1440
cugucuagcg ccgagaaggg aaacaccggc uucaucaucg	ugaucuccu gaucgccgug	1500
cugggcagcu ccaugauccu gguguccauc uucaucauu	ucaagaagac caagaagccc	1560
accggcguc cuccagaacu gagcggagug accaacaug	gcuuauccc ucacaac	1617

<210> SEQ ID NO 131
 <211> LENGTH: 1617
 <212> TYPE: RNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 131

augagcugga aggguguc auucuucagc cugcugauca caccucagca	cgccugaaa	60
gagagcuacc uggaagaguc cugcagcacc aucacagagg gcuaccuguc	ugugcugaga	120
accggcuggu acaccaacgu guucacacug gaagugggcg acgucgagaa	ucugacaugc	180
ucugauggcc cuagccugau caagaccgag cuggaucugc ucaagagcgc	ccugagagaa	240
cucaagaccg ugucugccga ucagcuggcc agagaggaa agaucagagaa	uccuggcagc	300
ggcagcuuug ugcugggagc cauugcucu ggaguggcug cugcugcagc	uguuacagca	360
ggcguggcca ucgcuagac caucagacug gaaagcgaag ugaccgccau	caacaacgcc	420
cugaagaaga caaacgaggc cgucagcaca cucggcaaug gcuuagagu	gcuggccaca	480
gccgugcgcg agcugaagga cuucgugcuu aagaaccuga caccggccau	uaacaagaac	540
aagugcgaca uccugaccu gaagauggcc guguccuuu gccagucaa	ccggcgguuu	600
cugaacgucg ugcggcaguu uagcgacaac gccggaauca caccagccau	cagccuggac	660
cugaugacag augcugagcu ggcuaagacc gugccuaaca ugccuacuc	ugccggccag	720
aucaagcuga ugcucgagaa uagagccaug guccgacgga aaggcuucgg	cauucugauu	780
ggcguguacg gcagcagcgu gaucuauaug gucgagcugc cuaucuucgg	cgugaucgac	840
acaccucgcu ggaauugaa ggccgcuccu agcuguagcg agaagaagg	cauuuacgcc	900
ugccugcuga gagaggacca aggcugguau ugucagaacg ccggcagcac	cguguacuac	960
ccuaacgaga aggacugcga gacaagaggc gaccacgugu ucugugauac	cgccgcugga	1020
aucaaugugg ccgagcagag caaagagugc aacaucaaca ucagcaccac	caacuauccc	1080
ugcaaggugu ccaccggcag gcaccuuuu ucuauaggug cucugucucc	ucugggagcc	1140
cuggugguuu guuaaaggcg cguguccugu agcaucggca gcaacagagu	gggcaucauc	1200
aagcagcuga acaaggcgug cagcuacauc accaaccagg acgccgauac	cgugaccauc	1260
gacaacaccg uguauacgu gagcaaggug gaaggcgaac agcacgugau	caagggcaga	1320
ccugugucca gcagcuucga ccuaucaag uucccugagg aucaguucca	gguggcccug	1380
gaccaggugu ucgagaacau cgagaauucc caggcucugg	uggaccaguc caacagaau	1440
cugucuagcg ccgagaaggg aaacaccggc uucaucaucg	ugaucuccu gaucgccgug	1500
cugggcagcu ccaugauccu gguguccauc uucaucauu	ucaagaagac caagaagccc	1560
accggcguc cuccagaacu gagcggagug accaacaug	gcuuauccc ucacaac	1617

<210> SEQ ID NO 132
 <211> LENGTH: 1617

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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 132

augagcugga aggguggucau caucuucagc cugcugauca caccucagca cggccugaaa      60
gagagcuacc uggaagaguc cugcagcacc aucacagagg gcuaccuguc ugugcugaga      120
accggcuggu acaccaacgu guucacacug gaagugggcg acgucgagaa ucugacaugc      180
ucugauggcc cuagccugau caagaccgag cuggaucugc ucaagagcgc ccugagagaa      240
cucaagaccg ugucugccga ucagcuggcc agagaggaac agaucgagaa uccuggcagc      300
ggcagcuuug ugcugggagc cauugcucu ggaguggcug cugcugcagc uguuacagca      360
ggcguggcca ucgcuagac caucagacug gaaagcgaag ugaccgccau caacaacgcc      420
cugaagaaga caaacgaggc cgucagcaca cucggcaaug gcguaagagu gcuggccaca      480
gccgugcgcg agcugaagga cuucgugcuu aagaaccuga cacgggccau uaacaagaac      540
aagugcgaca uccugaccu gaagauggcc guguccuuu gccaguuaa ccggcgguuu      600
cugaacgucg ugcggcaguu uagcgacaac gccggaauca caccagccau cagccuggac      660
cugaugacag augcugagcu ggcuaagacc gugccuaaca ugccuacauc ugccggccag      720
aucaagcuga ugcucgagaa uagagccaug guccgacgga aaggcuucgg cauucugauu      780
ggcguguacg gcagcagcgu gaucuauaug gugcagcugc cuaucuucgg cgugaucgac      840
acaccucgcu ggaauuguaa ggccgcuccu agcuguagcg agaagaaggg caauuacgcc      900
ugccugcuga gagaggacca aggcugguau ugucagaacg ccggcagcac cguguacuac      960
ccuaacgaga aggacugcga gacaagaggc gaccacgugu ucugugauac cgccgcugga      1020
aucaaugugg ccgagcagag caaagagugc aacaucacaa ucagcaccac caacuauccc      1080
ugcaaggugu ccaccggcag gcaaccuuu ucuauaggug cucugucucc ucuggggagcc      1140
cuggugggcu guuaaaaggg cguguccugu agcaucggca gcaacagagu gggcaucauc      1200
aagcagcuga acaaggcgug cagcuacauc accaaccagg acgccgauac cgugaccauc      1260
gacaacaccg uguauacgu gagcaaggug gaaggcgaac agcacgugau caagggcaga      1320
ccugugucca gcagcuucga ccuaucaag uucccugaga accaguucca gguggcccug      1380
gaccaggugu ucgagaacau cgagaauucc caggcucugg uggaccaguc caacagaaucc      1440
cugucuagcg ccgagaaggg aaacaccggc uucaucaucg ugaucauccu gaucgccgug      1500
cugggcagcu ccaugauccu gguguccauc uucaucauuu ucaagaagac caagaagccc      1560
accggcguc cuccagaacu gagcggagug accaacaauug gcuucauccc ucacaac      1617

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<210> SEQ ID NO 133
<211> LENGTH: 1617
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 133

augagcugga aggguggucau caucuucagc cugcugauca caccucagca cggccugaaa      60
gagagcuacc uggaagaguc cugcagcacc aucacagagg gcuaccuguc ugugcugaga      120
accggcuggu acaccaacgu guucacacug ccugugggcg acgucgagaa ucugacaugc      180

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ucugauggcc cuagccugau caagaccgag cuggaucugc ucaagagcgc ccugagagaa	240
cucaagaccg ugucugccga ucagcuggcc agagaggaac agaucgagaa uccuggcagc	300
ggcagcuuug ugcugggagc cauugcucu ggaguggcug cugcugcagc uguuacagca	360
ggcguggcca ugcuaagac caucagacug gaaagcgaag ugaccgccau caacaacgcc	420
cugaagaaga caaacgaggc cgucagcaca cucggcaaug gcguaagagu gcuggccaca	480
gccgugcgcg agcugaagga cuucgugucc aagaaccuga cacgggccau uaacaagaac	540
aagugcgaca ucgacgaccu gaagauggcc guguccuuu gccagucaa cggcgguuu	600
cugaacgucg ugcggcaguu uagcgacaac gccggaauca caccagccau cagccuggac	660
cugaugacag augcugagcu ggcuaagacc gugccuaaca ugccuacauc ugccggccag	720
aucaagcuga ugcucgagaa uagagccaug guccgacgga aaggcuucgg cauucugauu	780
ggcguguacg gcagcagcgu gaucuauaug gugcagcugc cuaucuucgg cgugaucgac	840
acaccucgcu ggauugugaa ggccgcuccu agcuguagcg agaagaaggg caauuacgcc	900
ugccugcuga gagaggacca aggcugguau ugucagaacg ccggcagcac cguguacuac	960
ccuaacgaga aggacugcga gacaagaggc gaccacgugu ucugugauac cgccgcugga	1020
aucaaugugg ccgagcagag caaagagugc aacaucaaca ucagcaccac caacuauccc	1080
ugcaaggugu ccaccggcag gcaccuauu ucuauggugg cucugucucc ucugggagcc	1140
cugguggguu guuaaaggg cguguccugu agcaucggca gcaacagagu gggcauac	1200
aagcagcuga acaaggcgug cagcuacauc accaaccagg acgccgauac cgugaccauc	1260
gacaacaccg uguauacgu gagcaaggug gaaggcgaac agcacgugau caagggcaga	1320
ccugugucca gcagcuucga ccuaucaag uucccugagg aucaguucca gguggccug	1380
gaccaggugu ucgagaacau cgagaauucc caggcucugg uggaaccaguc caacagaau	1440
cugucuagcg ccgagaaggg aaacaccggc uucaucaucg ugaucauccu gaucgccgug	1500
cugggcagcu ccaugauccu gguguccauc uucaucauu ucaagaagac caagaagccc	1560
accggcguc cuccagaacu gagcggagug accaacaau gcuucaucc ucacaac	1617

<210> SEQ ID NO 134

<211> LENGTH: 1617

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 134

augagcugga agguggucau caucuacgc cugcugauca caccucagca cggccugaaa	60
gagagcuacc uggaagaguc cugcagcacc aucacagagg gcuaccuguc ugugcugaga	120
accggcuggu acaccaacgu guucacacug ccugugggag acgucgagaa ucugacaugc	180
ucugauggcc cuagccugau caagaccgag cuggaucugc ucaagagcgc ccugagagaa	240
cucaagaccg ugucugccga ucagcuggcc agagaggaac agaucgagaa uccuggcagc	300
ggcagcuuug ugcugggagc cauugcucu ggaguggcug cugcugcagc uguuacagca	360
ggcguggcca ugcuaagac caucagacug gaaagcgaag ugaccgccau caacaacgcc	420
cugaagaaga caaacgaggc cgucagcaca cucggcaaug gcguaagagu gcuggccaca	480
gccgugcgcg agcugaagga cuucgugucc aagaaccuga cacgggccau uaacaagaac	540

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aagugcgaca	ucgacgaccu	gaagauggcc	guguccuuua	gccaguucua	ccggcgguuu	600
cugaacgucg	ugcggcaguu	uagcgacaac	gccggaauca	caccagccau	cagccuggac	660
cugaugacag	augcugagcu	ggcuagagcc	gugccuaaca	ugccuacauc	ugccggccag	720
aucaagcuga	ugcucgagaa	uagagccaug	guccgacgga	aaggcuucgg	cauucugauu	780
ggcguguacg	gcagcagcgu	gaucuauaug	gugcagcugc	cuauucucgg	cgugaucgac	840
acaccugcu	ggauugugaa	ggccgcuccu	agcuguagcg	agaagaagg	caauuacgcc	900
ugccugcuga	gagaggacca	aggcugguau	ugucagaacg	ccggcagcac	cguguacuac	960
ccuaacgaga	aggacugcga	gacaagaggc	gaccacgugu	ucugugauac	cgccgcugga	1020
aucaaugugg	ccgagcagag	caaagagugc	aacaucaaca	ucagcaccac	caacuauccc	1080
ugcaaggugu	ccaccggcag	gcaccuauu	ucuauggugg	cucugucucc	ucugggagcc	1140
cugguggguu	guuuaagg	cguguccugu	agcaucggca	gcaacagagu	gggcauac	1200
aagcagcuga	acaagggcug	cagcuacauc	accaaccagg	acgccgauac	cgugaccauc	1260
gacaacaccg	uguauacgu	gagcaaggug	gaaggcgaa	agcacgugau	caagggcaga	1320
ccugugucca	gcagcuucga	cccuaucag	uucccugaga	accaguucca	gguggcccug	1380
gaccaggugu	ucgagaacau	cgagaauucc	caggcucugg	uggaccaguc	caacagaau	1440
cugucuagcg	ccgagaagg	aaacaccggc	uucaucaucg	ugaucauccu	gaucgccgug	1500
cugggcagcu	ccaugauccu	gguguccauc	uucaucauu	ucaagaagac	caagaagccc	1560
accggcguc	cuccagaacu	gagcggagug	accaacaau	gcucauucc	ucacaac	1617

<210> SEQ ID NO 135

<211> LENGTH: 1617

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 135

augagcugga	aggugguac	caucuucagc	cugcugauca	caccucagca	cgccugaaa	60
gagagcuacc	uggaagaguc	cugcagcacc	aucacagagg	gcuaccuguc	ugugcugaga	120
accggcuggu	acaccaacgu	guucacacug	gaaguggg	acgucgagaa	ucugacaugc	180
ucugauggcc	cuagccgau	caagaccgag	cuggaucugc	ucaagagcgc	ccugagagaa	240
cucaagaccg	ugucugccga	ucagcuggcc	agagagggaac	agaucgagaa	uccuggcagc	300
ggcagcuuug	ugcugggagc	cauugcucu	ggaguggcug	cugcugcagc	uguuacagca	360
ggcguggcca	ucgcuaagac	caucagacug	gaaagcgaag	ugaccgccau	caacaacgcc	420
cugaagaaga	caaacgaggc	cgucagcaca	cucggcaaug	gcuuagagu	gcuggccaca	480
gccgugcgcg	agcugaagga	cuucgugucc	aagaaccuga	cacgggccau	uaacaagaac	540
aagugcgaca	ucgacgaccu	gaagauggcc	guguccuuua	gccaguucua	ccggcgguuu	600
cugaacgucg	ugcggcaguu	uagcgacaac	gccggaauca	caccagccau	cagccuggac	660
cugaugacag	augcugagcu	ggcuagagcc	gugccuaaca	ugccuacauc	ugccggccag	720
aucaagcuga	ugcucgagaa	uagagccaug	guccgacgga	aaggcuucgg	cauucugauu	780
ggcguguacg	gcagcagcgu	gaucuauaug	gugcagcugc	cuauucucgg	cgugaucgac	840
acaccugcu	ggauugugaa	ggccgcuccu	agcuguagcg	agaagaagg	caauuacgcc	900

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ugccugcuga gagaggacca aggcugguau ugucagaacg cggcgagcac cguguacuac	960
ccuaacgaga aggacugcga gacaagaggc gaccacgugu ucugugauac cgccgcugga	1020
aucaaugugg ccgagcagag caaagagugc aacaucaaca ucagcaccac caacuauccc	1080
ugcaaggugu ccaccggcag gcacccuauu ucuauuggug cucugucucc ucugggagcc	1140
cuggugguuu guuauaaggg cguguccugu agcaucggca gcaacagagu gggcaucauc	1200
aagcagcuga acaagggcug cagcuacauc accaaccagg acgccgauac cgugaccauc	1260
gacaacaccg uguauacgu gagcaaggug gaaggcgaac agcacgugau caagggcaga	1320
ccugugucca gcagcuucga ccuaucaag uucccugagg aucaguucca gguggccug	1380
gaccaggugu ucgagaacau cgagaauucc caggcucugg uggaccaguc caacagaau	1440
cugucuagcg ccgagaaggg aaacaccggc uucaucaucg ugaucauccu gaucgccgug	1500
cugggcagcu ccaugauccu gguguccauc uucaucauu ucaagaagac caagaagccc	1560
accggcguc cuccagaacu gagcggagug accaacaau gcuucaucc ucacaac	1617

<210> SEQ ID NO 136

<211> LENGTH: 1617

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 136

augagcugga agguggucau caucuacgc cugcugauca caccucagca cggccugaaa	60
gagagcuacc uggaagaguc cugcagcacc aucacagagg gcuaccuguc ugugcugaga	120
accggcuggu acaccaacgu guucacacug gaagugggag accucgagaa ucugacaugc	180
ucugauggcc cuagccgau caagaccgag cuggaucuga ccaagagcgc ccugagagaa	240
cucaagaccg ugucugccga ucagcuggcc agagaggaac agaucgagaa uccuggcagc	300
ggcagcuuug ugcugggagc cauugcucu ggaguggcug cugcugcagc uguuacagca	360
ggcguggcca ugcuaagac caucagacug gaaagcgaag ugaccgccau caacaacgcc	420
cugaagaaga caaacgaggc cgucagcaca cugggcaaug gcguaagagu gcuggccaca	480
gccgugcgc agcugaagga cuucgugucc aagaaccuga cacgggccau uaacaagaac	540
aagugcgaca ugcagcaccu gaagauggcc guguccuuu gccaguuaa ccggcgguuu	600
cugaacgucg ugcggcaguu uagcgacaac gccggaauca caccagccau cagccuggac	660
cugaugacag augcugagcu ggcuaagacc gugccuaaca ugccuacau ucgcggccag	720
aucaagcuga ugcucgagaa uagagccaug guccgacgga aaggcuucgg cauucgauu	780
ggcguguacg gcagcagcgu gaucuauaug gucgagcugc cuaucuucgg cgugaucgac	840
acaccucgu ggauugugaa ggccgcuccu agcuguagcg agaagaaggg caauuacgcc	900
ugccugcuga gagaggacca aggcugguau ugucagaacg cggcgagcac cguguacuac	960
ccuaacgaga aggacugcga gacaagaggc gaccacgugu ucugugauac cgccgcugga	1020
aucaaugugg ccgagcagag caaagagugc aacaucaaca ucagcaccac caacuauccc	1080
ugcaaggugu ccaccggcag gcacccuauu ucuauuggug cucugucucc ucugggagcc	1140
cuggugguuu guuauaaggg cguguccugu agcaucggca gcaacagagu gggcaucauc	1200
aagcagcuga acaagggcug cagcuacauc accaaccagg acgccgauac cgugaccauc	1260

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gacaacacccg	uguauacgcu	gagcaaggug	gaaggcgaac	agcacgugau	caagggcaga	1320
ccugugucca	gcagcuucga	cccuaucaag	uucccugagg	aucaguucca	gguggcccug	1380
gaccaggugu	ucgagaacau	cgagaauucc	caggcucugg	uggaccaguc	caacagaau	1440
cugucuagcg	ccgagaagg	aaacaccggc	uucaucuucg	ugaucuuccu	gaucgccgug	1500
cugggcagcu	ccaugauccu	gguguccauc	uucaucuuu	ucaagaagac	caagaagccc	1560
accggcguc	cuccagaacu	gagcggagug	accaacaau	gcuucaucc	ucacaac	1617

<210> SEQ ID NO 137

<211> LENGTH: 1617

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 137

augagcugga	aggugguc	caucucagc	cugcugauca	caccucagca	cgccugaaa	60
gagagcuacc	uggaagaguc	cugcagcacc	aucacagagg	gcuaccuguc	ugugcugaga	120
accggcuggu	acaccaacgu	guucacacug	gaaguggg	acgucgagaa	ucugacaugc	180
ucugauggcc	cuagccugau	caagaccgag	cuggaucuga	ccaagagcgc	ccugagagaa	240
cucaagaccg	ugucugccga	ucagcuggcc	agagaggaa	agaucgagaa	uccuggcagc	300
ggcagcuuug	ugcugggagc	cauugcucu	ggaguggcug	cugcugcagc	uguuacagca	360
ggcguggcca	ucgcuaagac	caucagacug	gaaagcgaag	ugaccgccau	caacaacgcc	420
cugaagaaga	caaacgaggc	cgucagcaca	cucggcaau	gcuuagagu	gcuggccaca	480
gccgugcgcg	agcugaagga	cuucgugcu	aagaaccuga	cacgggccau	uaacaagaac	540
aagugcgaca	ucgacgaccu	gaagauggcc	guguccuuu	gccaguuc	ccggcgguu	600
cugaacgucg	ugcggcaguu	uagcgacaac	gccggauca	caccagccau	cagccuggac	660
cugaugacag	augcugagcu	ggcuagagcc	gugccuaca	ugccuacau	ugccggccag	720
aucaagcuga	ugcucgagaa	uagagccaug	guccgacgga	aaggcuucgg	cauucugauu	780
ggcguguacg	gcagcagcgu	gaucuaau	gugcagcugc	cuaucucgg	cgugaucgac	840
acaccucgcu	ggauugugaa	ggccgcuccu	agcuguagcg	agaagaagg	caauuacgcc	900
ugccugcuga	gagaggacca	aggcugguau	ugucagaacg	ccggcagcac	cguguacuac	960
ccuaacgaga	aggacugcga	gacaagaggc	gaccacgugu	ucugugauac	cgccgcugga	1020
aucaaugugg	ccgagcagag	caaagagugc	aacaucaaca	ucagcaccac	caacuauccc	1080
ugcaaggugu	ccaccggcag	gcacccuauu	ucuauggugg	cucugucucc	ucugggagcc	1140
cuggugggcu	guuauaagg	cguguccugu	agcaucggca	gcaacagagu	gggcaucauc	1200
aagcagcuga	acaagggcug	cagcuacauc	accaaccagg	acgccgauac	cgugaccauc	1260
gacaacacccg	uguauacgcu	gagcaaggug	gaaggcgaac	agcacgugau	caagggcaga	1320
ccugugucca	gcagcuucga	cccuaucaag	uucccugagg	aucaguucca	gguggcccug	1380
gaccaggugu	ucgagaacau	cgagaauucc	caggcucugg	uggaccaguc	caacagaau	1440
cugucuagcg	ccgagaagg	aaacaccggc	uucaucuucg	ugaucuuccu	gaucgccgug	1500
cugggcagcu	ccaugauccu	gguguccauc	uucaucuuu	ucaagaagac	caagaagccc	1560
accggcguc	cuccagaacu	gagcggagug	accaacaau	gcuucaucc	ucacaac	1617

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<210> SEQ ID NO 138

<211> LENGTH: 1617

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 138

augagcugga agggugucau caucuucagc cugcugauca caccucagca cggccugaaa 60
gagagcuacc uggaagaguc cugcagcacc aucacagagg gcuaccuguc ugugcugaga 120
accggcuggu acaccaacgu guucacacug gaagugggag acgucgagaa ucugacaugc 180
ucugauggcc cuagccugau caagaccgag cuggaucuga ccaagagcgc ccugagagaa 240
cucaagaccg ugucugccga ucagcuggcc agagaggaac agaucgagaa uccuggcagc 300
ggcagcuuug ugcugggagc cauugcucu ggaguggcug cugcugcagc uguuacagca 360
ggcguggcca ucgcuagac caucagacug gaaagcgaag ugaccgccau caacaacgcc 420
cugaagaaga caaacgaggc cgucagcaca cugggcaaug gcguuagagu gcuggccaca 480
gccgugcgcg agcugaagga cuucgugucc aagaaccugu ggcgggccau uaacaagaac 540
aagugcgaca ucgacgaccu gaagauggcc guguccuuua gccaguuaa ccggcgguuu 600
cugaacgucg ugccgcaguu uagcgacaac gccggaauca caccagccau cagccuggac 660
cugaugacag augcugagcu ggcuaagacc gugccuaaca ugccuacauc ugccggccag 720
aucaagcuga ugcucgagaa uagagccaug guccgacgga aaggcuucgg cauucugauu 780
ggcguguaag gcagcagcgu gaucuauaug gugcagcugc cuaucuucgg cgugaucgac 840
acaccucgcu ggauugugaa ggcgcucucu agcuguagcg agaagaaggg caauuacgcc 900
ugccugcuga gagaggacca aggcugguau ugucagaacg ccggcagcac cguguacuac 960
ccuaacgaga aggacugcga gacaagaggc gaccacgugu ucugugauac cggcgucgga 1020
aucaaugugg ccgagcagag caaagaguc aacaucaaca ucagcaccac caacuauccc 1080
ugcaaggugu ccaccggcag gcaccuauu ucuauaggug cucugucucc ucugggagcc 1140
cugguggcuu guuauaaggg cguguccugu agcaucggca gcaacagagu gggcaucauc 1200
aagcagcuga acaaggcgug cagcuacauc accaaccagg acgccgauac cgugaccauc 1260
gacaacaccg uguauacgu gagcaaggug gaaggcgaac agcacgugau caagggcaga 1320
ccugugucca gcagcuucga ccuaucaag uucccugagg aucaguucca gguggcccug 1380
gaccaggugu ucgagaacau cgagaauucc caggcucugg uggaccaguc caacagaau 1440
cugucuagcg ccgagaaggg aaacaccggc uucaucaucg ugaucauccu gaucgccgug 1500
cugggcagcu ccaugauccu gguguccauc uucaucauuu ucaagaagac caagaagccc 1560
accggcguc cuccagaacu gagcggagug accaacaauug gcuucauccc ucacaac 1617

<210> SEQ ID NO 139

<211> LENGTH: 1617

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 139

augagcugga agggugucau caucuucagc cugcugauca caccucagca cggccugaaa 60

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gagagcuacc	uggaagaguc	cugcagcacc	aucacagagg	gcuaccuguc	ugugcugaga	120
accggcuggu	acaccaacgu	guucacacug	gaagugggcg	accucgagaa	ucugacaugc	180
ucugauggcc	cuagccgau	caagaccgag	cuggaucugc	ucaagagcgc	ccugagagaa	240
cucaagaccg	ugucugccga	ucagcuggcc	agagaggaac	agaucgagaa	uccuggcagc	300
ggcagcuuug	ugcugggagc	cauugcucu	ggaguggcug	cugcugcagc	uguuacagca	360
ggcguggcca	ucgcuaagac	caucagacug	gaaagcgaag	ugaccgccau	caacaacgcc	420
cugaagaaga	caaacgaggc	cgucagcaca	cucggcaaug	gcguaagagu	gcuggccaca	480
gccgugcgcg	agcugaagga	cuucgugcu	aagaaccugu	ggcgggccau	uaacaagaac	540
aagugcgaca	ucgacgaccu	gaagauggcc	guguccuuua	gccaguuaa	ccggcgguu	600
cugaacgucg	ugcggcaguu	uagcgacaac	gccggaauca	caccagccau	cagccuggac	660
cugaugacag	augcugagcu	ggcuagagcc	gugccuaaca	ugccuacauc	ugccggccag	720
aucaagcuga	ugcucgagaa	uagagccaug	guccgacgga	aaggcuucgg	cauucugauu	780
ggcguguacg	gcagcagcgu	gaucuauaug	gugcagcugc	cuaucucgg	cgugaucgac	840
acaccucgcu	ggauugugaa	ggccgcuccu	agcuguagcg	agaagaaggg	cauuuacgcc	900
ugccugcuga	gagaggacca	aggcugguau	ugucagaacg	ccggcagcac	cguguacuac	960
ccuaacgaga	aggacugcga	gacaagaggc	gaccacgugu	ucugugauac	cgccgcugga	1020
aucaaugugg	ccgagcagag	caaagagugc	aacaucaaca	ucagcaccac	caacuauccc	1080
ugcaaggugu	ccaccggcag	gcaccuauu	ucuauggugg	cucugucucc	ucugggagcc	1140
cugguggcuu	guuauaaggg	cguguccugu	agcaucggca	gcaacagagu	gggcaucauc	1200
aagcagcuga	acaagggcug	cagcuacauc	accaaccagg	acgccgauac	cgugaccauc	1260
gacaacaccg	uguauacgcu	gagcaaggug	gaaggcgaac	agcacgugau	caagggcaga	1320
ccugugucca	gcagcuucga	cccuaucaag	uucccugagg	aucaguucca	gguggcccug	1380
gaccaggugu	ucgagaacau	cgagaauucc	caggcucugg	uggaccaguc	caacagaau	1440
cugucuagcg	ccgagaaggg	aaacaccggc	uucaucaucg	ugaucuccu	gaucgcccug	1500
cugggcagcu	ccaugauccu	gguguccauc	uucaucauuu	ucaagaagac	caagaagccc	1560
accggcguc	cuccagaacu	gagcggagug	accaacaau	gcuucauccc	ucacaac	1617

<210> SEQ ID NO 140

<211> LENGTH: 1617

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 140

augagcugga	agguggucau	caucuucagc	cugcugauca	caccucagca	cggccugaaa	60
gagagcuacc	uggaagaguc	cugcagcacc	aucacagagg	gcuaccuguc	ugugcugaga	120
accggcuggu	acaccaacgu	guucacacug	ccugugggcg	acgucgagaa	ucugacaugc	180
ucugauggcc	cuagccgau	caagaccgag	cuggaucuga	ccaagagcgc	ccugagagaa	240
cucaagaccg	ugucugccga	ucagcuggcc	agagaggaac	agaucgagaa	uccuggcagc	300
ggcagcuuug	ugcugggagc	cauugcucu	ggaguggcug	cugcugcagc	uguuacagca	360
ggcguggcca	ucgcuaagac	caucagacug	gaaagcgaag	ugaccgccau	caacaacgcc	420

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cugaagaaga caaacgaggg cgucagcaca cucggcaaug gcguuagagu gcuggccaca	480
gccgugcgcg agcugaagga cuucgugucc aagaaccuga cacgggccau uaacaagaac	540
aagugcgaca ucgacgaccu gaagauggcc guguccuuua gccaguuaa cggcgguuu	600
cugaacgucg ugcggcaguu uagcgacaac gccggaauca caccagccau cagccuggac	660
cugaugacag augcugagcu ggcuagagcc gugccuaaca ugccuacauc ugccggccag	720
aucaagcuga ugcucgagaa uagagccaug guccgacgga aaggcuucgg cauucugauu	780
ggcgugugacg gcagcagcgu gaucuauaug gugcagcugc cuaucuucgg cgugaucgac	840
acaccucgcu ggauugugaa ggccgcuccu agcuguagcg agaagaaggg cauuuacgcc	900
ugccugcuga gagaggacca aggcugguau ugucagaacg ccggcagcac cguguacuac	960
ccuaacgaga aggacugcga gacaagaggc gaccacgugu ucugugauac cgccgcugga	1020
aucaaugugg ccgagcagag caaagagugc aacaucaaca ucagcaccac caacuauccc	1080
ugcaaggugu ccaccggcag gcaccuauu ucuauggugg cucugucucc ucugggagcc	1140
cugguggcuu guuauaaggg cguguccugu agcaucggca gcaacagagu gggcaucauc	1200
aagcagcuga acaagggcug cagcuacauc accaaccagg acgccgauac cgugaccauc	1260
gacaacaccg uguauacgcu gagcaaggug gaaggcgaac agcacgugau caagggcaga	1320
ccugugucca gcagcuucga ccuaucaag uucccugagg aucaguucca gguggcccug	1380
gaccaggugu ucgagaacau cgagaauucc caggcucugg uggaccaguc caacagaau	1440
cugucuagcg ccgagaaggg aaacaccggc uucaucaucg ugaucauccu gaucgccgug	1500
cugggcagcu ccaugauccu gguguccauc uucaucauuu ucaagaagac caagaagccc	1560
accggcguc cuccagaacu gagcgagug accaacaauug gcuucauccc ucacaac	1617

<210> SEQ ID NO 141

<211> LENGTH: 1617

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 141

augagcugga aggugguau caucuucagc cugcugauca caccucagca cggccugaaa	60
gagagcuacc uggaagaguc cugcagcacc aucacagagg gcuaaccuguc ugugcugaga	120
accggcuggu acaccaacgu guucacacug gaaguggggcg acgucgagaa ucugacaugc	180
ucugauggcc cuagccugau caagaccgag cuggaucuga ccaagagcgc ccugagagaa	240
cucaagaccg ugucugccga ucagcuggcc agagaggaa agaucgagaa uccuggcagc	300
ggcagcuuug ugcugggagc cauugcucu ggaguggcug cugcugcagc uguuacagca	360
ggcguggcca ucgcuaagac caucagacug gaaagcgaag ugaccgccau caacaacgcc	420
cugaagaaga caaacgaggg cgucagcaca cucggcaaug gcguuagagu gcuggccaca	480
gccgugcgcg agcugaagga cuucgugucc aagaaccuga cacgggccau uaacaagaac	540
aagugcgaca ucccgaccu gaagauggcc guguccuuua gccaguuaa cggcgguuu	600
cugaacgucg ugcggcaguu uagcgacaac gccggaauca caccagccau cagccuggac	660
cugaugacag augcugagcu ggcuagagcc gugccuaaca ugccuacauc ugccggccag	720
aucaagcuga ugcucgagaa uagagccaug guccgacgga aaggcuucgg cauucugauu	780

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ggcguguaacg gcagcagcgu gaucuaauaug gugcagcugc cuaucuuagg cgugaucgac	840
acaccucgcu ggauugugaa ggccgcuccu agcuguagcg agaagaaggg caauuacgcc	900
ugccugcuga gagaggacca aggcugguau ugucagaacg ccggcagcac cguguacuac	960
ccuaacgaga aggacugcga gacaagaggc gaccacgugu ucugugauac cgccgcugga	1020
aucaaugugg ccgagcagag caaagagugc aacaucaaca ucagcaccac caacuaucac	1080
ugcaaggugu ccaccggcag gaccccuauu ucuauggugg cucugucucc ucugggagcc	1140
cugguggcuu guuauaaggg cguguccugu agcaucggca gcaacagagu gggcaucauc	1200
aagcagcuga acaagggcug cagcuacauc accaaccagg acgccgauac cgugaccauc	1260
gacaacaccg uguaucagcu gagcaaggug gaaggcgaac agcacgugau caagggcaga	1320
ccugugucca gcagcuucga ccuaucaag uucccugagg aucaguucca gguggcccug	1380
gaccaggugu ucgagaacau cgagaauucc caggcucugg uggaccaguc caacagauc	1440
cugucuagcg ccgagaaggg aaacaccggc uucaucaucg ugaucauccu gaucgccgug	1500
cugggcagcu ccaugauccu gguguccauc uucaucauaa ucaagaagac caagaagccc	1560
accggcgcuc cuccagaacu gagcggagug accaacaauu gcuucauccc ucacaac	1617

<210> SEQ ID NO 142

<211> LENGTH: 1617

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 142

augagcugga agguggucau caucuuacgc cugcugauca caccucagca cggccugaaa	60
gagagcuacc uggaagaguc cugcagcacc aucacagagg gcuaccuguc ugugcugaga	120
accggcuggu acaccaacgu guucacacug gaagugggcg acgucgagaa ucugacaugc	180
ucugauggcc cuagccugau caagaccgag cuggaucuga ccaagagcgc ccugagagaa	240
cucaagaccg ugucugccga ucagcuggcc agagagggaac agaucgagaa uccuggcagc	300
ggcagcuuug ugucgggagc cauugcucu ggaguggcug cugcugcagc uguuacagca	360
ggcguggcca ucgcuagac caucagacug gaaagcgaag ugaccgccau caacaacgcc	420
cugaagaaga caaacgaggc cgucagcaca cucggcaaug gcguuagagu gcuggccaca	480
gccgugcgcg agcugaagga cuucgugucc aagaaccuga caccggccau uaacaagaac	540
aagugcccua ucgacgaccu gaagauggcc guguccuua gccaguuaa ccggcgguuu	600
cugaacgucg ugccgcaguu uagcgacaac gccggauca caccagccau cagccuggac	660
cugaugacag augcugagcu ggcuaagagg guggcuuaca ugccuacauc ugccggccag	720
aucaagcuga ugucugagaa uagagccaug guccgacgga aaggcuucgg cauucugauu	780
ggcguguaacg gcagcagcgu gaucuaauaug gugcagcugc cuaucuuagg cgugaucgac	840
acaccucgcu ggauugugaa ggccgcuccu agcuguagcg agaagaaggg caauuacgcc	900
ugccugcuga gagaggacca aggcugguau ugucagaacg ccggcagcac cguguacuac	960
ccuaacgaga aggacugcga gacaagaggc gaccacgugu ucugugauac cgccgcugga	1020
aucaaugugg ccgagcagag caaagagugc aacaucaaca ucagcaccac caacuaucac	1080
ugcaaggugu ccaccggcag gaccccuauu ucuauggugg cucugucucc ucugggagcc	1140

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cugguggcuu guuauaaggg cguguccugu agcaucggca gcaacagagu gggcaucauc	1200
aagcagcuga acaagggcug cagcuacauc accaaccagg acgccgauac cgugaccauc	1260
gacaacaccg uguauacgcu gagcaaggug gaaggcgaac agcacgugau caagggcaga	1320
ccugugucca gcagcuucga ccuaucaag uucccugagg aucaguucca gguggcccug	1380
gaccaggugu ucgagaacau cgagaauucc caggcucugg uggaccaguc caacagaau	1440
cugucuagcg ccgagaaggg aaacaccggc uucaucaucg ugaucauccu gaucgccgug	1500
cugggcagcu ccaugauccu gguguccauc uucaucauuu ucaagaagac caagaagccc	1560
accggcguc cuccagaacu gagcggagug accaacaug gcuucaucc ucacaac	1617

<210> SEQ ID NO 143

<211> LENGTH: 1617

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 143

augagcugga agguggucau caucuucagc cugcugauca caccucagca cggccugaaa	60
gagagcuacc uggaagaguc cugcagcacc aucacagagg gcuaccuguc ugugcugaga	120
accggcuggu acaccaacgu guucacacug gaagugggcg acgucgagaa ucugacaugc	180
ucugauggcc cuagccugau caagaccgag cuggaucuga ccaagagcgc ccugagagaa	240
cucaagaccg ugucugccga ucagcuggcc agagaggaa agaucgagaa uccuggcagc	300
ggcagcuuug ugucgggagc cauugcucu ggaguggcug cugcugcagc uguuacagca	360
ggcguggcca ugcuaagac caucagacug ccuagcgaag ugaccgccau caacaacgcc	420
cugaagaaga caaacgaggc cgcagcacaca cucggcaaug gcguuagagu gcuggccaca	480
gccgugcgcg agcugaagga cuucgugucc aagaaccuga caccggccau uaacaagaac	540
aagugcgaca ucgacgaccu gaagauggcc guguccuuu gccaguuaa ccggcgguuu	600
cugaacgucg ugccggcagu uagcgacaac gccggauca caccagccau cagccuggac	660
cugaugacag augcugagcu ggcuaagagg guggcuuaca ugccuacauc ugccggccag	720
aucaagcuga ugcucgagaa uagagccaug guccgacgga aaggcuucgg cauucugauu	780
ggcgugucg gcagcagcgu gaucuauaug gugcagcugc cuaucuucgg cgugaucgac	840
acaccucgcu ggauugugaa ggccgcuccu agcuguagcg agaagaaggg caauuacgcc	900
ugccugcuga gagaggacca aggcugguau ugucagaacg ccggcagcac cguguacuac	960
ccuaacgaga aggacugcga gacaagaggc gaccacgugu ucugugauac cggcgugga	1020
aucaaugugg ccgagcagag caaagagugc aacaaucaac ucagcaccac caacuauccc	1080
ugcaaggugu ccaccggcag gcaccuauu ucuauggugg cucugucucc ucugggagcc	1140
cugguggcuu guuauaaggg cguguccugu agcaucggca gcaacagagu gggcaucauc	1200
aagcagcuga acaagggcug cagcuacauc accaaccagg acgccgauac cgugaccauc	1260
gacaacaccg uguauacgcu gagcaaggug gaaggcgaac agcacgugau caagggcaga	1320
ccugugucca gcagcuucga ccuaucaag uucccugagg aucaguucca gguggcccug	1380
gaccaggugu ucgagaacau cgagaauucc caggcucugg uggaccaguc caacagaau	1440
cugucuagcg ccgagaaggg aaacaccggc uucaucaucg ugaucauccu gaucgccgug	1500

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cugggcagcu ccaugauccu gguguccauc uucaucauuu ucaagaagac caagaagccc 1560

accggcguc cuccagaacu gagcggagug accaacaauug gcuucaucc ucacaac 1617

<210> SEQ ID NO 144

<211> LENGTH: 1617

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 144

augagcugga aggguguc aucauucagc cugcugauca caccucagca cggccugaaa 60

gagagcuacc uggaagaguc cugcagcacc aucacagagg gcuaccuguc ugugcugaga 120

accggcuggu acaccaacgu guucacacug gaagugggag acgucgagaa ucugacaugc 180

ucugauggcc cuagccugau caagaccgag cuggaucuga ccaagagcgc ccugagagaa 240

cucaagaccg ugucugccga ucagcuggcc agagaggaac agaucgagaa uccuggcagc 300

ggcagcuuug ugcugggagc cauugcucu ggaguggcug cugcugcagc uguuacagca 360

ggcugggcca ugcuaagac caucagacug gaaagcgaag ugaccgccau caacaacgcc 420

cugaagaaga caaacgaggc cgucagcaca cucggcaaug gcguuagagu gcuggccaca 480

gccgugcgcg agcugaagga cuucgugucc aagaaccuga caccggccau uaacaagaac 540

aagugcgaca ucgacgaccu gaagauggcc guguccuuua gccaguuaa ccggcgguuu 600

cugaacgucg ugccggcagu uagcgacaac gccggaauca caccagccau cagccuggac 660

cugaugacag augcugagcu ggcuagagcc gggccuaua ugccuauac ugccggccag 720

aucaagcuga ugcucgagaa uagagccaug guccgacgga aaggcuucgg cauucugauu 780

ggcgugucg gcagcagcgu gcucauauug ggcagcugc cuauucucgg cgugaucgac 840

acaccucgcu ggauugugaa ggccgucucc agcuguagcg agaagaaggg caauuacgcc 900

ugccucguga gagaggacca aggcugguau ugucagaacg ccggcagcac cguguacuac 960

ccuaacgaga aggacugcga gacaagaggc gaccacgugu ucugugauac cggcgugga 1020

aucaaugugg ccgagcagag caaagagugc aacaauaaca ucagcaccac caacuauccc 1080

ugcaaggugu ccaccggcag gcaccuauu ucuauggugg cucugucucc ucugggagcc 1140

cugggugcuu guuauaaggg cguguccugu agcaucgga gcaacagagu gggcauauac 1200

aagcagcuga acaaggcgug cagcuauac accaaccagg acgcccgauc cgugaccauc 1260

gacaacaccg uguauacgu gagcaaggug gaagcggaac agcagugau caagggcaga 1320

ccugugucca gcagcuucc accuaucaag uucccugagg aucaguucca gguggcccug 1380

gaccaggugu ucgagaacau cgagaauucc caggcucugg uggaaccagc caacagaauac 1440

cugucuagcg ccgagaaggg aaacaccggc uucaucaucg ugaucuccu gaucgcccug 1500

cugggcagcu ccaugauccu gguguccauc uucaucauuu ucaagaagac caagaagccc 1560

accggcguc cuccagaacu gagcggagug accaacaauug gcuucaucc ucacaac 1617

<210> SEQ ID NO 145

<211> LENGTH: 1617

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 145

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augagcugga agguuggucau caucuucagc cugcugauca caccucagca cggccugaaa    60
gagagcuacc uggaagaguc cugcagcacc aucacagagg gcuaccuguc ugugcugaga    120
accggcuggu acaccaacgu guucacacug gaagugggcg acgucgagaa ucugacaugc    180
ucugauggcc cuagccugau caagaccgag cuggaucuga ccaagagcgc ccugagagaa    240
cucaagaccg ugucugccga ucagcuggcc agagaggaac agaucgagaa uccuggcagc    300
ggcagcuuug ugcugggagc cauugcucu ggaguggcug cugcugcagc uguuacagca    360
ggcguggcca ugcuaagac caucagacug gaaagcgaag ugaccgccau caacaacgcc    420
cugaagaaga caaacgaggc cgucagcaca cucggcaaug gcguuagagu gcuggccaca    480
gccgugcgcg agcugaagga cuucgugucc aagaaccuga caccggccau uaacaagaac    540
aagugcgaca ucgacgaccu gaagauggcc guguccuuu gccaguucua ccggcgguuu    600
cugaacgucg ugcggcaguu uagcgacaac gccggauca caccagccau cagccuggac    660
cugaugacag augcugagcu ggcuagagcc gugccuaaca ugccuacauc ugccggccag    720
aucaagcuga ugcucgagaa uagagccaug guccgacgga aaggcuucgg cauucugauu    780
ggcgugucg gcagcagcgu gaucuauaug gugcagcugc cuaucuucgg cgugaucgac    840
acaccucgcu ggaauuguaa ggccgcuccu agcuguagcg agaagaaggg caauuacgcc    900
ugccugcuga gagaggacca aggcugguau ugucagaacg ccggcagcac cguguacuac    960
ccuaacgaga aggacugcga gacaagaggc gaccacgugu ucugugauac cgccgcugga    1020
aucaaugugg ccgagcagag caaagagugc aacaucaaca ucagcaccac caacuauccc    1080
ugcaaggugu ccaccggcag gcaccuauu ucuauuggug cucugucucc ucugggagcc    1140
cugguggcuu guuauaaggg cguguccugu agcaucggca gcaacagagu gggcaucauc    1200
aagcagcuga acaagggcug cagcuacauc accaaccagg acgccgauac cgugaccauc    1260
gacaacaccg uguauacgcu gagcaaggug gaaggcgaac agcacgugau caagggcaga    1320
ccugugucca gcagcuucga ccuaucaag ucccugaga accaguucca gguggcccug    1380
gaccaggugu ucgagaacau cgagaauucc caggcucugy uggaccaguc caacagaau    1440
cugucuagcg ccgagaaggg aaacaccggc uucaucaucg ugaucauccu gaucgcccug    1500
cugggcagcu ccaugauccu gguguccauc uucaucauuu ucaagaagac caagaagccc    1560
accggcguc cuccagaacu gagcggagug accaacaauy gcuucauccc ucacaac    1617

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<210> SEQ ID NO 146

<211> LENGTH: 1617

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 146

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augagcugga agguuggucau caucuucagc cugcugauca caccucagca cggccugaaa    60
gagagcuacc uggaagaguc cugcagcacc aucacagagg gcuaccuguc ugugcugaga    120
accggcuggu acaccaacgu guucacacug gaagugggcg acgucgagaa ucugacaugc    180
ucugauggcc cuagccugau caagaccgag cuggaucuga ccaagagcgc ccugagagaa    240
cucaagaccg ugucugccga ucagcuggcc agagaggaac agaucgagaa uccuggcagc    300

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ggcagcuuug	ugcugggagc	cauugcucu	ggaguggcug	cugcugcagc	uguuacagca	360
ggcguggcca	ucgcuaagac	caucagacug	gaaagcgaag	ugaccgccau	caacaacgcc	420
cugaagaaga	caaacgaggc	cgucagcaca	cucggcaaug	gcguuagagu	gcuggccaca	480
gccgugcgcg	agcugaagga	cuucgugucc	aagaaccuga	cacgggccau	uaacaagaac	540
aagugcgaca	ucgacgaccu	gaagauggcc	guguccuuua	gccaguucua	ccggcgguuu	600
cugaacgucg	ugcggcaguu	uagcgacaac	gccggaauca	caccagccau	cagccuggac	660
cugaugacag	augcugagcu	ggcuagagcc	gugccuaaca	ugccuacauc	ugccggccag	720
aucaagcuga	ugcucgagaa	uagagccaug	guccgacgga	aaggcuucgg	cauucugauu	780
ggcguguaag	gcagcagcgu	gaucuauaug	gugcagcugc	cuauucucgg	cgugaucgac	840
acaccucgcu	ggauugugaa	ggccgcuccu	agcuguagcg	agaagaaggg	caauuacgcc	900
ugccugcuga	gagaggacca	aggcugguau	ugucagaacg	ccggcagcac	cguguacuac	960
ccuaacgaga	aggacugcga	gacaagaggc	gaccacgugu	ucugugauac	cgccgcugga	1020
aucaaugugg	ccgagcagag	caaagagugc	aacaucuaaca	ucagcaccac	caacuauccc	1080
ugcaaggugu	ccaccggcag	gcaccuauu	ucuauuggug	cucugucucc	ucugggagcc	1140
cuggguggcu	guuauaagg	cguguccugu	agcaucggca	gcaacagagu	gggcaucauc	1200
aagcagcuga	acaaggcgug	cagcuacauc	accaaccagg	acgccgauac	cgugaccauc	1260
gacaacaccg	uguauacgcu	gagcaaggug	gaaggcgaac	agcagugau	caagggcaga	1320
ccugugucca	gcagcuucga	cccuaucaag	uucccucagg	aucaguucca	gguggcccug	1380
gaccaggugu	ucgagaacau	cgagaauucc	caggcucugg	uggaccaguc	caacagaau	1440
cugucuagcg	ccgagaagg	aaacaccggc	uucaucaucg	ugaucuccu	gaucgcccug	1500
cugggcagcu	ccaugauccu	gguguccauc	uucaucuuu	ucaagaagac	caagaagccc	1560
accggcguc	cuccagaacu	gagcggagug	accaacaau	gcuucaucc	ucacaac	1617

<210> SEQ ID NO 147

<211> LENGTH: 1617

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 147

augagcugga	agguggucau	caucuucagc	cugcugauca	caccucagca	cgccugaaa	60
gagagcuacc	uggaagaguc	cugcagcacc	aucacagagg	gcuaccuguc	ugugcugaga	120
accggcuggu	acaccaacgu	guucacacug	gaaguggcg	acgucgagaa	ucugacaugc	180
ucugauggcc	cuagccugau	caagaccgag	cuggaucuga	ccaagagcgc	ccugagagaa	240
cucaagaccg	ugucugccga	ucagcuggcc	agagaggaac	agaucgagaa	uccuggcagc	300
ggcagcuuug	ugcugggagc	cauugcucu	ggaguggcug	cugcugcagc	uguuacagca	360
ggcguggcca	ucgcuaagac	caucagacug	gaaagcgaag	ugaccgccau	caacaacgcc	420
cugaagaaga	caaacgaggc	cgucagcaca	cucggcaaug	gcguuagagu	gcuggccaca	480
gccgugcgcg	agcugaagga	cuucgugucc	aagaaccuga	cacgggccau	uaacaagaac	540
aagugcgaca	ucgacgaccu	gaagauggcc	guguccuuua	gccaguggaa	ccggcgguuu	600
cugaacgucg	ugcggcaguu	uagcgacaac	gccggaauca	caccagccau	cagccuggac	660

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cugaugacag augcugagcu ggcuagagcc gugccuaaca ugccuacauc ugccggccag	720
aucaagcuga ugcucgagaa uagagccaug guccgacgga aaggcuucgg cauucugauu	780
ggcguguacg gcagcagcgu gaucuaauaug gugcagcugc cuaucuucgg cgugaucgac	840
acaccucgcu ggauugugaa ggccgcuccu agcuguagcg agaagaaggg caauuacgcc	900
ugccugcuga gagaggacca aggcugguau ugucagaacg ccggcagcac cguguacuac	960
ccuaacgaga aggacugcga gacaagaggc gaccacgugu ucugugauac cgccgcugga	1020
aucaaugugg ccgagcagag caaagagugc aacaucaaca ucagcaccac caacuauccc	1080
ugcaaggugu ccaccggcag gcaccuauu ucuauaggugg cucugucucc ucugggagcc	1140
cugguggcuu guuauaaggg cguguccugu agcaucggca gcaacagagu gggcaucauc	1200
aagcagcuga acaagggcug cagcuacauc accaaccagg acgccgauac cgugaccauc	1260
gacaacaccg uguaucagcu gagcaaggug gaaggcgaac agcacgugau caagggcaga	1320
ccugugucca gcagcuucga ccuaucaag ucccugagg aucaguucca gguggcccug	1380
gaccaggugu ucgagaacau cgagaauucc caggcucugg uggaccaguc caacagaau	1440
cugucuagcg ccgagaaggg aaacaccggc uucaucaucg ugaucauccu gaucgcccug	1500
cugggcagcu ccaugauccu gguguccauc uucaucauuu ucaagaagac caagaagccc	1560
accgggcguc cuccagaacu gagcggagug accaacaauug gcuucauccc ucacaac	1617

1.-12. (canceled)

33. A human parainfluenza virus type 3 (hPIV3) vaccine, comprising:

an isolated ribonucleic acid (RNA) polynucleotide comprising an open reading frame encoding an antigenic hPIV3 Fusion (F) protein formulated in a lipid nanoparticle that comprises a molar ratio of 20-60% ionizable cationic lipid, 5-25% non-cationic lipid, 25-55% sterol, and 0.5-15% PEG-modified lipid, wherein the isolated mRNA polynucleotide is not self-replicating RNA.

34.-95. (canceled)

96. A method of inducing an antigen-specific immune response in a subject, the method comprising administering to the subject the vaccine of claim 33 in an amount effective to produce an antigen-specific immune response in the subject.

97.-135. (canceled)

136. The hPIV3 vaccine of claim 33, wherein the isolated mRNA polynucleotide further encodes a 5' terminal cap, 7mG(5')ppp(5')NlmpNp.

137. The hPIV3 vaccine of claim 33, wherein at least 80% of the uracil in the open reading frame comprises a chemical modification selected from N1-methyl-pseudouridine and N1-ethyl-pseudouridine.

138. The hPIV3 vaccine of claim 33, wherein the chemical modification is in the 5-position of the uracil.

139. The hPIV3 vaccine of claim 33, wherein the open reading frame encoding an antigenic hPIV3 F protein comprises a RNA sequence that has at least 90% identity to the RNA sequence set forth in SEQ ID NO: 64.

140. The hPIV3 vaccine of claim 139, wherein the open reading frame encoding an antigenic hPIV3 F protein comprises a RNA sequence set forth as SEQ ID NO: 64.

141. The hPIV3 vaccine of claim 33, wherein the antigenic hPIV3 F protein comprises an amino acid sequence that has at least 90% identity to the amino acid sequence set forth as SEQ ID NO: 13.

142. The hPIV3 vaccine of claim 141, wherein the antigenic hPIV3 F protein comprises an amino acid sequence set forth as SEQ ID NO: 13.

143. The hPIV3 vaccine of claim 33, formulated in an effective amount, wherein the effective amount is a total dose of 25 µg-200 µg.

144. The hPIV3 vaccine of claim 33, wherein the isolated RNA polynucleotide further comprises 5' terminal cap, a 5' UTR, a 3' UTR, and a polyA tail.

145. The hPIV3 vaccine of claim 144, wherein the open reading frame encoding an antigenic hPIV3 F protein comprises a RNA sequence that has at least 90% identity to the RNA sequence set forth in SEQ ID NO: 64.

146. The hPIV3 vaccine of claim 145, wherein the open reading frame encoding an antigenic hPIV3 F protein comprises a RNA sequence set forth as SEQ ID NO: 64.

147. The hPIV3 vaccine of claim 33, wherein the efficacy of the vaccine in vaccinated subjects is at least 60%, relative to unvaccinated subjects, following a single dose of the vaccine.

148. The hPIV3 vaccine of claim 33, wherein a single dose of the vaccine administered to a subject is sufficient to produce detectable levels of hPIV3 F protein as measured in serum of a subject vaccinated with at least one dose of the vaccine at 1-72 hours post administration.

149. The hPIV3 vaccine of claim **33**, wherein a single dose of the vaccine administered to a subject is sufficient to produce a 1,000-10,000 neutralization titer produced by neutralizing antibody against the antigenic hPIV3 F protein as measured in serum of a subject vaccinated with at least one dose of the vaccine at 1-72 hours post administration.

150. The hPIV3 vaccine of claim **149**, wherein the 1,000-10,000 neutralization titer is produced in the absence of antibody-dependent enhancement (ADE) of a hPIV3-associated disease.

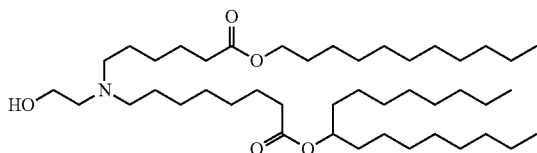
151. The hPIV3 vaccine of claim **150**, wherein the hPIV3-associated disease is alevolitis interstitial pneumonia.

152. The hPIV3 vaccine of claim **33**, wherein an anti-hPIV3 F protein antibody titer produced in a subject vaccinated with at least one dose of the vaccine is increased by at least 1 log relative to a control, wherein the control is an anti-hPIV3 F protein antibody titer produced in a subject who has not been administered a vaccine against hPIV3.

153. The hPIV3 vaccine of claim **33**, wherein an anti-hPIV3 F protein antibody titer produced in a subject vaccinated with at least one dose of the vaccine is increased at least 2 times relative to a control, wherein the control is an anti-hPIV3 F protein antibody titer produced in a subject who has not been administered a vaccine against hPIV3.

154. The hPIV3 vaccine of claim **33**, wherein the ionizable cationic lipid comprises the following compound:

(Compound 25)



155. The hPIV3 vaccine of claim **33**, wherein the noncationic lipid is DSPC (1,2-Distearoyl-sn-glycero-3 -phosphocholine).

156. The hPIV3 vaccine of claim **33**, wherein the PEG-modified lipid is DMG-PEG (1,2-dimyristoyl-racglycero-3-methoxypolyethylene glycol-2000).

157. The method of claim **33**, wherein the lipid nanoparticle comprises 40-50% ionizable cationic lipid, 5-15% DSPC, 25-40% cholesterol, and 1-3.5% DMG-PEG.

158. The method of claim **157**, wherein the lipid nanoparticle comprises 50% ionizable cationic lipid, 10% DSPC, 38.5% cholesterol, and 1.5% DMG-PEG.

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